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(54) Title: UNDECAPRENYL PYROPHOSPHATE SYNTHASE (UPPS) ENZYME AND METHODS OF USE

(57) Abstract: A novel *Streptococcus pneumoniae* UPPS native crystalline structure and a novel *Streptococcus pneumoniae* UPPS complex with the substrates FPP and IPP are identified.

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## UNDECAPRENYL PYROPHOSPHATE SYNTHASE (UPPS) ENZYME AND METHODS OF USE

### Technical Field of the Invention

5           The present invention relates generally to the identification of a novel undecaprenyl pyrophosphate synthase (herein "UPPS") crystalline structure. In addition, it provides a novel undecaprenyl pyrophosphate synthase active site of a crystalline structure in complex with Isopentenyl pyrophosphate and in complex with farnesyl pyrophosphate and methods to use these crystalline forms and their active sites to identify and improve undecaprenyl  
10       pyrophosphate synthase inhibitor compounds, among other uses. These compounds are characterized by the ability to competitively inhibit binding of substrates or other like-molecules to the active site of UPPS.

### Background of the Invention

15           Polyisoprenoid molecules constitute a diverse and essential group of cellular polymers that function as sugar transporters, pigments, vitamins, hormones, *etc.* These molecules are products of a condensation of isopentenyl units that are produced by either of two pathways, a mevalonate-dependent or a mevalonate-independent pathway. IPP is a building block in the synthesis of squalene from which steroids are produced, and it is also  
20       precursor of geranyl pyrophosphate from which polyisoprenols are synthesized (C. K. Mathews, and K. E. van Holde, 1996, *Biochemistry*). The successive condensation reactions to produce polyisoprenols from IPP are catalyzed by prenyltransferases of which there are at least 16 different enzyme forms in four distinct classes. These classes differ in the stereochemistry of the reaction they catalyze, the chain length of the substrates they use, and  
25       the chain length of their products. In the proposed two-step general mechanism of prenyltransferases, the first step is the elimination of the diphosphate from the allylic substrate, followed by the attack of the incoming IPP substrate to form a new carbon-carbon bond, followed by a stereospecific removal of a proton and formation of a new double bond (K. Ogura, and T. Koyama (1998) *Chemical Reviews* 98, 1263-1276; S. Ohnuma, T.  
30       Koyama, and K. Ogura (1989) *FEBS Letters* 257, 71-74).

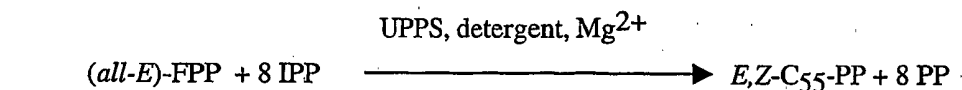
          In one of their many functions throughout the cell, polyisoprenol molecules are used as essential sugar carriers in the biosynthesis of glycoproteins in mammalian cells, and as essential sugar carriers in the biosynthesis of the bacterial cell wall. The peptidoglycan of the bacterial cell wall of Gram positive bacteria is formed by alternating units of N-  
35       acetylglucosamine, NAcGlc and N-acetylmuramic acid, NacMur. A pentapeptide chain with

sequence: (L-Ala)-(D-Glu)-(L-Lys)-(D-Ala)-(D-Ala) is linked through the N-terminal amino group of the peptide with the carboxyl group of the lactate moiety of NAcMur. These peptidoglycan chains are further cross-linked by connecting pentaglycine units. The NAcMur-pentapeptide is synthesized from UDP-NAcMur by successive additions of the corresponding amino acids catalyzed by various ligases, after which the NAcMur-pentapeptide is transferred to undecaprenolphosphate with the release of UMP. While linked to the undecaprenol carrier, NAcGlc and five glycine residues are added from Gly-tRNA. Subsequently, the NAcGlc-NAcMur-pentapeptide-pentaglycine intermediate is transferred to a peptidoglycan acceptor with the release of undecaprenyl pyrophosphate. In the next step, the terminal D-Ala is cleaved and released as adjacent peptidoglycan chains are cross-linked between the penultimate D-Ala of the first chain and the  $\epsilon$ -NH group of the lysine in the second chain. It is noteworthy that several molecules with antibacterial activity block various steps along this pathway. For example, bacitracin blocks the hydrolysis of the phosphodiester bond of undecaprenyl pyrophosphate to produce undecaprenylphosphate; vancomycin blocks the transfer of NAcGlc-NAcMur-pentapeptide-pentaglycine to the acceptor; and penicillin and cephalosporins block the transpeptidation, or cross-linking, between adjacent peptidoglycan chains.

The sugar-carrier function of undecaprenolphosphate in bacteria is performed in mammalian cells by dolicholphosphate during N-linked glycosylation of peptides in the ER. The human and bacterial homologous enzymes share about 34% amino acid sequence identity. Unlike undecaprenol, formed by 11 isopentenyl units, the dolichol molecule is nearly twice as large with 19-21 units. The amino acid sequence alignment of related UPPSs shows that contrary to other prenyl transferases, UPPS does not have the DDXXD sequence motif (A. Chen, P. A. Kroon, and C. D. Poulter (1994) *Protein Science* 3, 600-607). Instead, several stretches of highly conserved residues are localized around a shallow cleft on the surface of the protein around the active site. This observation is consistent with the topology observed in the crystal structure of UPPS from *Micrococcus luteus* B-P 26, (M. Fujihashi, N. Shimizu, Y-W. Zhang, T. Koyama, and K. Miki (1999) *Acta Crystallographica* D55, 1606-1607; M. Fujihashi, Y-W. Zhang, Y. Higuchi, X-Y. Li, T. Koyama, and K. Miki (2001) *Proceedings of the National Academy of Sciences*, U.S.A. 98, 4337-4342).

UPP is synthesized by the consecutive action of two enzymes: FPPS and UPPS. The crystal structure of FPPS in complex with FPP shows the FPP molecule bound in a deep pocket at a domain interface with a magnesium ion coordinated between the pyrophosphate and two aspartate residues in the DDXXD motif characteristic of these class of farnesyltransferases (L. C. Tarshis, M. Ynag, C. D. Poulter, and J. C. Sachettini (1994)

*Biochemistry* 33, 10871-10877). The FPPS product is an (*all-E*)-farnesyl diphosphate, one of the substrates for UPPS. UPPS is a (*Z*)-polyprenyldiphosphate synthase (prenyltransferase type IV) that catalyzes the sequential *Z*-addition of eight IPP molecules to an *all-E*-FPP to produce a *E,Z*-mixed-C<sub>55</sub>-isoprenyldiphosphate product, undecaprenyl pyrophosphate (M. Ito, M. Kobayashi, T. Koyama, and K. Ogura (1987) *Biochemistry* 26, 4745-4750):



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The *S. pneumoniae* UPPS has a <sup>FPP</sup> $K_m$  of 0.5 $\mu$ M and a <sup>IPP</sup> $K_m$  of 3.6 $\mu$ M with a pH optimum of 7.5 - 8.0. The monomer has a pI of 5.1, a Mr • 29,000Da and is physiologically and catalytically active as a dimer. UPPS is an essential enzyme present in both Gram-positive and Gram-negative pathogens, except in *Mycoplasma* (J. D. Mutle, and C. M. Allen (1989) *Archives in Biochemistry and Biophysics* 230, 49-60; I. Takahashi, and K. Ogura (1982) *Journal of Biochemistry* 92, 1527-1537; N. Shimizu, T. Kagawa, and K. Ogura (1998) *Journal of Biological Chemistry* 273, 19476-19481; C. M. Apfel, B. Takaca, M. Fountoulakis, M. Stieger, and W. Keck (1999) *Journal of Bacteriology* 181, 483-492).

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The present invention provides a crystal structure of UPPS from *Streptococcus pneumoniae* in its native state, and in complex with the substrates FPP and IPP. The structures show that UPPS is a dimer with an extensive contact area along a dimer interface. A shallow cleft harbors numerous conserved residues and delimits an active site. Several of these residues are disordered in a native enzyme but become well ordered in substrate-bound complexes. The crystal structures of the complexes with each of two substrates, FPP and IPP, provide a detailed description of these substrates' mode of binding, a structure of the Michaelis complex, certain critical residues involved in binding of substrates. The bound substrates and the residues that appear responsible for catalysis indicate a reaction mechanism, and map the available binding pockets used by inhibitors.

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### 30 Summary of the Invention

In one aspect, the invention provides a composition comprising a UPPS in crystalline form.

In another aspect, the present invention relates to a UPPS protein that is derived from *Streptococcus pneumoniae* comprising the amino acid sequence shown in SEQ ID No. 1 having coordinates of any or all of Tables I-III, said protein in an essentially pure native

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form, or a homolog thereof. In a preferred embodiment, the invention provides a UPPS composition wherein said UPPS is a dimer.

In another aspect, the present invention provides a crystalline form of *Streptococcus pneumoniae* UPPS as derived from models of UPPS comprising coordinates of any or all of  
5 Tables I-III.

In yet another aspect, the invention provides a UPPS protein in crystalline form having coordinates of Table IA, and interatomic distances and angles of active site residues listed in Table IIA and/or Table IIIA, respectively, in an essentially pure native form or a  
10 homolog thereof.

In yet another aspect, the invention provides a prenyltransferase of a *Streptococcus pneumoniae* UPPS in its native crystalline form. A preferred embodiment of the invention provides a prenyltransferase wherein said prenyltransferase has an active site formed by the amino acids Arg247, Gly250, Arg206, Arg200, Ser208, Tyr217, Asp28, Tyr70, Ile26, Phe72, Asn76, Met27, Ala71, particularly as ligands to IPP.  
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In yet another aspect, the invention provides a prenyltransferase wherein said prenyltransferase has an active site formed by the amino acids Asp28-Arg32, Arg79, Met27, His45, Gly48, Met49, Leu52, Ala71, Tyr70, Leu90, Pro91, Phe94, Phe149, particularly as  
20 ligands to FPP.

In another aspect, the invention provides a composition comprising a  
20 prenyltransferase in complex with FPP as characterized by the coordinates selected from the group consisting of the coordinates of Tables IB, and interatomic distances and angles of active site residues listed in IIB and/or IIIB.

In yet another aspect, the invention provides a composition comprising a  
25 prenyltransferase in complex with IPP as characterized by the coordinates selected from the group consisting of the coordinates of Tables IC, and interatomic distances and angles of active site residues listed in IIC and/or IIIC.

In another aspect, the invention provides a heavy atom derivative of a *Streptococcus pneumoniae* UPPS crystal wherein the prenyltransferase comprises a protein having the coordinates represented in any of Figures 2, 3, 4 and/or 5, and listed in Tables IA-IC, IIA-  
30 IIC, and/or IIIA-IIIC.

In another aspect, the invention provides a characterized by an  $\alpha+\beta$  fold with three layers,  $\alpha\beta\alpha$ , wherein the  $\beta$ -strands form a six-strand parallel  $\beta$ -sheet and three  $\alpha$ -helices pack against one face of the sheet and three to four  $\alpha$ -helices located on the opposite face.

In yet another aspect, the invention provides a composition comprising a  
35 *Streptococcus pneumoniae* UPPS in orthorhombic crystalline form having a space group of

P2<sub>1</sub>2<sub>1</sub>2<sub>1</sub> wherein the lattice constants are a = 59.6Å, b = 118.0Å, c = 178.2Å and containing two 60 kDa dimers in an asymmetric unit.

In another aspect, the invention provides a composition comprising a *Streptococcus pneumoniae* UPPS in orthorhombic crystalline form having a space group of I2<sub>1</sub>2<sub>1</sub>2<sub>1</sub>.

5 In yet another aspect, the invention provides a composition comprising a co-crystal of *Streptococcus pneumoniae* UPPS in complex with IPP in orthorhombic crystalline form having a space group selected from the group consisting of P2<sub>1</sub>2<sub>1</sub>2<sub>1</sub> and I2<sub>1</sub>2<sub>1</sub>2<sub>1</sub>.

In yet another aspect, the invention provides a composition comprising a co-crystal of *Streptococcus pneumoniae* UPPS in complex with a substrate FPP in monoclinic  
10 crystalline form having a space group of P2<sub>1</sub> and the crystalline form has lattice constants of a = 58.1 Å, b = 44.6 Å, c = 115.5Å, β = 98.7°.

In another aspect, the invention provides a process for determining a crystal structure form using structural coordinates of a *Streptococcus pneumoniae* UPPS crystal or portions thereof, to determine a crystal form of a mutant, homologue, or co-complex of said  
15 active site by molecular replacement.

In yet another aspect, the invention provides a process of identifying an inhibitor compound capable of binding to and inhibiting an enzymatic activity of a *Streptococcus pneumoniae* UPPS said process comprising: introducing into a suitable computer program information defining an active site conformation of a UPPS molecule comprising a  
20 conformation defined by coordinates listed in Table IA, IIA, and/or IIIA wherein said program displays the three-dimensional structure thereof; creating a three dimensional structure of a test compound in said computer program; displaying and superimposing a model of said test compound on a model of said active site; incorporating said test compound in a biological prenyltransferase activity assay for a prenyltransferase  
25 characterized by said active site; and determining whether said test compound inhibits enzymatic activity in said assay.

In another aspect, the invention provides a process designing drugs useful for inhibiting UPPS activity using certain or all of the atomic coordinates of a *Streptococcus pneumoniae* UPPS crystal to computationally evaluate a chemical entity for associating with  
30 an active site of a UPPS enzyme.

In yet another aspect, the invention provides a method of modifying a test UPPS polypeptide comprising: providing a test UPPS polypeptide sequence having a characteristic that is targeted for modification; aligning the test UPPS polypeptide sequence with at least one reference UPPS polypeptide sequence for which an X-ray structure or other structure is  
35 available, wherein the at least one reference UPPS polypeptide sequence has a characteristic

that is desired for the test UPPS polypeptide; building a three-dimensional model for the test UPPS polypeptide using the three-dimensional coordinates of the X-ray structure(s) or other structure(s) of the at least one reference UPPS polypeptide and its sequence alignment with the test UPPS polypeptide sequence; examining the three-dimensional model of the test

5 UPPS polypeptide for a difference in an amino acid residue as compared to the at least one reference polypeptide, wherein the residues are associated with the desired characteristic; and mutating an amino acid residue in the test UPPS polypeptide sequence located at a difference identified to a residue associated with the desired characteristic, whereby the test UPPS polypeptide is modified.

10 In another aspect, the invention provides a process of identifying an inhibitor compound capable of inhibiting an enzymatic activity of a *Streptococcus pneumoniae* UPPS, said process comprising: carrying out an *in vitro* assay by introducing said compound in a biological prenyltransferase activity assay containing a prenyltransferase of the invention; and determining whether said test compound inhibits an enzymatic activity of the

15 prenyltransferase in said assay.

In yet another aspect, the invention provides a product of the process of identifying an inhibitor compound capable of inhibiting an enzymatic activity of a *Streptococcus pneumoniae* UPPS which is a peptide, peptidomimetic, or synthetic molecule and is useful for inhibiting the metallo-beta lactamase, preferably in the treatment of bacterial infections

20 in a mammal.

In another aspect, the invention provides a product of the process of identifying an inhibitor compound capable of inhibiting an enzymatic activity of a *Streptococcus pneumoniae* UPPS wherein said product is a competitive or non-competitive inhibitor of the *Streptococcus pneumoniae* prenyltransferase.

25 In another aspect, the invention provides a process of designing drugs useful for inhibiting *Streptococcus pneumoniae* UPPS comprising using atomic coordinates of a *Streptococcus pneumoniae* UPPS crystal or atomic coordinates of a *Streptococcus pneumoniae* UPPS in complex with FPP or IPP to computationally evaluate a chemical entity for associating with an active site of a *Streptococcus pneumoniae* UPPS.

30 In another aspect, the invention provides a process of designing drugs useful for inhibiting *Streptococcus pneumoniae* UPPS comprising the step of using structure coordinates of *Streptococcus pneumoniae* UPPS to identify an intermediate in a chemical reaction between said prenyltransferase and a compound that is a substrate or inhibitor of said prenyltransferase. In another aspect, the invention provides a process of designing

35 drugs useful for inhibiting *Streptococcus pneumoniae* UPPS wherein structure coordinates

comprise the coordinates corresponding to any of the structures shown in Figures 2, 3, 4 and/or 5 and/or listed in Tables IA-IC, IIA-IIC, and/or IIIA-IIIC.

5 In one aspect, the present invention relates to an UPPS that is derived from *Streptococcus pneumoniae* and comprising a protein having the amino acid sequence shown in SEQ ID No. 1, and coordinates of Table I, and interatomic distances and angles of active site residues listed in Table II and/or III, in an essentially pure native form or a homolog thereof.

10 In another aspect, the present invention provides a novel crystalline form of a UPPS enzyme active site in complex with IPP, having the coordinates of Table I, and interatomic distances and angles of active site residues listed in Table II, and/or III.

In yet another aspect, the present invention provides a novel crystalline form of the UPPS enzyme active site in complex with the substrate farnesyl pyrophosphate, identified herein FPP, having the coordinates of Table I, and interatomic distances and angles of active site residues listed in Table II, and/or III.

15 In yet another aspect, the invention provides a model of specific roles of residues in the active site responsible for the binding of substrates, substrate analogs, and inhibitors.

In yet another aspect, the invention provides a structural basis for the role of active site amino acid residues and metals bound in an active site in a catalytic activity of these enzymes. This aspect of the invention provides a method for identifying inhibitors of a UPPS, which methods comprise the steps of: providing coordinates of a UPP structure of the invention to a computerized modeling system; identifying compounds that bind to an active site; and screening the compounds identified for undecaprenyl pyrophosphate synthase inhibitory bio-activity.

20 Another aspect of this invention includes machine-readable media encoded with data representing coordinates of a three-dimensional structure of a UPPS crystal structure alone or in complex with IPP and/or FPP.

Other aspects and advantages of the present invention are described further in the following detailed description of the preferred embodiments thereof.

30 Description of the Figures:

Figure 1A provides a representation of the chemical structure of FPP, and the numbering scheme used.

Figure 1B provides a representation of the chemical structure of IPP, and the numbering scheme used.

Figure 2A provides a representation of the secondary structure elements of native UPPS, from *Streptococcus pneumoniae*.

Figure 2B provides a representation of the topology of UPPS. Triangles denote  $\beta$ -strands and circles denote  $\alpha$ -helices.

5        Figure 3A provides a schematic drawing of a UPPS enzyme from *Streptococcus pneumoniae* in complex with IPP bound in the active site.

Figure 3B provides a schematic drawing of a UPPS enzyme from *Streptococcus pneumoniae* in complex with FPP bound in the active site.

10        Figure 4A provides a schematic drawing of FPP bound in an active site of UPPS from *S. pneumoniae*. Shown and labeled in this view are the hydrophobic side chains of residues lining an FPP binding pocket, the interactions of the phosphate groups bound at the N-terminus of  $\alpha 1$ , a tightly bound water molecule, and the role of conserved arginine residues that are important for FPP binding.

15        Figure 4B provide a schematic drawing of FPP bound in the active site of UPPS from *S. pneumoniae*. In this view are shown, along the axis of the extended FPP molecule, the relative orientation of the important residues for catalysis, and those side chains important for substrate binding.

20        Figure 5 provides a schematic drawing of the interactions between the active site residues of a UPPS from *Streptococcus pneumoniae* and the substrate IPP. Important for the substrate binding are arginine side chains from the C-terminus of the other molecule in a dimer. Also shown is a pyrophosphate molecule that occupies the same position as the pyrophosphate moiety of FPP.

#### Detailed Description of the Invention

25        The present invention provides a *Streptococcus pneumoniae* UPPS crystalline structure of a native enzyme. In addition, it provides an undecaprenyl pyrophosphate synthase active site of the crystalline structure of the UPPS, in complex with IPP and in complex with FPP and methods to use these crystalline forms and their active sites to identify and improve UPPS inhibitor compounds (peptide, peptidomimetic or synthetic  
30        compositions). These compounds are characterized by an ability to competitively inhibit binding of substrates or other like-molecules to the active site of undecaprenyl pyrophosphate synthases.

A UPPS from *Streptococcus pneumoniae* crystalline three-dimensional structure and its complex with IPP and FPP

5 The crystal structures of aUPPS from *Streptococcus pneumoniae* in its native form, in complex with the substrate IPP (Figure 1B), and a substrate, FPP (Figure 1A) have been determined and refined to 2.3Å, 2.8Å and 3.3Å resolution, respectively.

Native UPPS from *Streptococcus pneumoniae* crystalline structure was determined. This crystal structure consists of two homodimers in the asymmetric unit, molecules A and B form one active dimer, and molecules C and D form the second dimer. A preferred model  
10 includes residues 17-72 and 77-248 in molecule A; residues 17-72 and 79-246 in molecule B; residues 17-73 and 77-248 in molecule C; residues 18-73 and 78-246 in molecule D; and a total of 410 water molecules (Figure 2A). Each polypeptide chain has an  $\alpha + \beta$  fold characterized by three layers:  $\alpha \cdot \cdot \cdot$ . Four  $\alpha$ -helices packed against one face of the central  $\beta$ -sheet, formed by six parallel  $\beta$ -strands with ordering 342156. Another three  $\alpha$ -helices  
15 located at the other side of the sheet form most of the dimer interface (Figure 2B). The central sheet is not continuous from one molecule to the other in the dimer, rather, the  $\beta$ -sheets from each monomer form an angle of approximately 90°. In the dimer, the N- and the C-terminus of molecule B are located near a shallow groove formed in molecule A, the  
20 proposed location of the active site suggesting that the termini on one molecule contribute to the binding of substrates in the other molecule. This may explain the need for the enzyme to be a dimer if catalysis is to occur, and the extensive 1,650 Å<sup>2</sup> of buried surface area at the dimer interface involving  $\alpha 5$ ,  $\alpha 6$ , and  $\alpha 7$ . The dimer interface include interactions between three pairs of charged side chains: Arg170NH2:Asp214OD2 (3.1Å), Arg226NE:Glu239OE2  
25 (2.8Å), and Glu239OE2:Arg226NE (2.6Å). Also across the interface interact Tyr237OH and Asn229ND2 (3.1Å).

There are three buried charged residues: Glu152, Arg200, His22. E152 is at the N-terminus of  $\alpha 5$  and contacts Wat146 (2.9Å), Tyr147OH (2.6Å), Gln214OE1 (3.2Å), Phe184N (2.8Å), and Gln214OE1 (3.1Å). Arg200 is located at the C-terminus of  $\beta 5$   
30 contacting with Ser218 OG (2.7Å), Arg216O (2.9Å), Asp46OD2 (3.1Å), and Wat410 (2.8Å). His22 is makes H-bonds with Leu192O (2.6Å) and Thr68OG1 (2.9Å).

There are five relatively small, and empty internal cavities. One cavity is next to Arg200, a residue presumably located in the active site. This cavity is bound by atoms in residues Ile198, Ile199, Arg200, Leu20, Leu22, Tyr221 and Phe222. Two more cavities are  
35 located on either side of  $\alpha$ -helix  $\alpha 3$ , one is lined by Leu90, Pro91, Phe94, Tyr95, Val99,

Ile109, Ala125, Leu126, Ala129, and Phe143. The cavity on the other side of  $\alpha 3$  is lined by His45, Phe86, Met49, Leu90, Leu52, Asn30, Ala71, Met27, and Trp227. The presence of these two cavities suggests that the helix may be displaced upon substrate binding and for product release or membrane association. Another cavity is located C-terminal to  $\alpha 6$  and a portion of  $\beta 3$  (His187, Phe184, Glu110, Ile112, Asn142, Met111) along the groove on the side of  $\alpha 5$ . This groove probably accommodates the product. N-terminal to  $\beta 5$  is the last cavity (Asp191, Leu192, Arg193, Asp194, Pro195, Asp196) that may allow the  $\alpha 6$ - $\beta 5$  connection slide sideways or back and forth when the product is being processed during catalysis. No solvent molecules have been found occupying these cavities.

In all four molecules in the asymmetric unit, residues 74-76 are disordered in a *S. pneumoniae* native UPPS structure, and residues in the immediate vicinity have higher B-factors than the average of the structure suggesting that these residues are highly mobile in the absence of ligands or substrates, and that they may be part of the active site. In addition, based on the alignment of UPPS amino acid sequences, the most conserved residues are located in the short  $\alpha$ -helix  $\alpha 1$  (residues 28-32) and  $\alpha 2$ - $\beta 3$  (residues 73-83), and in the  $\beta 5$ - $\alpha 7$  (residues 200-214) loops suggesting that the active site is located at the top of the sheet in a shallow groove, next to the disordered region. As discussed below, the crystal structures of the UPPS complexes with the substrates FPP and IPP confirm the location of the active site, the critical role played by the conserved residues for substrate binding and their role in catalysis, and show that the disordered residues become ordered upon substrate binding.

The undecaprenyl pyrophosphate synthases from *S. pneumoniae* and *M. luteus* share a 37% amino acid sequence identity and the polypeptide have the same fold. Superposition of the C $\alpha$  atoms of the *M. luteus* and *S. pneumoniae* native UPPS crystal structures results in an overall root mean square, rms, deviation of 0.6Å.

The present invention also provides a novel undecaprenyl pyrophosphate synthase crystalline structure based on the UPPS *Streptococcus pneumoniae* undecaprenyl pyrophosphate synthase in complex with the substrates IPP and FPP.

In the FPP complex, one FPP molecule is bound in the active site. However, in the IPP complex structure, two large, adjacent electron density peaks appear in the active site, the first one corresponds to a pyrophosphate onto which the pyrophosphate of FPP can be superimposed. The second electron density peak corresponds to an entire IPP molecule. In both complex structures, the major structural changes between the native and the substrate complex structures is the ordering of the polypeptide chain between residues 72-79, to form two turns of a  $3_{10}$  helix and the opening of the entrance to the long, narrow hydrophobic

pocket where FPP binds. In the IPP complex, the C-terminus of the other molecule in the dimer also becomes ordered to form part of the IPP binding site.

The interactions between the substrates and the enzyme are summarize as follows:

1. There are at least two substrate-binding sites, at least one of each corresponding to each of the two substrates. The FPP's pyrophosphate binds at the N-terminus of  $\alpha$ -helix  $\alpha$ 1 and the C-terminal end of strands  $\alpha$ 1 and  $\alpha$ 2. The farnesyl carbon chain runs across  $\alpha$ 2 and  $\alpha$ 3. The IPP's pyrophosphate binding site is located next to an FPP site and also runs across the top strands  $\alpha$ 1 and  $\alpha$ 2, but on the other side of the  $\alpha$ -sheet. The phosphate group interacts with Arg247 located on the C-terminus of the partner molecule in the dimer
2. The farnesyl chain binds into a tunnel lined by Met49, Leu52, Ala71, Leu90, Pro91, Phe94, Leu126, Phe143, and Leu145.
3. The isopentenyl chain binds into a shallow depression lined by Ile26, the C $\alpha$  carbon of Asp28, Tyr70, and Phe72. The isopentenyl chain is then substantially or completely enclosed by the farnesyl chain bound adjacent to it and by the C-terminus of the partner molecule in the dimer. They are bound in such a way that the *re* face of an attacking carbon is poised for the reaction.
4. The position of the Mg<sup>+2</sup> ions in a metal binding site may be indicated by a strong difference in an electron density peak modeled as a water molecule is located between the two pyrophosphate groups observed bound in the IPP complex.
5. The enzymatic turnover cycle starts with binding of FPP required for a subsequent binding of IPP. IPP binding must follow FPP because a binding interaction is with magnesium that is bridging the two pyrophosphates. Also, the carbon chain of FPP forms part of the IPP binding pocket. The orientation of C02 of IPP is such, that C1 of FPP is facing the *re* face of the double bond, ideal for the attack on C1. This is necessary, since the removal of a proton by Asp28 (or Arg200) occurs from the opposite side (on C9) to produce a Z-double bond.
6. A preferred mechanism provides a critical role for His45, in  $\alpha$ 2, to promote cleavage of the pyrophosphate moiety from FPP by positioning the NE2 atom to polarize C1 in FPP, in analogy to a mechanism of thiamine phosphate synthase. Another preferred mechanism involves a metal-triggered carbocation formation. Once an FPP is bound, the binding of IPP and Mg<sup>+2</sup> result in the formation of a carbocation analogously to a mechanism postulated for other prenyltransferases (*i.e.*, farnesyl synthase, or aristolochene synthase). In addition to His45, Asn30 and/or Asp28, or Arg200 in  $\alpha$ 1 is putatively important for a stereochemically- specific removal of a proton to form a double bond. These residues occupy suitable relative positions for catalysis as deduced from a comparison of



complex structures. Asn30, Asp28 or Arg200 are poised to assist a stereochemical-specific proton abstraction from an incoming isopentenyl unit from C09. These residues are highly conserved among UPPSs from a variety of organisms. Of 27 aligned amino acid sequences including bacterial, archaebacteria and eukariotic UPPS's, the stretch FGHKA that includes Gly44 is absolutely conserved while His45 is present in all but two known sequences. In these two known sequences, a tyrosine replaces the histidine. In the same alignment, an amino acid stretch that includes Asp28, IMDGN, Asp28, Gly29 and Asn30 is absolutely conserved. Site-directed mutagenesis of some conserved residues of UPPS from *E. coli* (Pan, J-J., Yang, L.-W. , and Liang, P-H. (2000) *Biochemistry* 39, 13856-13861) can now be rationally explained by the discoveries of the present invention. Mutation of Asp26 or Glu213 to alanine causes a 1000-fold drop in  $k_{cat}$ . In *S. pneumoniae* Asp28 is equivalent to *E. coli*'s Asp26. In a preferred catalytic mechanism provided by the invention, Asp28/Asp26 plays a key role in formation of a double bond in the product after condensation step has occurred by removing a proton that would result in a cis (Z) configuration. A second important mutation involves Glu213, in *S. pneumoniae* Glu219 is equivalent to *E. coli*'s Glu213. Glu219/Glu213 interacts with and helps to position Arg206 in a proper orientation to interact with IPP in an active site. Arg206 is an important residue for binding of IPP.

Certain mechanisms of the invention take into account the binding of the product's chain when the product exceeds 20 carbons. A model of a C30 intermediate having the preferred stereochemistry (trans, trans, cis, cis, cis) bound at the FPP binding site in an active site UPPS shows that the chain beyond the first 15 carbon atoms can exit the protein into the solvent or, more likely, into a phospholipid membrane or detergent micell through an opening created between helices •2 and •3. Creation of an opening requires the movement of side chains of Met49 and Tyr98, torsion of the side chains is sufficient to open a channel through which a product may exit. There is also the possibility, as has been suggested, that a product may fold on itself several times inside an FPP binding channel, but there does not seem possible since there is not enough space to accommodate a long carbon chain. The final product exits the protein by either a "pull" action from the pyrophosphate end, or by a "pull" action from the opposite end, but that implies that the pyrophosphate is dragged along an FPP binding channel and out through an inter-helix space.

Table I provides the atomic coordinates of preferred native and complex crystal structures of UPPS from *S. pneumoniae*. This preferred native model includes residues 37-92 and 97-268 in molecule A, 37-92 and 99-266 in molecule B, 37-93 and 97-268 in molecule C, 38-93 and 98-266 in molecule D, for the four molecules, A, B, C, and D, in the crystallographic asymmetric unit. The amino acid sequence of a UPPS from *S. pneumoniae*

is provided in SEQ ID No. 1. Table II provides the distances, in Å, between atoms within a 5.0Å radius in an active site including bound substrates FPP and IPP. Table III provides the angles (°) between active site atoms that are within 4.0Å of substrate FPP or IPP.

Small variations in the atomic coordinates shown in Tables I - III will occur such as upon refinement of a crystal structure from a different crystal form that will result in a new set of coordinates. The deviation on Cα atoms from the present coordinate set is not expected to substantially exceed a rms of 2.5Å. Similarly, bond angles and bond lengths will usually vary within a small range (Engh, R. A., and Huber, R. (1991) *Acta Crystallogr. A* 47, 392-400), however, the inter-atomic interactions in Tables I - III will remain constant, within the experimental error, as will the relative conformation and orientation or positioning of residues in an active site. The atomic coordinates of an active site residues, including bound substrates, are provided in Tables I-III.

#### Mutants and Derivatives

Herein, the terms "a" and "an" mean "one or more" when used in this application, including the claims.

The invention further provides homologues, co-complexes, mutants and derivatives of the UPPS crystal structure of the invention.

The term "homologue" means a protein having at least 30% amino acid sequence identity with a functional domain of UPPS. Preferably the percentage identity will be 40, or 50%, more preferably 60 or 70% and most preferably 80 or 90%. A 95% identity is most particularly preferred.

The term "co-complex" means a UPPS or a mutant or homologue of a UPPS in covalent or non-covalent association with a chemical entity or compound.

As used herein, the term "agonist" means an agent that supplements or potentiates the bioactivity of a functional UPPS gene or protein or of a polypeptide encoded by a gene that is up- or down-regulated by a UPPS polypeptide. By way of specific example, an "agonist" is a compound that interacts with a steroid hormone receptor to promote a transcriptional response. An agonist can induce changes in a receptor that places a receptor in an active conformation that allows them to influence transcription, either positively or negatively. There can be several different ligand-induced changes in a receptor's conformation. The term "agonist" specifically encompasses partial agonists.

As used herein, the terms "•-helix", "alpha-helix" and "alpha helix" are used interchangeably and mean the conformation of a polypeptide chain wherein the polypeptide backbone is wound around the long axis of the molecule in a left-handed or right-handed

direction, and the R groups of the amino acids protrude outward from the helical backbone, wherein the repeating unit of the structure is a single turn of the helix, which extends about 0.56 nm along the long axis.

As used herein, the term "antagonist" means an agent that decreases or inhibits a  
5 bioactivity of a functional UPPS gene or protein, or that supplements or potentiates a  
bioactivity of a naturally occurring or engineered non-functional UPPS gene or protein.  
Alternatively, an antagonist can decrease or inhibit a bioactivity of a functional gene or  
polypeptide encoded by a gene that is up- or down-regulated by a UPPS polypeptide. An  
antagonist can also supplement or potentiate the bioactivity of a naturally occurring or  
10 engineered non-functional gene or polypeptide encoded by a gene that is up- or down-  
regulated by a UPPS polypeptide. By way of specific example, an "antagonist" is a  
compound that interacts with a steroid hormone receptor to inhibit a transcriptional  
response. An antagonist can bind to a receptor but fail to induce conformational changes  
that alter a receptor's transcriptional regulatory properties or physiologically relevant  
15 conformations. Binding of an antagonist can also block the binding and therefore the actions  
of an agonist. The term "antagonist" specifically encompasses partial antagonists.

As used herein, the terms "α-sheet", "β-sheet" and "beta sheet" are used  
interchangeably and mean the conformation of a polypeptide chain stretched into an  
extended zig-zig conformation. Portions of polypeptide chains that run "parallel" all run in  
20 the same direction. Polypeptide chains that are "antiparallel" run in the opposite direction  
from the parallel chains.

As used herein, the term "binding pocket" refers to any moiety, part or region of  
UPPS that actually or is capable of binding to, directly participating with, adhering to, or  
otherwise associating with an atom, ion or molecule. Preferably, a large cavity within a  
25 UPPS ligand binding domain where an agonist or antagonist can bind is a binding pocket.  
Such a cavity can be empty, or can contain water molecules or other molecules from the  
solvent, or an agonist or antagonist moieties, atoms or molecules. Such a binding pocket  
also includes regions of space near the "main" binding pocket that are not occupied by  
atoms or moieties of UPPS, but that are near the "main" binding pocket, and that are  
30 contiguous with the "main" binding pocket. Preferably,

As used herein, the term "active site" refers to a specific region of UPPS binding  
pocket where a molecule binds and catalysis takes place. It is comprised and bound by  
amino acid residues that are in direct contact with the substrate or that interact with the  
substrate(s) through water molecules or those amino acids that, although not being in direct  
35 contact with the substrate(s), nonetheless are important for they allow the correct

positioning of those amino acids that are and which without the correct positioning they would not be able to interact favorably (i. e. in a way conducive to catalysis) with the substrate(s). These interactions between amino acids and substrate(s) are responsible for the binding of the substrate to UPPS, for the correct positioning of the substrate for catalysis, and for stabilization of any reaction intermediates and for the binding and possibly the release of the products from that active site. These are amino acids that may be replaced by site-directed mutagenesis, and their replacement will result in at the very least a several-fold, or more likely, in several orders of magnitude decrease in the binding affinity of the substrate(s). The active site is also comprised by amino acids that are directly responsible for catalysis. These amino acids interact with the substrate(s) through hydrogen bonds or are in close proximity to electron-donor or electron-acceptor centers in the substrate. These amino acids may act themselves as electron-donor or electron-acceptor centers for catalysis to take place. These are amino acids that may be replaced by site-directed mutagenesis, and their replacement will result in at the very least a several-fold, or more likely, in several orders of magnitude decrease in the catalytic efficiency, but no changes in the affinity of binding of the substrate(s). In some cases, the catalytic activity may be recovered by some chemicals that, by binding to the appropriate active site residues, will mimic the wild-type amino acid.

As used herein, the term "biological activity" means any observable effect flowing from interaction between a UPPS polypeptide and an agonist or antagonist. Representative, but non-limiting, examples of biological activity in the context of the present invention include transcription regulation, agonist or antagonist binding, and peptide binding.

As used herein, the terms "candidate substance" and "candidate compound" are used interchangeably and refer to a substance that is believed to interact with another moiety, for example an agonist or antagonist that is believed to interact with a complete, or a fragment of, a UPPS polypeptide, and which can be subsequently evaluated for such an interaction. Representative candidate substances or compounds include xenobiotics such as drugs and other therapeutic agents, carcinogens and environmental pollutants, natural products and extracts, as well as endobiotics such as glucocorticosteroids, steroids, fatty acids and prostaglandins. Other examples of candidate compounds that can be investigated using the methods of the present invention include, but are not restricted to, agonists and antagonists of a UPPS polypeptide, toxins and venoms, viral epitopes, hormones (e.g., glucocorticosteroids, opioid peptides, steroids, etc.), hormone receptors, peptides, enzymes, enzyme substrates, co-factors, lectins, sugars, oligonucleotides or nucleic acids, oligosaccharides, proteins, small molecules and monoclonal antibodies.

As used herein, the terms "cells," "host cells" or "recombinant host cells" are used interchangeably and mean not only to a particular subject cell, but also to any progeny or potential progeny of such a cell. Because certain modifications can occur in succeeding generations due to either mutation or environmental influences, such progeny might not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

As used herein, the terms "chimeric protein" or "fusion protein" are used interchangeably and mean a fusion of a first amino acid sequence encoding a UPPS polypeptide with a second amino acid sequence defining a polypeptide domain foreign to, and not homologous with, any domain of a UPPS polypeptide. A chimeric protein can include a foreign domain that is found in an organism that also expresses the first protein, or it can be an "interspecies" or "intergenic" fusion of protein structures expressed by different kinds of organisms. In general, a fusion protein can be represented by the general formula X—UPPS—Y, wherein UPPS represents a portion of the protein which is derived from a UPPS polypeptide, and X and Y are independently absent or represent amino acid sequences which are not related to a UPPS sequence in an organism, which includes naturally occurring mutants.

As used herein, the term "detecting" means confirming the presence of a target entity by observing the occurrence of a detectable signal, such as a radiologic or spectroscopic signal that will appear exclusively in the presence of the target entity.

As used herein, the term "DNA segment" means a DNA molecule that has been isolated free of total genomic DNA of a particular species. In a preferred embodiment, a DNA segment encoding a UPPS polypeptide refers to a DNA segment that comprises any of SEQ ID NO:1, but can optionally comprise fewer or additional nucleic acids, yet is isolated away from, or purified free from, total genomic DNA of a source species, such as *Streptococcus pneumoniae*. Included within the term "DNA segment" are DNA segments and smaller fragments of such segments, and also recombinant vectors, including, for example, plasmids, cosmids, phages, viruses, and the like.

As used herein, the term "DNA sequence encoding a UPPS polypeptide" can refer to one or more coding sequences within a particular individual. Moreover, certain differences in nucleotide sequences can exist between individual organisms, which are called alleles. It is possible that such allelic differences might or might not result in differences in amino acid sequence of the encoded polypeptide yet still encode a protein with the same biological activity. As is well known, genes for a particular polypeptide can exist in single or multiple copies within the genome of an individual. Such duplicate genes

can be identical or can have certain modifications, including nucleotide substitutions, additions or deletions, all of which still code for polypeptides having substantially the same activity.

As used herein, the term "expression" generally refers to the cellular processes by which a biologically active polypeptide is produced.

As used herein, the term "gene" is used for simplicity to refer to a functional protein, polypeptide or peptide encoding unit. As will be understood by those in the art, this functional term includes both genomic sequences and cDNA sequences. Preferred embodiments of genomic and cDNA sequences are disclosed herein.

As used herein, the term "crystal lattice" means the array of points defined by the vertices of packed unit cells.

As used herein, "hexagonal unit cell" means a unit cell wherein  $a = b \neq c$ ; and  $\alpha = \beta = 90^\circ, \gamma = 120^\circ$ . The vectors  $a$ ,  $b$ , and  $c$  describe the unit cell edges and the angles  $\alpha$ ,  $\beta$ , and  $\gamma$  describe the unit cell angles. In a preferred embodiment of the present invention, the unit cell has lattice constants of  $a = 59.6\text{\AA}$ ,  $b = 118.0\text{\AA}$ ,  $c = 178.2\text{\AA}$ . While preferred lattice constants are provided, a crystalline polypeptide of the present invention also comprises variations from the preferred lattice constants, wherein the variations range from about one to about two percent.

As used herein, the term "hybridization" means the binding of a probe molecule, a molecule to which a detectable moiety has been bound, to a target sample.

As used herein, the term "interact" means detectable interactions between molecules, such as can be detected using, for example, a yeast two hybrid assay. The term "interact" is also meant to include "binding" interactions between molecules. Interactions can, for example, be protein-protein or protein-nucleic acid in nature.

As used herein, the term "isolated" means oligonucleotides substantially free of other nucleic acids, proteins, lipids, carbohydrates or other materials with which they can be associated, such association being either in cellular material or in a synthesis medium. The term can also be applied to polypeptides, in which case the polypeptide will be substantially free of nucleic acids, carbohydrates, lipids and other undesired polypeptides.

As used herein, the term "labeled" means the attachment of a moiety, capable of detection by spectroscopic, radiologic or other methods, to a probe molecule.

As used herein, the term "modified" means an alteration from an entity's normally occurring state. An entity can be modified by removing discrete chemical units or by adding discrete chemical units. The term "modified" encompasses detectable labels as well as those entities added as aids in purification.

As used herein, the term "modulate" means an increase, decrease, or other alteration of any or all chemical and biological activities or properties of a wild-type or mutant UPPS polypeptide, preferably a wild-type or mutant UPPS polypeptide. The term "modulation" as used herein refers to both up-regulation (i.e., activation or stimulation) and down-regulation (i.e. inhibition or suppression) of a response, and includes responses that are upregulated in one cell type or tissue, and down-regulated in another cell type or tissue.

As used herein, the term "molecular replacement" means a method that involves generating a preliminary model of a wild-type UPPS ligand binding domain, or a UPPS mutant crystal whose structure coordinates are unknown, by orienting and positioning a molecule or model whose structure coordinates are known within the unit cell of the unknown crystal so as best to account for the observed diffraction pattern of the unknown crystal. Phases can then be calculated from this model and combined with the observed amplitudes to give an approximate Fourier synthesis of the structure whose coordinates are unknown. This, in turn, can be subject to any of the several forms of refinement to provide a final, accurate structure of the unknown crystal. See, e.g., *Lattman, (1985) Method Enzymol.*, 115: 55-77; *Rossmann, ed, (1972) The Molecular Replacement Method*, Gordon & Breach, New York. Using the structure coordinates of the active site of UPPS provided by this invention, molecular replacement can be used to determine the structure coordinates of a crystalline mutant or homologue of the UPPS active site, or of a different crystal form of the UPPS active site.

As used herein, the term "partial agonist" means an entity that can bind to a receptor and induce only part of the changes in the receptors that are induced by agonists. The differences can be qualitative or quantitative. Thus, a partial agonist can induce some of the conformation changes induced by agonists, but not others, or it can only induce certain changes to a limited extent.

As used herein, the term "partial antagonist" means an entity that can bind to a receptor and inhibit only part of the changes in the receptors that are induced by antagonists. The differences can be qualitative or quantitative. Thus, a partial antagonist can inhibit some of the conformation changes induced by an antagonist, but not others, or it can inhibit certain changes to a limited extent.

As used herein, the term "polypeptide" means any polymer comprising any of the 20 protein amino acids, regardless of its size. Although "protein" is often used in reference to relatively large polypeptides, and "peptide" is often used in reference to small polypeptides, usage of these terms in the art overlaps and varies. The term "polypeptide" as used herein refers to peptides, polypeptides and proteins, unless otherwise noted. As used

herein, the terms "protein", "polypeptide" and "peptide" are used interchangeably herein when referring to a gene product.

As used herein, the term "primer" means a sequence comprising two or more deoxyribonucleotides or ribonucleotides, preferably more than three, and more preferably  
5 more than eight and most preferably at least about 20 nucleotides of an exonic or intronic region. Such oligonucleotides are preferably between ten and thirty bases in length.

As used herein, the term "sequencing" means the determining the ordered linear sequence of nucleic acids or amino acids of a DNA or protein target sample, using conventional manual or automated laboratory techniques.

10 As used herein, the terms "structure coordinates" and "structural coordinates" mean mathematical coordinates derived from mathematical equations related to the patterns obtained on diffraction of a monochromatic beam of X-rays by the atoms (scattering centers) of a molecule in crystal form. The diffraction data are used to calculate an electron density map of the repeating unit of the crystal. The electron density maps are used to  
15 establish the positions of the individual atoms within the unit cell of the crystal.

Those of skill in the art understand that a set of coordinates determined by X-ray crystallography is not without standard error. In general, the error in the coordinates tends to be reduced as the resolution is increased, since more experimental diffraction data is available for the model fitting and refinement. Thus, for example, more diffraction data can  
20 be collected from a crystal that diffracts to a resolution of 2.8 angstroms than from a crystal that diffracts to a lower resolution, such as 3.5 angstroms. Consequently, the refined structural coordinates will usually be more accurate when fitted and refined using data from a crystal that diffracts to higher resolution. The design of agonists, antagonists, and modulators for UPPS depends on the accuracy of the structural coordinates. If the  
25 coordinates are not sufficiently accurate, then the design process will be ineffective. In most cases, it is very difficult or impossible to collect sufficient diffraction data to define atomic coordinates precisely when the crystals diffract to a resolution of only 3.5 angstroms or poorer. Thus, in most cases, it is difficult to use X-ray structures in structure-based agonist and antagonist design when the X-ray structures are based on crystals that diffract to a  
30 resolution of only 3.5 angstroms or poorer. However, common experience has shown that crystals diffracting to 2.8 angstroms or better can yield X-ray structures with sufficient accuracy to greatly facilitate structure-based drug design. Further improvement in the resolution can further facilitate structure-based design, but the coordinates obtained at 2.8 angstroms resolution are generally adequate for most purposes.

35 Also, those of skill in the art will understand that UPPS proteins can adopt different



conformations when different agonists, antagonists, and modulators are bound. Subtle variations in the conformation can also occur when different agonists are bound, and when different antagonists are bound. These variations can be difficult or impossible to predict from a single X-ray structure. Generally, structure-based design of UPPS modulators  
5 depends to some degree on a knowledge of the differences in conformation that occur when agonists and antagonists are bound. Thus, structure-based modulator design is most facilitated by the availability of X-ray structures of complexes with potent agonists as well as potent antagonists.

As used herein, the term "substantially pure" means that the polynucleotide or  
10 polypeptide is substantially free of the sequences and molecules with which it is associated in its natural state, and those molecules used in the isolation procedure. The term "substantially free" means that the sample is at least 50%, preferably at least 70%, more preferably 80% and most preferably 90% free of the materials and compounds with which is it associated in nature.

15 As used herein, the term "target cell" refers to a cell, into which it is desired to insert a nucleic acid sequence or polypeptide, or to otherwise effect a modification from conditions known to be standard in the unmodified cell. A nucleic acid sequence introduced into a target cell can be of variable length. Additionally, a nucleic acid sequence can enter a target cell as a component of a plasmid or other vector or as a naked sequence.

20 As used herein, the term "transcription" means a cellular process involving the interaction of an RNA polymerase with a gene that directs the expression as RNA of the structural information present in the coding sequences of the gene. The process includes, but is not limited to the following steps: (a) the transcription initiation, (b) transcript elongation, (c) transcript splicing, (d) transcript capping, (e) transcript termination, (f)  
25 transcript polyadenylation, (g) nuclear export of the transcript, (h) transcript editing, and (i) stabilizing the transcript.

As used herein, the term "transcription factor" means a cytoplasmic or nuclear protein which binds to such gene, or binds to an RNA transcript of such gene, or binds to another protein which binds to such gene or such RNA transcript or another protein which  
30 in turn binds to such gene or such RNA transcript, so as to thereby modulate expression of the gene. Such modulation can additionally be achieved by other mechanisms; the essence of "transcription factor for a gene" is that the level of transcription of the gene is altered in some way.

As used herein, the term "unit cell" means a basic parallelepiped shaped block. The  
35 entire volume of a crystal can be constructed by regular assembly of such blocks. Each unit

cell comprises a complete representation of the unit of pattern, the repetition of which builds up the crystal. Thus, the term "unit cell" means the fundamental portion of a crystal structure that is repeated infinitely by translation in three dimensions. A unit cell is characterized by three vectors a, b, and c, not located in one plane, which form the edges of a parallelepiped. Angles  $\alpha$ ,  $\beta$ , and  $\gamma$  define the angles between the vectors: angle  $\alpha$  is the angle between vectors b and c; angle  $\beta$  is the angle between vectors a and c; and angle  $\gamma$  is the angle between vectors a and b. The entire volume of a crystal can be constructed by regular assembly of unit cells; each unit cell comprises a complete representation of the unit of pattern, the repetition of which builds up the crystal.

As used herein, the term "mutant" or "mutation" carries its traditional connotation and means a change, inherited, naturally occurring or introduced, in a nucleic acid or polypeptide sequence, and is used in its sense as generally known to those of skill in the art. For example, a UPPS polypeptide, i.e., a polypeptide displaying the biological activity of wild-type UPPS activity, characterized by the replacement of at least one active-site amino acid from the wild-type prenyltransferase sequence. Such a mutant may be prepared, for example, by expression of the UPPS prenyltransferase cDNA previously altered in its coding sequence by oligonucleotide-directed mutagenesis.

UPPS mutants may also be generated by site-specific incorporation of unnatural amino acids into the UPPS protein using the general biosynthetic method of C. J. Noren et al, *Science*, 244:182-188 (1989). In this method, the codon encoding the amino acid of interest in wild-type UPPS is replaced by a "blank" nonsense codon, TAG, using oligonucleotide-directed mutagenesis. A suppressor directed against this codon is then chemically aminoacylated *in vitro* with the desired unnatural amino acid. The aminoacylated residue is then added to an *in vitro* translation system to yield a mutant UPPS enzyme with the site-specific incorporated unnatural amino acid.

Selenocysteine or selenomethionine may be incorporated into wild-type or mutant metallo UPPS prenyltransferase by expression of UPPS-encoding cDNAs in auxotrophic *E. coli* strains (W. A. Hendrickson et al, *EMBO J.*, 9(5):1665-1672 (1990)) or a normal strain grown in a medium supplemented with appropriate nutrients that will prevent endogenous synthesis of methionine. In either of these methods, the wild-type or mutated undecaprenyl pyrophosphate synthase cDNA may be expressed in a host organism on a growth medium depleted of either natural cysteine or methionine (or both) but enriched in selenocysteine or selenomethionine (or both).

The term "heavy atom derivative" refers to derivatives of UPPS produced by chemically modifying a crystal of UPPS. In practice, a native crystal is treated by

immersing it in a solution containing the desired metal salt, or organometallic compound, e.g., lead chloride, gold thiomalate, thimerosal or uranyl acetate, which upon diffusion into the protein crystal can bind to the protein. The location of the bound heavy metal atom site(s) can be determined by X-ray diffraction analysis of the treated crystal. This  
5 information, in turn, is used to generate the phase angle information needed to construct a three-dimensional electron density map from which a model of the atomic structure of the enzyme is derived (T. L. Blundel and N. L. Johnson, *Protein Crystallography*, Academic Press (1976)).

The term "space group" refers to the arrangement of symmetry elements (i.e.  
10 molecules) throughout the crystal. There are only 132 possible arrangements, each one unique and identified by a symbol. The space group symbol is formed by a letter (P, F, I, C) and numbers with or without subscripts, for example:  $P2_1$ ,  $I222$ ,  $C2_12_12_1$ , etc.

#### 15 Methods of Identifying Inhibitors of UPPS from *Streptococcus pneumoniae* Crystalline Structure

An aspect of this invention involves a method for identifying inhibitors of a UPPS characterized by the crystal structure and novel active site described herein, and the crystal structures of the complexes with its substrates. The novel prenyltransferase crystalline structure of the invention permits the identification of inhibitors of prenyltransferase  
20 activity. Such inhibitors may be competitive, binding to all or a portion of the active site of UPPS; or non-competitive and bind to and inhibit undecaprenyl pyrophosphate synthase whether or not it is bound to another chemical entity.

One design approach is to probe a UPPS crystal of the invention with molecules composed of a variety of different chemical entities to determine optimal sites for  
25 interaction between candidate UPPS inhibitors and the enzyme. For example, high resolution X-ray diffraction data collected from crystals saturated with solvent allows the determination of where each type of solvent molecule binds. Small molecules that bind tightly to those sites can then be designed and synthesized and tested for a UPPS inhibitor activity (J. Travis, *Science*, 262:1374 (1993)).

30 This invention also enables the development of compounds that can isomerize to short-lived reaction intermediates in the chemical reaction of a substrate or other compound that binds to or with a UPPS. Thus, the time-dependent analysis of structural changes in a UPPS during its interaction with other molecules is permitted. The reaction intermediates of the UPPS can also be deduced from the reaction product in co-complex with a UPPS. Such  
35 information is useful to design improved analogues of known UPPS inhibitors or to design

novel classes of inhibitors based on the reaction intermediates of a UPPS enzyme and UPPS inhibitor co-complex. This provides a novel route for designing UPPS inhibitors with both high specificity and stability.

Another approach made possible by this invention, is to screen computationally  
5 small molecule data bases for chemical entities or compounds that can bind in whole, or in part, to a UPPS enzyme. In this screening, the quality of fit of such entities or compounds to the binding site may be judged either by shape complementarity or by estimated interaction energy (E. C. Meng et al, *J. Comp. Chem.*, 13:505-524 (1992)).

Because UPPS may crystallize in more than one crystal form, the structure  
10 coordinates of UPPS, or portions thereof, as provided by this invention are particularly useful to solve the structure of those other crystal forms of UPPS. They may also be used to solve the structure of UPPS mutant co-complexes, or of the crystalline form of any other protein with significant amino acid sequence homology to any functional domain of UPPS.

One method that may be employed for this purpose is molecular replacement. In  
15 this method, the unknown crystal structure, whether it is another crystal form of UPPS, a UPPS mutant, a UPPS co-complex, a UPPS from a different bacterial species, or the crystal of some other protein with significant amino acid sequence homology to any domain of UPPS, may be determined using the UPPS structure coordinates of this invention as provided in Figures 1-5 and Tables I - III. This method will provide an accurate structural  
20 form for the unknown crystal more quickly and efficiently than attempting to determine such information *ab initio*.

Thus, preferred UPPS structures provided herein permits the screening of known molecules and/or the designing of new molecules which bind to the structure, particularly at the binding pocket or active site, via the use of computerized evaluation systems. For  
25 example, computer modeling systems are available in which the sequence of a UPPS, and a UPPS structure (i.e., the atomic coordinates, bond distances between atoms in the active site region, etc. as provided by Tables I - III herein) may be input. Thus, a machine readable medium may be encoded with data representing the coordinates of Tables I - III. The computer then generates structural details of the site into which a test compound should  
30 bind, thereby enabling the determination of the complementary structural details of said test compound.

More particularly, the design of compounds that bind to or inhibit UPPS according to this invention generally involves consideration of two factors. First, the compound must be capable of physically and structurally associating with UPPS. Non-covalent molecular

interactions important in the association of UPPS with its substrate include hydrogen bonding, van der Waals, and hydrophobic interactions.

Second, the compound must be able to assume a conformation that allows it to associate with UPPS. Although certain portions of the compound will not directly participate in this association with UPPS, those portions may still influence the overall conformation of the molecule. This, in turn, may have a significant impact on potency. Such conformational requirements include the overall three-dimensional structure and orientation of the chemical entity or compound in relation to all or a portion of the binding site, e.g., binding pocket, active site, or substrate binding sites of UPPS, or the spacing between functional groups of a compound comprising several chemical entities that directly interact with UPPS.

Another approach made possible by this invention is to screen computationally small molecule databases for chemical entities or compounds that can bind in whole, or in part, to a UPPS enzyme. Details on this process and the results it can provide are now documented in the art. For a description of this type of technology please refer to PCT application WO 97/16177 published 09 May 1997; the techniques described there for computer modeling are incorporated herein by reference.

Once identified by the modeling techniques, the prenyltransferase inhibitor may be tested for bio-activity using standard techniques. For example, the structure of the invention may be used in enzymatic activity assays to determine the inhibitory activity of the compounds or binding assays using conventional formats to screen inhibitors. One particularly suitable assay format includes the enzyme-linked immunosorbent assay (herein "ELISA"). Other assay formats may be used; these assay formats are not a limitation on the present invention.

The potential inhibitory or binding effect of a chemical compound on UPPS may be analyzed prior to its actual synthesis and testing by the use of computer modelling techniques. If the theoretical structure of the given compound suggests insufficient interaction and association between it and UPPS, synthesis and testing of the compound is obviated. However, if computer modelling indicates a strong interaction, the molecule may then be synthesized and tested for its ability to bind to UPPS and inhibit using a suitable assay. In this manner, synthesis of inoperative compounds may be avoided.

An inhibitory or other binding compound of UPPS may be computationally evaluated and designed by means of a series of steps in that chemical entities or fragments are screened and selected for their ability to associate with the individual binding pockets or other areas of UPPS.

One skilled in the art may use one of several methods to screen chemical entities or fragments for their ability to associate with UPPS and more particularly with the individual binding pockets of the UPPS active site or accessory binding site. This process may begin by visual inspection of, for example, the active site on the computer screen based on the UPPS coordinates in Tables I-III. Selected fragments or chemical entities may then be positioned in a variety of orientations, or docked, within an binding pocket or active site of UPPS. Docking may be accomplished using software such as Quanta and Sybyl, followed by energy minimization and molecular dynamics with standard molecular mechanics forcefields, such as CHARMM and AMBER.

Specialized computer programs may also assist in the process of selecting fragments or chemical entities. These include:

1. GRID (P. J. Goodford, "A Computational Procedure for Determining Energetically Favorable Binding Sites on Biologically Important Macromolecules", *J. Med. Chem.*, 28:849-857 (1985)). GRID is available from Oxford University, Oxford, UK.

2. MCSS (A. Miranker and M. Karplus, "Functionality Maps of Binding Sites: A Multiple Copy Simultaneous Search Method", *Proteins: Structure, Function and Genetics*, 11:29-34 (1991)). MCSS is available from Molecular Simulations, Burlington, MA.

3. AUTODOCK (D. S. Goodsell and A. J. Olsen, "Automated Docking of Substrates to Proteins by Simulated Annealing", *Proteins: Structure, Function, and Genetics*, 8:195-202 (1990)). AUTODOCK is available from Scripps Research Institute, La Jolla, CA.

4. DOCK (I. D. Kuntz et al., "A Geometric Approach to Macromolecule-Ligand Interactions", *J. Mol. Biol.*, 161:269-288 (1982)). DOCK is available from University of California, San Francisco, CA.

In addition, other commercially available computer databases for small molecular compounds includes Cambridge Structural Database, Fine Chemical Database, and CONCORD, for a review see Rusinko, A., *Chem. Des. Auto. News* 8, 44-47 (1993).

Once suitable chemical entities or fragments have been selected, they can be assembled into a single compound or inhibitor. Assembly may be proceed by visual inspection of the relationship of the fragments to each other on the three-dimensional image displayed on a computer screen in relation to the structure coordinates of UPPS. This would be followed by manual model building using software such as Quanta or Sybyl.

Useful programs to aid one of skill in the art in connecting the individual chemical entities or fragments include:

1. CAVEAT (P. A. Bartlett et al, "CAVEAT: A Program to Facilitate the Structure-Derived Design of Biologically Active Molecules", in *Molecular Recognition in Chemical and Biological Problems*, Speical Pub., Royal Chem. Soc. 78, pp. 182-196 (1989)]. CAVEAT is available from the University of California, Berkeley, CA.
  - 5 2. 3D Database systems such as MACCS-3D (MDL Information Systems, San Leandro, CA). This area is reviewed in Y. C. Martin, "3D Database Searching in Drug Design," *J. Med. Chem.*, 35:2145-2154 (1992).
  3. HOOK (available from Molecular Simulations, Burlington, MA).
- Instead of proceeding to build a UPPS inhibitor in a step-wise fashion one fragment
- 10 or chemical entity at a time as described above, inhibitory or other UPPS binding compounds may be designed as a whole or "*de novo*" using either an empty active site or optionally including some portion(s) of a known ligand(s). These methods include:
1. LUDI (H.J. Bohm, "The Computer Program LUDI: A New Method for the De Novo Design of Enzyme Inhibitors", *J. Comp. Aid. Molec. Design*, 6:61-78 (1992)).
  - 15 LUDI is available from Biosym Technologies, San Diego, CA.
  2. LEGEND (Y. Nishibata and A. Itai, *Tetrahedron*, 47:8985 (1991)).  
LEGEND is available from Molecular Simulations, Burlington, MA.
  3. LeapFrog (available from Tripos Associates, St. Louis, MO).
- Other molecular modelling techniques may also be employed in accordance with
- 20 this invention. See, e.g., N. C. Cohen et al, "Molecular Modeling Software and Methods for Medicinal Chemistry", *J. Med. Chem.*, 33:883-894 (1990). See also, M. A. Navia and M. A. Murcko, "The Use of Structural Information in Drug Design", *Current Opinions in Structural Biology*, 2:202-210 (1992). For example, where the structures of test compounds are known, a model of the test compound may be superimposed over the model of the
- 25 structure of the invention. Numerous methods and techniques are known in the art for performing this step, any of which may be used. See, e.g., P.S. Farmer, *Drug Design*, Ariens, E.J., ed., Vol. 10, pp 119-143 (Academic Press, New York, 1980); U.S. Patent No. 5,331,573; U.S. Patent No. 5,500,807; C. Verlinde, *Structure*, 2:577-587 (1994); and I. D. Kuntz, *Science*, 257:1078-1082 (1992). The model building techniques and computer
- 30 evaluation systems described herein are not a limitation on the present invention.
- Thus, using these computer evaluation systems, a large number of compounds may be quickly and easily examined and expensive and lengthy biochemical testing avoided. Moreover, the need for actual synthesis of many compounds is effectively eliminated.
- In another aspect, the undecaprenyl pyrophosphate synthase structure of the
- 35 invention permit the design and identification of synthetic compounds and/or other

molecules which are characterized by the conformation of the undecaprenyl pyrophosphate synthase of the invention. Using known computer systems, the coordinates of the undecaprenyl pyrophosphate synthase structure of the invention may be provided in machine readable form, the test compounds designed and/or screened and their

5 conformations superimposed on the structure of the undecaprenyl pyrophosphate synthase of the invention. Subsequently, suitable candidates identified as above may be screened for the desired undecaprenyl pyrophosphate synthase inhibitory bio-activity, stability, and the like.

Once identified and screened for biological activity, these inhibitors may be used

10 therapeutically or prophylactically to block undecaprenyl pyrophosphate synthase activity, and thus, overcome bacterial resistance to antibiotics, for example, of the beta-lactam class, eg. imipenem, penicillins, cephalosporins, etc. by using an entirely different mechanism of attacking bacteria in diseases produced by bacterial infection.

15 Abbreviations used herein

	ATP	adenosine triphosphate
	ADP	adenosine diphosphate
	AR	androgen receptor
	CAT	chloramphenicol acyltransferase
20	CBP	CREB binding protein
	cDNA	complementary DNA
	DBD	DNA binding domain
	DMSO	dimethyl sulfoxide
	DNA	deoxyribonucleic acid
25	DTT	dithiothreitol
	EDTA	ethylenediaminetetraacetic acid
	ER	estrogen receptor
	FPP	farnesyl pyrophosphate
	GST	glutathione S-transferase
30	HEPES	N-2-Hydroxyethylpiperazine-N'-2-ethanesulfonic acid
	HSP	heat shock protein
	IPP	Isopentenyl pyrophosphate
	kDa	kilodalton(s)
	LBD	ligand binding domain
35	MR	mineralcorticoid receptor



	NDP	nucleotide diphosphate
	NID	nuclear receptor interaction domain
	NTP	nucleotide triphosphate
	PAGE	polyacrylamide gel electrophoresis
5	PCR	polymerase chain reaction
	pI	isoelectric point
	PPAR	peroxisome proliferator-activated receptor
	PR	progesterone receptor
	RAR	retinoid acid receptor
10	RXR	retinoid X receptor
	SDS	sodium dodecyl sulfate
	SDS-PAGE	sodium dodecyl sulfate polyacrylamide gel electrophoresis
	TIF2	transcription intermediary factor 2
	TR	thyroid receptor
15	UPPS	undecaprenyl pyrophosphate synthase
	VDR	vitamin D receptor

Amino Acid Abbreviations used herein

	<u>Single-Letter Code</u>	<u>Three-Letter Code</u>	<u>Name</u>
20	A	Ala	Alanine
	V	Val	Valine
	L	Leu	Leucine
	I	Ile	Isoleucine
	P	Pro	Proline
25	F	Phe	Phenylalanine
	W	Trp	Tryptophan
	M	Met	Methionine
	G	Gly	Glycine
	S	Ser	Serine
30	T	Thr	Threonine
	C	Cys	Cysteine
	Y	Tyr	Tyrosine
	N	Asn	Asparagine
	Q	Gln	Glutamine
35	D	Asp	Aspartic Acid

E	Glu	Glutamic Acid
K	Lys	Lysine
R	Arg	Arginine
H	His	Histidine

Functionally Equivalent Codons

	<u>Amino Acid</u>			<u>Codons</u>
	Alanine	Ala	A	GCA GCC GCG GCU
	Cysteine	Cys	C	UGC UGU
5	Aspartic Acid	Asp	D	GAC GAU
	Glumatic acid	Glu	E	GAA GAG
	Phenylalanine	Phe	F	UUC UUU
	Glycine	Gly	G	GGA GGC GGG GGU
	Histidine	His	H	CAC CAU
10	Isoleucine	Ile	I	AUA AUC AUU
	Lysine	Lys	K	AAA AAG
	Methionine	Met	M	AUG
	Asparagine	Asn	N	AAC AAU
	Proline	Pro	P	CCA CCC CCG CCU
	Glutamine	Gln	Q	CAA CAG
15	Threonine	Thr	T	ACA ACC ACG ACU
	Valine	Val	V	GUA GUC GUG GUU
	Tryptophan	Trp	W	UGG
	Tyrosine	Tyr	Y	UAC UAU
	Leucine	Leu	L	UUA UUG CUA CUC CUG CUU
20	Arginine	Arg	R	AGA AGG CGA CGC CGG CGU
	Serine	Ser	S	ACG AGU UCA UCC UCG UCU

25 The following examples illustrate various aspects of this invention. These examples do not limit the scope of this invention that is defined by the appended claims.

Example 1- Expression and purification of UPPS prenyltransferase from *Streptococcus pneumoniae* in *Escherichia coli*

30 UPPS from *Streptococcus pneumoniae* with an additional 20 residues at the amino terminus that include the hexa-histidine tag was over expressed in *E. coli*, strain BL21(DE3), and purified by NiNTA (nickel nitrilo-tri-acetic acid) column. A plasmid pET28-UPPS was transformed into *E. coli* BL21 (DE3). For expression *E. coli* BL21 (pET28-UPPS) was grown at 37 °C in LB medium containing 1% glucose and 50 ug/ml kanamycin to OD600 0.5 and then induced with 1 mM IPTG for 3 hrs. The induced cultures

were harvested by centrifugation. The cell paste was suspended in 25 ml Buffer A (10mM imidazole, 50mM Na-phosphate, 0.5M NaCl pH7.5) containing 0.1mg/ml of lysozyme. After incubating on ice 30 min, the cell suspension was put through 4 cycles of sonication, freeze and thaw. The lysate was centrifuged and the supernatant applied to the NiNTA, column. The column was washed with 18 ml of Buffer A and 12.5ml of Buffer B (100 mM imidazole, 50mM Na-phosphate, 0.5M NaCl pH7.5). The His-tagged UPPS was eluted with 10 ml of Buffer C (500 mM imidazole, 50mM Na-phosphate, 0.5M NaCl pH7.5). The eluted His-UPPS was dialyzed overnight at 4 °C against 2L of 50mM Tris-HCl pH 7.5, 0.2M NaCl and 1mM EDTA. The soluble polypeptide includes 272 amino acid residues with a molecular weight of 29,000. This product was greater than 95% pure by SDS PAGE, has the desired enzymatic activity, and N-terminal amino acid analysis confirmed its identity.

#### 1.A. Measurement of UPPS activity

Enzymatic activity of UPPS was assayed by measuring the incorporation of (1-14C)IPP (isopentenyl diphosphate) into butanol-soluble materials from the condensations of FPP and (1-14C)IPP using a butanol extraction assay (Shimizu et al. 1998). A typical assay of 100 ul contained 100 mM Tris-HCl, pH7.5, 50 mM KCl, 0.5 mM MgCl<sub>2</sub>, 0.05% Triton X-100, 0.5 uM FPP, 3.6 uM (1-14C)IPP, and 6 nM purified *S. pneumoniae* His-UPPS. The reaction was incubated at 25 °C for 25 min and stopped by addition of EDTA to 50 mM. The reaction was extracted with equal volume of 1-butanol and the radioactivity in the butanol phase was measured with a liquid scintillation counter (Shimizu, N., T. Koyama, and K. Ogura. (1998) *J Biol. Chem.* 273:19476-19481).

#### 1.B. Ligand binding to UPPS

It is also possible to define ligand interactions with UPPS in experiments that are not dependent upon enzyme catalyzed turnover of substrates. This type of experiment can be done in a number of ways:

##### 1.B.1. Effects of ligand binding upon enzyme intrinsic fluorescence (e.g. of tryptophan)

Binding of either natural ligands or inhibitors may result in enzyme conformational changes which alter enzyme fluorescence. Using stopped-flow fluorescence equipment, this can be used to define the microscopic rate constants that describe binding. Alternatively, steady-state fluorescence titration methods can yield the overall dissociation constant for binding in the same way that these are accessed through enzyme inhibition experiments.

Example 2 Crystallization, structure determination and refinement of a crystal structure of UPPS from *Streptococcus pneumoniae*

2.A. Crystallization

5           Single crystals of native UPPS grew from sitting or hanging drops prepared by mixing 2  $\mu$ L protein (9.5 mg/ml in 50mM Tris-HCl, pH 7.5, 0.2M NaCl, 1mM EDTA) with 2 $\mu$ L of reservoir solution containing either 10-20% ethanol, 0.1M Tris-HCl, pH 8.5 or 4-5% PEG6000, 0.1M HEPES, pH 7.5. The drops were left to equilibrate at room temperature against 500 $\mu$ L of the reservoir solution. The crystals belong to the orthorhombic crystalline form having a space group  $P2_12_12_1$  with unit cell parameters:  $a = 59.6\text{\AA}$ ,  $b = 118.0\text{\AA}$ ,  $c = 178.2\text{\AA}$ , and two 60 kDa dimers in the asymmetric unit. Some crystals were found to belong to the orthorhombic crystalline form having a space group  $I2_12_12_1$  with the similar cell parameters as the primitive cell. In the primitive cell, a pseudo-translation of nearly  $1/2$ ,  $1/2$ ,  $1/2$  along the cell edges, results in a diffraction pattern in which the  $h + k + l = \text{odd}$  are, on the average, markedly weaker than the  $h + k + l = \text{even}$  reflections resulting in a pseudo body centered lattice. The crystals were quickly transferred to a solution of mother liquor containing 30% xylitol as cryo-protective agent and flash frozen under the cold stream before data collection. The Se-Met substituted protein was expressed in *E. coli* fed with an amino acid mixture that inhibited the endogenous biosynthesis of methionine and forced the uptake of selenium-labeled methionine from the medium. The protein was crystallized under similar conditions with the exception that the crystallization drops were flushed with argon gas before sealing them in order to prevent oxidation. The crystal structure of UPPS in complex with IPP was determined using native crystals soaked at room temperature for 20-30 minutes in mother liquor containing 2-3mM IPP and 2mM  $\text{MgCl}_2$ . The co-crystals of UPPS in complex with the substrate IPP crystals belong to the orthorhombic crystalline form having the space groups  $P2_12_12_1$  and  $I2_12_12_1$ , similar to the native crystal. The co-crystals of UPPS in complex with the substrate FPP were grown at room temperature from sitting drops prepared by mixing 2 $\mu$ L of protein solution ( $\sim 10\text{mg/ml}$ , 2mM FPP, 1mM  $\text{MgCl}_2$ , 50mM Tris-HCl pH 7.5 and 200mM NaCl) with 2 $\mu$ L of reservoir solution containing 100mM sodium cacodylate, pH 6.4, 120-240 mM sodium acetate. These crystals belong to the monoclinic crystalline form having a space group  $P2_1$  with unit cell dimensions  $a = 58.1\text{\AA}$ ,  $b = 44.6\text{\AA}$ ,  $c = 115.5\text{\AA}$ ,  $\beta = 98.7^\circ$ .

## 2.B. X-ray diffraction data collection

A native UPPS crystal structure was determined by multiwavelength anomalous diffraction, MAD, using the K absorption edge of selenium incorporated into the amino acid methionine. Three diffraction data sets to 2.3Å resolution were collected at the NSLS's  
5 X12C beamline. The wavelengths were determined by analyzing the x-ray fluorescence of the UPPS crystal around the selenium absorption edge. These correspond to the peak (0.9795Å), the inflection point (0.9791Å) and at a remote wavelength on the high-energy side of the edge (0.9500Å). Diffraction intensities from each wavelength were independently integrated, merged and scaled using DENZO/SCALEPACK (Otwinowsky, et  
10 al. (1999) *Methods in Enzymology* Vol. 267). Diffraction data from UPPS in complex with FPP or IPP were collected at the 17ID beamline at the Advanced Photon Source, APS, at Argonne National Laboratory, using 1.000Å wavelength.

## 2.C. Structure Determination

15 A selenium substructure was determined by automatic Patterson map peak search and peak correlation implemented in the program SOLVE (Terwilliger, T. C., and Berendsen, J. (1999) *Acta Crystallogr. D* 55: 849-861). A Fourier map was calculated to 2.7Å resolution using phases calculated from 15 of the possible 24 Se sites in the asymmetric unit. After solvent modification, this map afforded the determination of the  
20 boundaries of the four monomers and tracing of the polypeptide chains. The tracing was used to find the rotation and translation transformations used in 4-fold electron density averaging (CCP4, DM). The improved, averaged map was also used in tracing of the chains.

## 2.D. Model Building and Refinement

25 This averaged electron density map was of high quality and afforded the complete tracing of the four molecules using the interactive computer graphics program O (Jones, T.A. *et al.* (1991) *Acta Crystallogr. A* 47: 110-119). The initial model was refined against diffraction data collected at the remote wavelength by successive rounds of simulated annealing with torsion angle dynamics, positional refinement and restrained B-factor  
30 refinement using CNS (A. Brunger *et al.*, *Science*, 235: 458-460 (1987)) followed by manual intervention. The refinement and manual rebuilding was monitored by the quality of the 2Fo-Fc and Fo-Fc electron density maps and the value of the crystallographic R and  $R_{free}$ . At the beginning of the refinement, the four molecules in the asymmetric unit (A, B, C, and D) were forced to obey strict non-crystallographic symmetry. This constraint was  
35 released as the refinement proceeded.

A final R is 0.20 and the  $R_{\text{free}}$  is 0.25 for 53,642 reflections to 2.3Å resolution. The rms deviation from the reference bond lengths and bond angles (Engh & Huber (1991) *Acta Crystallogr. A* 47: 392-400) are 0.01 and 1.4, respectively. The refined model includes residues 17-72, 77-248 in molecule A, 17-72, 79-246 in molecule B, 17-73, 77-248 in molecule C and 18-73, 78-246 in molecule D according to the amino acid sequence SEQ ID NO:1. The N-terminal residues 1-16 were disordered in the four molecules. Also were disordered the residues in the vicinity of the loop formed by amino acids 72-80. A number of conserved amino acids that may form part of the active site (see below) are located in this region. The six residues 247-252 at the C-terminus were also disordered. In the refined model, all the main chain conformations fall in the "allowed" regions of the Ramachandran plot. Molecules A and B form one of the dimers and molecules C and D the second dimer in the asymmetric unit. The C $\alpha$ -carbon atoms of the two pairs of molecules in each dimer, molecules A and B, and C and D, superimpose with a rms deviation of 1.2Å and 1.1Å, respectively, with very large differences at the N- (6.1Å) and C-termini (1.5Å), the turn formed by residues 35-41 (1.2Å), the long helix formed by residues 79-104 (7.1Å), the short turn formed by residues 115-127 (2.2Å), and residues 157-171 (1.7Å) that form an  $\alpha$ -helix and a turn. Omitting these residues from the comparison gives a rms of 0.3Å or both pairs of molecules. The turn formed by residues 35-41 (1.2Å) in molecule A has no crystal contacts or contacts with the partner in the dimer, however, in molecule B it is making contacts with the same region in molecule D. The long helix from 79-104 is not making contacts in molecules A or D but in C is contacting residues in the region of B177, and in B is contacting D117 of a symmetry related molecule; this region leads to a disordered loop that may be involved in substrate binding. B115 region is in contact with symmetry related D119-D121, and D115 is contacting symmetry related B85-B88 region. A166 is in contact with symmetry related B240, C166 is in contact with symmetry related D240, but neither B166 nor D166 are making any crystal contacts.

A crystal structure of a UPPS in complex with FPP was determined by molecular replacement with the program package AMoRe (Navaza, J. (1994) *Acta Cryst. A* 50, 157-163) using the native structure as search model and refined as described before. The cross rotation and translation searches were carried using data from 20Å to 4Å resolution and a radius of integration of 20Å. The top two solutions of the cross rotation function corresponding to the two molecules in the dimer in the asymmetric unit were unambiguously discriminated from the noise peaks. The search for the correct translation for each molecule in the asymmetric unit produced a solution for the tetramer with an R-factor

of 0.60 and a correlation coefficient of 0.34 after rigid body refinement in. The crystal structure of the complex with IPP was determined by Fourier methods.

5 All documents cited herein and patent applications to which priority is claimed are incorporated by reference herein in their entirety. This invention is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description. Such modifications are intended to fall within the scope of the appended claims. The disclosures of the patents, patent applications and publications  
10 cited herein are incorporated by reference in their entirety.



## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Néstor O. Concha, and Cheryl A. Janson  
(ii) TITLE OF INVENTION: Novel UPPS Enzyme  
(iii) NUMBER OF SEQUENCES: 1  
(iv) CORRESPONDENCE ADDRESS:  
10 (A) ADDRESSEE: GlaxoSmithKline Corporation  
(B) STREET: 709 Swedeland Road - P.O. Box 1539  
(C) CITY: King of Prussia  
(D) STATE: Pennsylvania  
(E) COUNTRY: USA  
(F) ZIP: 19406-2799  
15  
(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM:  
20 (D) SOFTWARE:  
  
(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
25 (C) CLASSIFICATION:  
  
(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
30  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
  
(viii) ATTORNEY/AGENT INFORMATION:  
35 (A) NAME:  
(B) REGISTRATION NUMBER:  
(C) REFERENCE/DOCKET NUMBER:

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE:

(B) TELEFAX:

5

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 272 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: protein

## (iii) SEQUENCE DESCRIPTION: SEQ ID NO:1:

20

-20        -10        1        11        21  
MGSSHHHHHH SSSLVPRGSH MFGFFKKDKA VEVPTQVP AHIGIIMDGN

31        41        51        61        71  
GRWAKKRMQP RVFGHKAGME ALQTVTKAAN KLGVKVITVY AFSTENWTRP

25

81        91        101        111        121  
DQEVKFIMNL PVEFYDNYVP ELHANNVKIQ MIGETDRLPK QTFEALTKAE

30

131        141        151        161        171  
ELTKNNTGLI LNFALNYGGR AEITQALKLI SQDVLDKIN PGDITEELIG

181        191        201        211        221  
NYLFTQHLPK DLRDPDLIIR TSGELRLSNF LPWQGAYSEL YFTDTLWPDF

35

231        241        251  
DEAALQEAIL AYNRRHRRFG GV

Figure 1A

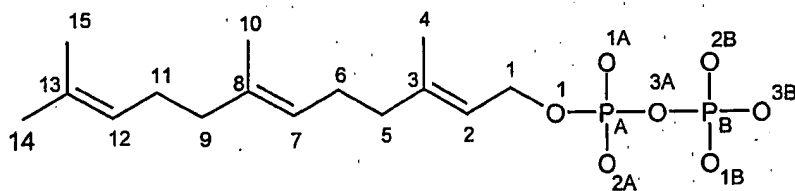


Figure 1B

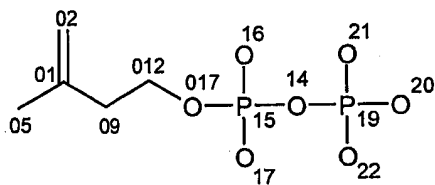


Figure 2A

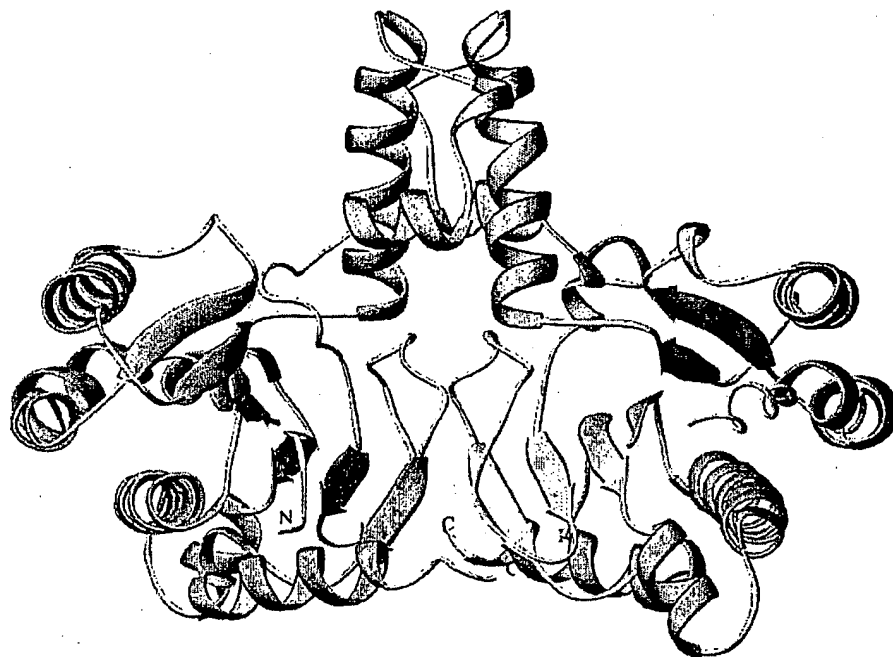


Figure 2B

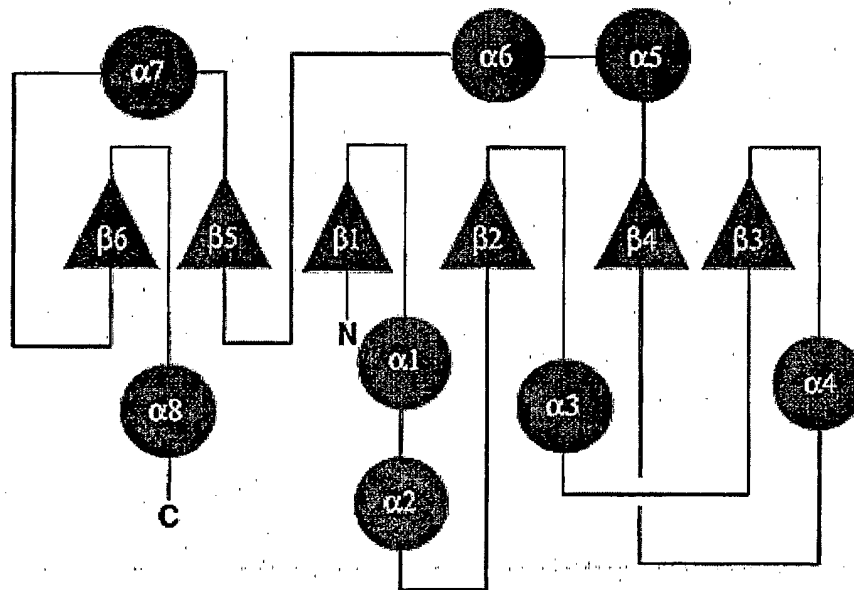
UPS ( *S. pneumoniae* )

Figure 3A

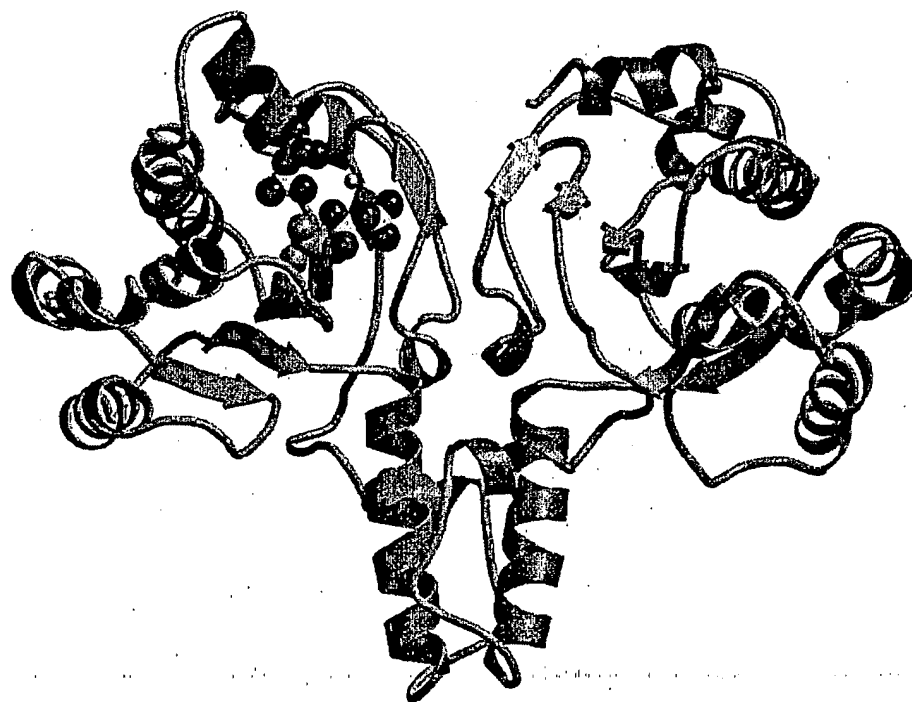


Figure 3B

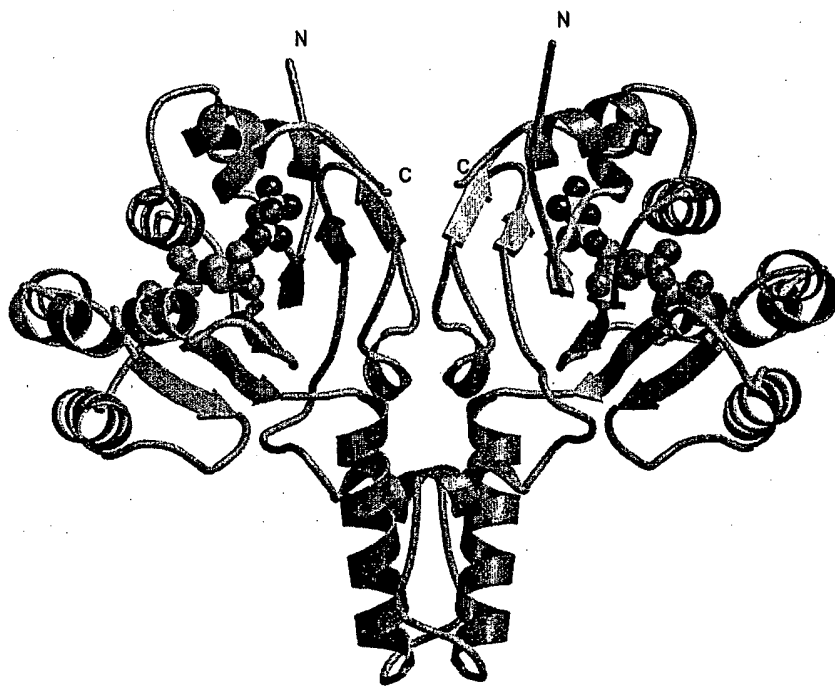




Figure 4A

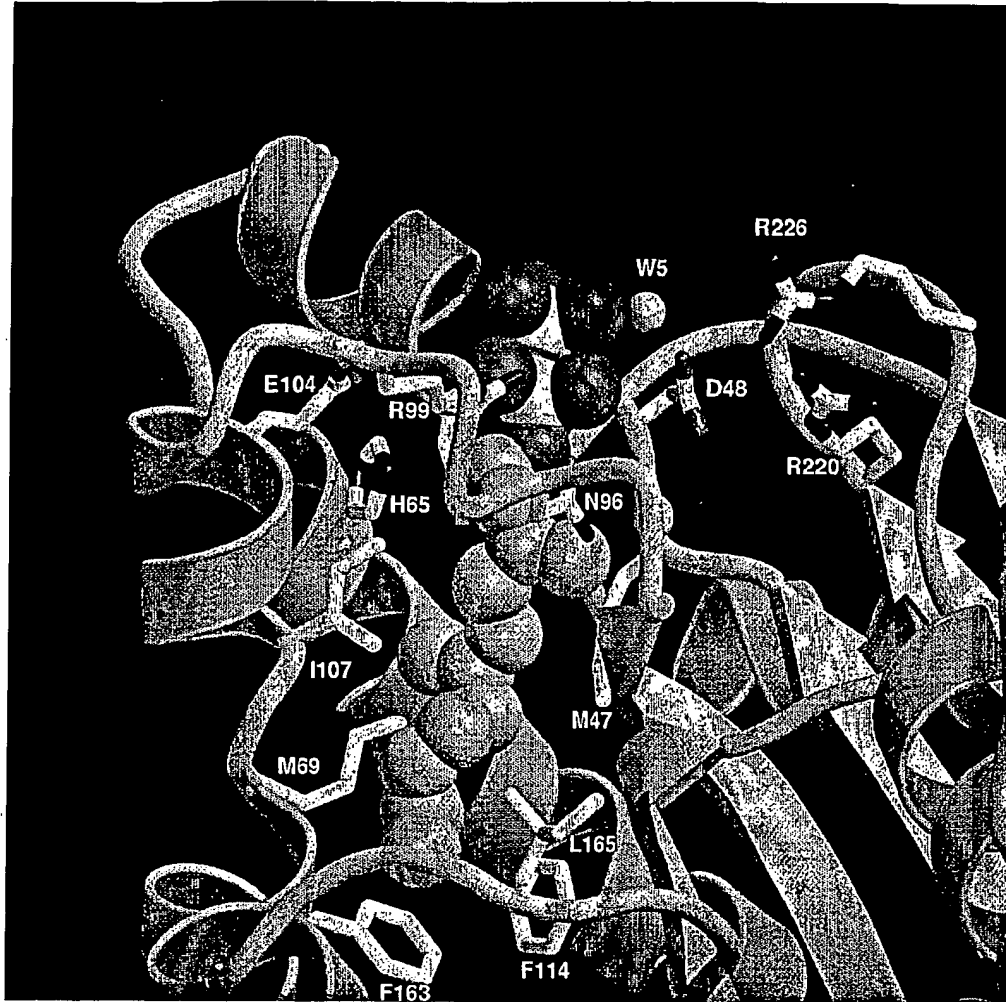


Figure 4B

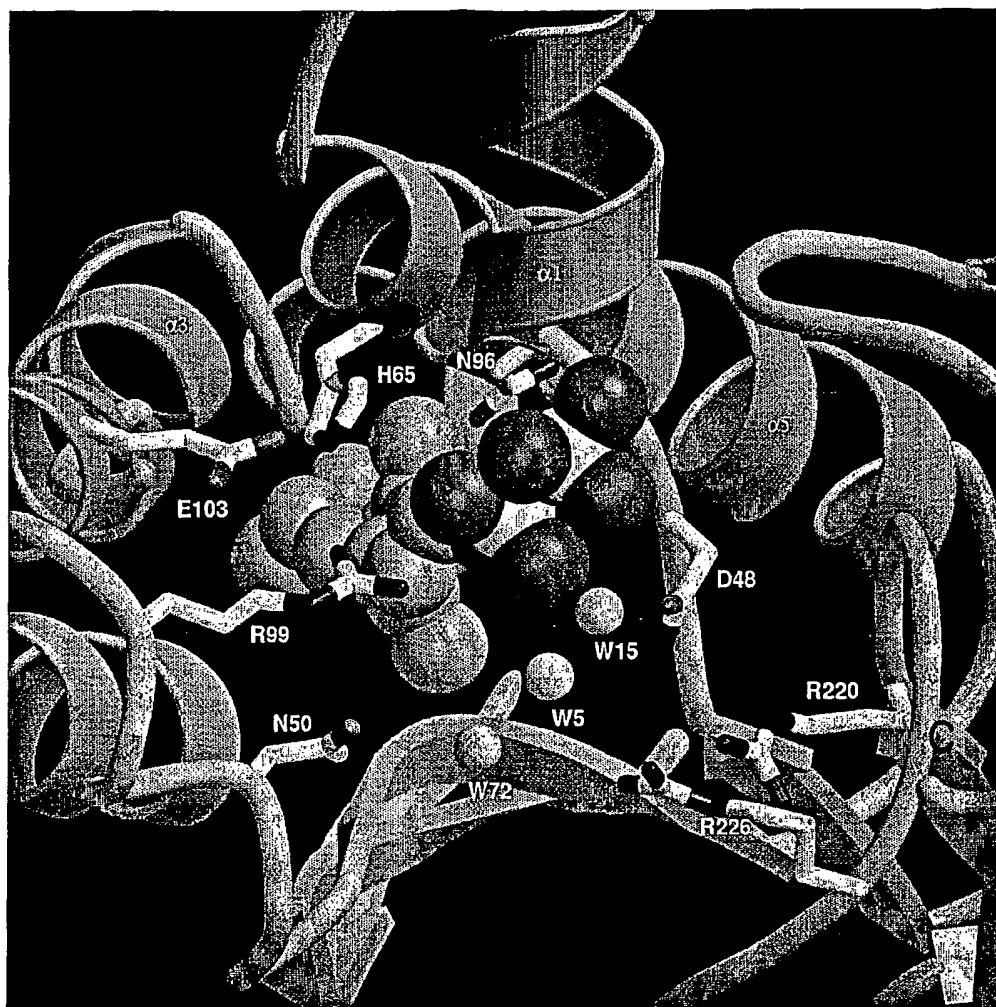
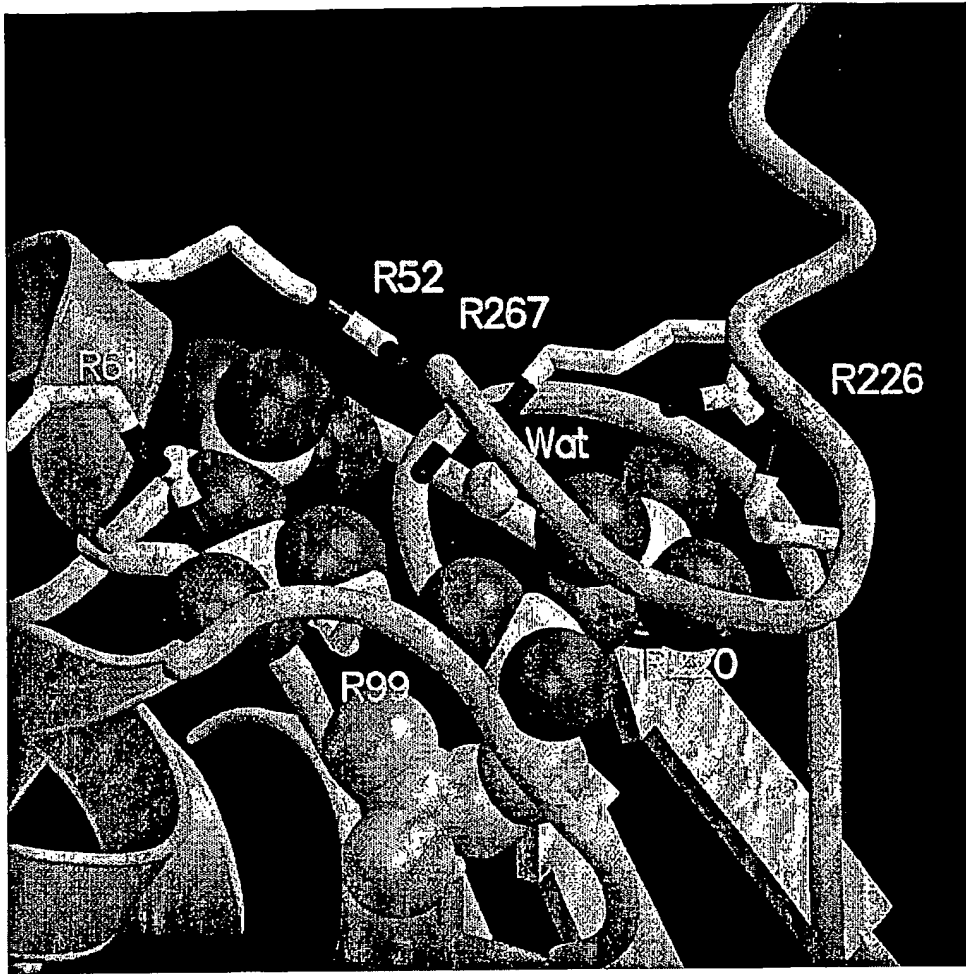


Figure 5



## TABLE I

Table IA. Atomic coordinates of native UPPS structure

5 Table IB. Atomic coordinates of active of UPPS in complex with FPP

Table IC. Atomic coordinates of active of UPPS in complex with IPP

## TABLE II

Table IIA. Interatomic distances in an active site of the native UPPS

10 Table IIB. Interatomic distances in an active site of UPPS in complex with FPP

Table IIC. Interatomic distances in an active site of UPPS in complex with IPP

## TABLE III

Table IIIA. Interatomic angles in an active site of the native UPPS

15 Table IIIB. Interatomic angles in an active of UPPS in complex with FPP

Table IIIC. Interatomic angles in an active of UPPS in complex with IPP

## Legend:

1. Under the heading ATOM appears a "atom number" (e.g. 1,2,3,4...etc) and the "atom name" (e.g. CA, CB, N,... etc) such that to each "atom name" in the coordinate list  
 20 corresponds an "atom number".
2. Under the heading RESIDUE appears a three-letter "residue name" (e.g. THR, ASP, etc), a "chain identifier" represented by a capital letter (e.g. A, B, C D, etc) and a "residue number", such that to each residue (or amino acid) in the amino acid sequence of the  
 25 particular protein in the structure corresponds a name that identifies it, a number according to its position along the amino acid sequence, and a chain name. The chain name identifies a particular molecule in the crystal structure. For instance, if there are more than one molecule that form the unit that is repeated throughout the crystal lattice, then each unit is identified  
 30 as molecule A, or molecule B, or molecule C, etc.
3. Under the headings X, Y, or Z appear the Cartesian coordinates of the atoms in the structure.

4. Under the heading OCC appears the "occupancy factor" for each atom. If the entity is present and observed in the structure then occupancy of 1.00 is assigned to it. If the atom is present but not observed, occupancy of 0.00 is assigned to it. Also, factors between 0.00 and 1.00 are also acceptable and represent the degree of confidence in observing that atom at a particular position.

5. Under the heading B appears the "B-factor" or "temperature factor" which can adopt, in principle, any value. It is meant to represent the atomic displacement around that position.

# 10 Table IA

## Atomic coordinates of native UPPS

CRYST1 59.600 118.000 178.200 90.00 90.00 90.00							
ATOM		RESIDUE		X	Y	Z	Occ B
1	CB	THR A	17	18.414	87.195	103.592	1.00 93.58
15	2	OG1	THR A	17	18.502	87.203	105.024 1.00 94.14
	3	CG2	THR A	17	17.190	88.014	103.149 1.00 93.23
	4	C	THR A	17	19.637	84.999	103.347 1.00 89.94
	5	O	THR A	17	20.525	85.538	104.017 1.00 91.11
	6	N	THR A	17	17.169	85.002	103.724 1.00 90.66
20	7	CA	THR A	17	18.311	85.723	103.077 1.00 91.60
	8	N	GLN A	18	19.761	83.783	102.808 1.00 86.41
	9	CA	GLN A	18	20.949	82.945	102.991 1.00 80.31
	10	CB	GLN A	18	22.219	83.757	102.767 1.00 83.93
	11	CG	GLN A	18	22.233	84.548	101.482 1.00 89.19
25	12	CD	GLN A	18	23.150	85.747	101.583 1.00 94.65
	13	OE1	GLN A	18	24.334	85.612	101.914 1.00 95.46
	14	NE2	GLN A	18	22.608	86.934	101.306 1.00 95.13
	15	C	GLN A	18	20.918	82.433	104.429 1.00 73.54
	16	O	GLN A	18	21.875	81.846	104.922 1.00 71.59
30	17	N	VAL A	19	19.793	82.678	105.085 1.00 64.52
	18	CA	VAL A	19	19.567	82.272	106.464 1.00 56.20
	19	CB	VAL A	19	18.912	83.445	107.244 1.00 53.44
	20	CG1	VAL A	19	18.089	82.935	108.392 1.00 51.55
	21	CG2	VAL A	19	19.991	84.383	107.750 1.00 55.06
35	22	C	VAL A	19	18.667	81.024	106.548 1.00 50.21
	23	O	VAL A	19	17.570	80.997	105.979 1.00 47.54
	24	N	PRO A	20	19.132	79.967	107.243 1.00 42.84
	25	CD	PRO A	20	20.450	79.772	107.880 1.00 36.61
	26	CA	PRO A	20	18.304	78.763	107.358 1.00 35.73
40	27	CB	PRO A	20	19.193	77.808	108.161 1.00 36.35

	28	CG	PRO	A	20	20.132	78.727	108.916	1.00	33.42
	29	C	PRO	A	20	16.998	79.119	108.063	1.00	35.84
	30	O	PRO	A	20	17.004	79.851	109.040	1.00	41.13
	31	N	ALA	A	21	15.877	78.607	107.572	1.00	34.58
5	32	CA	ALA	A	21	14.580	78.932	108.153	1.00	30.24
	33	CB	ALA	A	21	13.469	78.609	107.158	1.00	28.08
	34	C	ALA	A	21	14.256	78.267	109.474	1.00	35.80
	35	O	ALA	A	21	13.469	78.805	110.261	1.00	32.51
	36	N	HIS	A	22	14.811	77.076	109.694	1.00	30.51
10	37	CA	HIS	A	22	14.577	76.339	110.925	1.00	24.73
	38	CB	HIS	A	22	13.542	75.232	110.678	1.00	24.49
	39	CG	HIS	A	22	13.197	74.430	111.893	1.00	17.70
	40	CD2	HIS	A	22	13.751	74.389	113.130	1.00	23.53
	41	ND1	HIS	A	22	12.134	73.555	111.921	1.00	15.36
15	42	CE1	HIS	A	22	12.041	73.011	113.122	1.00	22.80
	43	NE2	HIS	A	22	13.010	73.502	113.878	1.00	19.49
	44	C	HIS	A	22	15.911	75.772	111.420	1.00	31.35
	45	O	HIS	A	22	16.583	74.987	110.731	1.00	29.44
	46	N	ILE	A	23	16.309	76.213	112.608	1.00	32.00
20	47	CA	ILE	A	23	17.561	75.789	113.215	1.00	28.24
	48	CB	ILE	A	23	18.429	76.991	113.554	1.00	28.68
	49	CG2	ILE	A	23	19.744	76.532	114.171	1.00	23.27
	50	CG1	ILE	A	23	18.652	77.826	112.294	1.00	30.89
	51	CD1	ILE	A	23	19.637	78.959	112.501	1.00	33.77
25	52	C	ILE	A	23	17.295	75.034	114.512	1.00	29.56
	53	O	ILE	A	23	16.616	75.551	115.412	1.00	24.41
	54	N	GLY	A	24	17.812	73.809	114.595	1.00	23.15
	55	CA	GLY	A	24	17.654	73.016	115.803	1.00	19.84
	56	C	GLY	A	24	18.910	73.238	116.624	1.00	24.53
30	57	O	GLY	A	24	19.996	73.315	116.044	1.00	22.45
	58	N	ILE	A	25	18.795	73.352	117.954	1.00	26.50
	59	CA	ILE	A	25	19.989	73.577	118.778	1.00	24.89
	60	CB	ILE	A	25	20.104	75.055	119.251	1.00	25.41
	61	CG2	ILE	A	25	21.464	75.292	119.914	1.00	21.04
35	62	CG1	ILE	A	25	19.944	76.012	118.067	1.00	28.76
	63	CD1	ILE	A	25	20.044	77.491	118.452	1.00	32.26
	64	C	ILE	A	25	20.036	72.712	120.031	1.00	26.29
	65	O	ILE	A	25	19.111	72.731	120.833	1.00	26.84
	66	N	ILE	A	26	21.120	71.965	120.208	1.00	25.54
40	67	CA	ILE	A	26	21.271	71.146	121.402	1.00	27.16
	68	CB	ILE	A	26	21.943	69.782	121.063	1.00	26.76
	69	CG2	ILE	A	26	22.035	68.919	122.318	1.00	20.62
	70	CG1	ILE	A	26	21.103	69.043	120.017	1.00	28.54

	71	CD1	ILE	A	26	21.659	67.702	119.623	1.00	28.49
	72	C	ILE	A	26	22.150	71.959	122.358	1.00	27.16
	73	O	ILE	A	26	23.348	72.075	122.162	1.00	24.98
	74	N	MET	A	27	21.543	72.551	123.378	1.00	31.61
5	75	CA	MET	A	27	22.293	73.374	124.325	1.00	32.29
	76	CB	MET	A	27	21.344	74.337	125.036	1.00	34.76
	77	CG	MET	A	27	20.458	75.121	124.084	1.00	39.19
	78	SD	MET	A	27	19.237	76.248	124.852	1.00	43.39
	79	CE	MET	A	27	18.191	75.134	125.772	1.00	18.61
10	80	C	MET	A	27	23.016	72.498	125.348	1.00	34.24
	81	O	MET	A	27	22.438	72.057	126.337	1.00	37.76
	82	N	ASP	A	28	24.289	72.247	125.096	1.00	35.03
	83	CA	ASP	A	28	25.090	71.407	125.966	1.00	32.47
	84	CB	ASP	A	28	25.640	70.232	125.159	1.00	34.38
15	85	CG	ASP	A	28	26.173	69.105	126.036	1.00	40.92
	86	OD1	ASP	A	28	26.213	69.270	127.278	1.00	42.58
	87	OD2	ASP	A	28	26.547	68.050	125.474	1.00	38.43
	88	C	ASP	A	28	26.246	72.251	126.461	1.00	32.33
	89	O	ASP	A	28	26.677	73.167	125.764	1.00	27.95
20	90	N	GLY	A	29	26.740	71.949	127.656	1.00	29.74
	91	CA	GLY	A	29	27.875	72.689	128.182	1.00	37.03
	92	C	GLY	A	29	27.680	73.527	129.436	1.00	38.13
	93	O	GLY	A	29	28.664	73.928	130.054	1.00	42.42
	94	N	ASN	A	30	26.436	73.796	129.818	1.00	37.31
25	95	CA	ASN	A	30	26.161	74.607	131.000	1.00	39.04
	96	CB	ASN	A	30	24.671	74.602	131.300	1.00	36.01
	97	CG	ASN	A	30	23.874	75.303	130.228	1.00	37.46
	98	OD1	ASN	A	30	22.652	75.356	130.280	1.00	47.26
	99	ND2	ASN	A	30	24.568	75.856	129.250	1.00	40.27
30	100	C	ASN	A	30	26.934	74.167	132.229	1.00	40.31
	101	O	ASN	A	30	27.595	74.980	132.873	1.00	39.08
	102	N	GLY	A	31	26.855	72.879	132.553	1.00	42.35
	103	CA	GLY	A	31	27.575	72.369	133.710	1.00	42.40
	104	C	GLY	A	31	29.079	72.587	133.617	1.00	43.17
35	105	O	GLY	A	31	29.697	73.121	134.539	1.00	39.84
	106	N	ARG	A	32	29.659	72.168	132.494	1.00	45.90
	107	CA	ARG	A	32	31.092	72.294	132.234	1.00	47.63
	108	CB	ARG	A	32	31.393	71.837	130.810	1.00	47.86
	109	CG	ARG	A	32	32.544	70.865	130.693	1.00	56.91
40	110	CD	ARG	A	32	32.571	70.243	129.307	1.00	61.73
	111	NE	ARG	A	32	33.821	70.517	128.603	1.00	69.19
	112	CZ	ARG	A	32	34.004	70.310	127.301	1.00	72.54
	113	NH1	ARG	A	32	33.015	69.827	126.554	1.00	72.99

	114	NH2	ARG	A	32	35.173	70.594	126.743	1.00	72.13
	115	C	ARG	A	32	31.516	73.743	132.406	1.00	47.36
	116	O	ARG	A	32	32.564	74.047	132.984	1.00	46.24
	117	N	TRP	A	33	30.668	74.630	131.907	1.00	46.56
5	118	CA	TRP	A	33	30.897	76.063	131.968	1.00	46.35
	119	CB	TRP	A	33	29.789	76.771	131.191	1.00	45.33
	120	CG	TRP	A	33	29.962	78.233	131.043	1.00	48.41
	121	CD2	TRP	A	33	29.468	79.242	131.923	1.00	48.75
	122	CE2	TRP	A	33	29.797	80.489	131.352	1.00	49.59
10	123	CE3	TRP	A	33	28.774	79.214	133.143	1.00	52.10
	124	CD1	TRP	A	33	30.566	78.884	130.010	1.00	46.04
	125	NE1	TRP	A	33	30.466	80.238	130.185	1.00	49.62
	126	CZ2	TRP	A	33	29.453	81.705	131.954	1.00	51.56
	127	CZ3	TRP	A	33	28.431	80.425	133.743	1.00	52.07
15	128	CH2	TRP	A	33	28.771	81.653	133.145	1.00	52.75
	129	C	TRP	A	33	30.928	76.554	133.417	1.00	46.64
	130	O	TRP	A	33	31.821	77.308	133.804	1.00	47.86
	131	N	ALA	A	34	29.951	76.134	134.214	1.00	46.47
	132	CA	ALA	A	34	29.895	76.541	135.616	1.00	45.91
20	133	CB	ALA	A	34	28.668	75.952	136.285	1.00	44.55
	134	C	ALA	A	34	31.151	76.091	136.353	1.00	46.40
	135	O	ALA	A	34	31.833	76.886	136.993	1.00	45.15
	136	N	LYS	A	35	31.461	74.809	136.255	1.00	50.44
	137	CA	LYS	A	35	32.633	74.275	136.920	1.00	57.01
25	138	CB	LYS	A	35	32.849	72.817	136.516	1.00	59.31
	139	CG	LYS	A	35	33.962	72.150	137.285	1.00	64.17
	140	CD	LYS	A	35	34.135	70.704	136.871	1.00	67.56
	141	CE	LYS	A	35	35.217	70.031	137.705	1.00	71.91
	142	NZ	LYS	A	35	35.386	68.592	137.351	1.00	74.18
30	143	C	LYS	A	35	33.883	75.100	136.615	1.00	60.35
	144	O	LYS	A	35	34.630	75.437	137.528	1.00	65.64
	145	N	LYS	A	36	34.111	75.432	135.343	1.00	61.78
	146	CA	LYS	A	36	35.283	76.231	134.963	1.00	61.26
	147	CB	LYS	A	36	35.263	76.571	133.464	1.00	66.65
35	148	CG	LYS	A	36	35.750	75.462	132.547	1.00	69.63
	149	CD	LYS	A	36	35.772	75.918	131.091	1.00	73.05
	150	CE	LYS	A	36	36.190	74.773	130.175	1.00	77.08
	151	NZ	LYS	A	36	36.137	75.147	128.736	1.00	78.10
	152	C	LYS	A	36	35.361	77.528	135.752	1.00	59.62
40	153	O	LYS	A	36	36.444	77.957	136.132	1.00	58.71
	154	N	ARG	A	37	34.204	78.147	135.975	1.00	59.80
	155	CA	ARG	A	37	34.090	79.396	136.718	1.00	57.35
	156	CB	ARG	A	37	32.776	80.105	136.376	1.00	59.57



	157	CG	ARG	A	37	32.527	80.387	134.902	1.00	63.20
	158	CD	ARG	A	37	33.261	81.621	134.440	1.00	66.92
	159	NE	ARG	A	37	32.981	81.948	133.044	1.00	70.08
	160	CZ	ARG	A	37	33.178	81.114	132.027	1.00	74.26
5	161	NH1	ARG	A	37	33.649	79.893	132.247	1.00	73.92
	162	NH2	ARG	A	37	32.926	81.506	130.783	1.00	75.48
	163	C	ARG	A	37	34.096	79.111	138.220	1.00	60.36
	164	O	ARG	A	37	33.850	80.006	139.026	1.00	63.86
	165	N	MET	A	38	34.345	77.863	138.599	1.00	62.29
10	166	CA	MET	A	38	34.369	77.489	140.011	1.00	64.24
	167	CB	MET	A	38	35.506	78.227	140.724	1.00	67.10
	168	CG	MET	A	38	36.885	77.800	140.280	0.50	70.38
	169	SD	MET	A	38	37.169	76.085	140.705	0.50	77.34
	170	CE	MET	A	38	38.285	76.262	142.112	0.50	76.14
15	171	C	MET	A	38	33.050	77.799	140.716	1.00	63.85
	172	O	MET	A	38	33.003	77.880	141.939	1.00	65.90
	173	N	GLN	A	39	31.985	77.974	139.944	1.00	63.31
	174	CA	GLN	A	39	30.671	78.290	140.492	1.00	62.45
	175	CB	GLN	A	39	30.023	79.381	139.648	1.00	61.29
20	176	CG	GLN	A	39	30.575	80.745	139.923	1.00	69.13
	177	CD	GLN	A	39	30.115	81.260	141.266	1.00	76.78
	178	OE1	GLN	A	39	28.943	81.601	141.444	1.00	81.67
	179	NE2	GLN	A	39	31.026	81.303	142.228	1.00	80.44
	180	C	GLN	A	39	29.767	77.063	140.536	1.00	62.86
25	181	O	GLN	A	39	30.064	76.051	139.915	1.00	63.48
	182	N	PRO	A	40	28.649	77.133	141.279	1.00	64.92
	183	CD	PRO	A	40	28.105	78.262	142.059	1.00	65.41
	184	CA	PRO	A	40	27.753	75.972	141.343	1.00	65.47
	185	CB	PRO	A	40	26.764	76.367	142.442	1.00	62.80
30	186	CG	PRO	A	40	26.657	77.854	142.265	1.00	64.53
	187	C	PRO	A	40	27.072	75.728	139.987	1.00	65.74
	188	O	PRO	A	40	26.856	76.675	139.219	1.00	64.28
	189	N	ARG	A	41	26.747	74.467	139.694	1.00	64.20
	190	CA	ARG	A	41	26.098	74.111	138.434	1.00	66.35
35	191	CB	ARG	A	41	25.553	72.678	138.478	1.00	69.33
	192	CG	ARG	A	41	26.592	71.590	138.246	1.00	78.61
	193	CD	ARG	A	41	25.997	70.436	137.431	1.00	86.11
	194	NE	ARG	A	41	25.524	70.896	136.120	1.00	92.86
	195	CZ	ARG	A	41	24.937	70.125	135.204	1.00	95.17
40	196	NH1	ARG	A	41	24.737	68.836	135.439	1.00	98.23
	197	NH2	ARG	A	41	24.542	70.646	134.048	1.00	93.83
	198	C	ARG	A	41	24.956	75.058	138.088	1.00	65.18
	199	O	ARG	A	41	24.770	75.425	136.927	1.00	65.36

	200	N	VAL A	42	24.188	75.441	139.101	1.00	63.07
	201	CA	VAL A	42	23.067	76.347	138.919	1.00	60.84
	202	CB	VAL A	42	22.500	76.791	140.269	1.00	63.29
	203	CG1	VAL A	42	21.505	77.925	140.071	1.00	63.95
5	204	CG2	VAL A	42	21.842	75.605	140.958	1.00	67.91
	205	C	VAL A	42	23.482	77.586	138.155	1.00	59.87
	206	O	VAL A	42	22.743	78.074	137.304	1.00	59.07
	207	N	PHE A	43	24.671	78.090	138.469	1.00	59.46
	208	CA	PHE A	43	25.192	79.289	137.829	1.00	60.02
10	209	CB	PHE A	43	26.591	79.604	138.385	1.00	62.61
	210	CG	PHE A	43	27.054	81.007	138.107	1.00	67.33
	211	CD1	PHE A	43	26.269	82.099	138.478	1.00	68.38
	212	CD2	PHE A	43	28.264	81.242	137.449	1.00	70.16
	213	CE1	PHE A	43	26.680	83.407	138.191	1.00	70.34
15	214	CE2	PHE A	43	28.686	82.543	137.157	1.00	68.91
	215	CZ	PHE A	43	27.891	83.626	137.528	1.00	69.60
	216	C	PHE A	43	25.230	79.102	136.307	1.00	56.05
	217	O	PHE A	43	24.746	79.949	135.552	1.00	52.49
	218	N	GLY A	44	25.792	77.978	135.872	1.00	54.61
20	219	CA	GLY A	44	25.881	77.683	134.452	1.00	53.75
	220	C	GLY A	44	24.536	77.695	133.753	1.00	52.38
	221	O	GLY A	44	24.414	78.158	132.625	1.00	54.02
	222	N	HIS A	45	23.504	77.199	134.415	1.00	54.75
	223	CA	HIS A	45	22.207	77.191	133.777	1.00	54.21
25	224	CB	HIS A	45	21.240	76.279	134.528	1.00	57.02
	225	CG	HIS A	45	21.348	74.851	134.097	1.00	63.86
	226	CD2	HIS A	45	20.681	74.161	133.139	1.00	63.65
	227	ND1	HIS A	45	22.343	74.012	134.549	1.00	63.95
	228	CE1	HIS A	45	22.291	72.871	133.887	1.00	61.59
30	229	NE2	HIS A	45	21.292	72.937	133.024	1.00	63.72
	230	C	HIS A	45	21.619	78.562	133.575	1.00	53.07
	231	O	HIS A	45	20.935	78.796	132.577	1.00	54.86
	232	N	LYS A	46	21.875	79.484	134.496	1.00	50.85
	233	CA	LYS A	46	21.341	80.827	134.309	1.00	49.20
35	234	CB	LYS A	46	21.469	81.647	135.596	1.00	53.63
	235	CG	LYS A	46	20.468	81.185	136.648	1.00	60.57
	236	CD	LYS A	46	20.600	81.921	137.965	1.00	65.48
	237	CE	LYS A	46	19.666	81.315	139.006	1.00	65.75
	238	NZ	LYS A	46	19.786	81.997	140.319	1.00	66.82
40	239	C	LYS A	46	22.091	81.470	133.151	1.00	42.28
	240	O	LYS A	46	21.508	82.170	132.331	1.00	46.03
	241	N	ALA A	47	23.386	81.209	133.071	1.00	38.72
	242	CA	ALA A	47	24.177	81.749	131.983	1.00	38.08

	243	CB	ALA A	47	25.634	81.331	132.153	1.00	36.54
	244	C	ALA A	47	23.592	81.169	130.691	1.00	41.82
	245	O	ALA A	47	23.613	81.801	129.625	1.00	42.67
	246	N	GLY A	48	23.059	79.955	130.809	1.00	37.99
5	247	CA	GLY A	48	22.467	79.286	129.671	1.00	39.35
	248	C	GLY A	48	21.180	79.921	129.164	1.00	42.61
	249	O	GLY A	48	20.954	79.943	127.950	1.00	42.20
	250	N	MET A	49	20.330	80.421	130.068	1.00	42.02
	251	CA	MET A	49	19.071	81.054	129.659	1.00	43.54
10	252	CB	MET A	49	18.151	81.303	130.865	1.00	43.46
	253	CG	MET A	49	17.787	80.066	131.668	0.50	43.91
	254	SD	MET A	49	16.447	80.362	132.865	0.50	50.86
	255	CE	MET A	49	17.404	80.914	134.277	0.50	47.30
	256	C	MET A	49	19.460	82.382	129.018	1.00	45.42
15	257	O	MET A	49	18.838	82.843	128.049	1.00	43.63
	258	N	GLU A	50	20.510	82.981	129.572	1.00	43.49
	259	CA	GLU A	50	21.035	84.231	129.058	1.00	45.80
	260	CB	GLU A	50	22.293	84.641	129.829	1.00	48.10
	261	CG	GLU A	50	22.023	85.475	131.063	1.00	60.89
20	262	CD	GLU A	50	21.662	86.904	130.716	1.00	67.75
	263	OE1	GLU A	50	22.528	87.602	130.137	1.00	70.54
	264	OE2	GLU A	50	20.519	87.322	131.017	1.00	68.32
	265	C	GLU A	50	21.392	83.976	127.608	1.00	41.06
	266	O	GLU A	50	20.943	84.687	126.715	1.00	40.41
25	267	N	ALA A	51	22.213	82.957	127.389	1.00	37.44
	268	CA	ALA A	51	22.624	82.582	126.044	1.00	35.18
	269	CB	ALA A	51	23.406	81.295	126.093	1.00	32.93
	270	C	ALA A	51	21.396	82.403	125.153	1.00	35.31
	271	O	ALA A	51	21.337	82.946	124.042	1.00	35.44
30	272	N	LEU A	52	20.409	81.654	125.641	1.00	31.44
	273	CA	LEU A	52	19.212	81.421	124.844	1.00	37.68
	274	CB	LEU A	52	18.217	80.499	125.559	1.00	33.73
	275	CG	LEU A	52	16.936	80.245	124.741	1.00	35.94
	276	CD1	LEU A	52	17.281	79.633	123.392	1.00	28.69
35	277	CD2	LEU A	52	16.006	79.313	125.504	1.00	30.87
	278	C	LEU A	52	18.527	82.725	124.486	1.00	39.83
	279	O	LEU A	52	18.235	82.966	123.316	1.00	41.72
	280	N	GLN A	53	18.276	83.569	125.483	1.00	41.29
	281	CA	GLN A	53	17.627	84.855	125.224	1.00	38.17
40	282	CB	GLN A	53	17.621	85.736	126.475	1.00	37.50
	283	CG	GLN A	53	16.823	87.019	126.283	1.00	34.75
	284	CD	GLN A	53	15.328	86.803	126.441	1.00	41.28
	285	OE1	GLN A	53	14.826	85.683	126.284	1.00	37.82

	286	NE2	GLN	A	53	14.601	87.882	126.747	1.00	43.24
	287	C	GLN	A	53	18.320	85.625	124.104	1.00	35.35
	288	O	GLN	A	53	17.670	86.092	123.173	1.00	39.14
	289	N	THR	A	54	19.639	85.765	124.185	1.00	35.55
5	290	CA	THR	A	54	20.349	86.510	123.147	1.00	39.49
	291	CB	THR	A	54	21.778	86.877	123.573	1.00	34.39
	292	OG1	THR	A	54	22.699	86.357	122.612	1.00	37.55
	293	CG2	THR	A	54	22.096	86.332	124.914	1.00	35.25
	294	C	THR	A	54	20.421	85.800	121.788	1.00	43.21
10	295	O	THR	A	54	20.531	86.460	120.743	1.00	47.35
	296	N	VAL	A	55	20.373	84.468	121.789	1.00	38.92
	297	CA	VAL	A	55	20.410	83.743	120.527	1.00	34.48
	298	CB	VAL	A	55	20.832	82.242	120.712	1.00	33.78
	299	CG1	VAL	A	55	20.427	81.439	119.487	1.00	30.66
15	300	CG2	VAL	A	55	22.341	82.132	120.914	1.00	25.19
	301	C	VAL	A	55	19.028	83.806	119.875	1.00	33.18
	302	O	VAL	A	55	18.928	83.961	118.656	1.00	30.59
	303	N	THR	A	56	17.958	83.701	120.665	1.00	28.69
	304	CA	THR	A	56	16.646	83.748	120.041	1.00	35.13
20	305	CB	THR	A	56	15.506	83.123	120.923	1.00	38.19
	306	OG1	THR	A	56	14.478	84.092	121.141	1.00	36.89
	307	CG2	THR	A	56	16.023	82.599	122.227	1.00	31.64
	308	C	THR	A	56	16.263	85.154	119.611	1.00	39.44
	309	O	THR	A	56	15.424	85.331	118.731	1.00	45.04
25	310	N	LYS	A	57	16.884	86.158	120.214	1.00	44.77
	311	CA	LYS	A	57	16.612	87.546	119.836	1.00	45.55
	312	CB	LYS	A	57	17.077	88.521	120.933	1.00	46.12
	313	CG	LYS	A	57	15.959	89.004	121.868	1.00	47.10
	314	CD	LYS	A	57	16.509	89.555	123.189	1.00	52.73
30	315	CE	LYS	A	57	17.626	90.587	122.987	1.00	53.56
	316	NZ	LYS	A	57	18.195	91.049	124.283	1.00	53.28
	317	C	LYS	A	57	17.364	87.817	118.541	1.00	43.53
	318	O	LYS	A	57	16.792	88.340	117.579	1.00	43.78
	319	N	ALA	A	58	18.644	87.452	118.513	1.00	40.56
35	320	CA	ALA	A	58	19.446	87.654	117.307	1.00	46.38
	321	CB	ALA	A	58	20.894	87.252	117.563	1.00	39.19
	322	C	ALA	A	58	18.882	86.864	116.114	1.00	48.40
	323	O	ALA	A	58	18.774	87.392	115.003	1.00	51.66
	324	N	ALA	A	59	18.516	85.604	116.349	1.00	48.78
40	325	CA	ALA	A	59	17.971	84.757	115.291	1.00	48.87
	326	CB	ALA	A	59	17.621	83.374	115.840	1.00	45.90
	327	C	ALA	A	59	16.731	85.395	114.691	1.00	47.59
	328	O	ALA	A	59	16.611	85.498	113.473	1.00	45.52

	329	N	ASN	A	60	15.809	85.812	115.558	1.00	51.23
	330	CA	ASN	A	60	14.558	86.447	115.130	1.00	51.13
	331	CB	ASN	A	60	13.742	86.897	116.346	1.00	51.74
	332	CG	ASN	A	60	12.412	87.549	115.964	1.00	49.53
5	333	OD1	ASN	A	60	11.654	87.037	115.132	1.00	47.90
	334	ND2	ASN	A	60	12.118	88.674	116.592	1.00	44.22
	335	C	ASN	A	60	14.820	87.637	114.230	1.00	48.73
	336	O	ASN	A	60	14.028	87.936	113.345	1.00	45.02
	337	N	LYS	A	61	15.948	88.300	114.451	1.00	51.94
10	338	CA	LYS	A	61	16.300	89.456	113.652	1.00	54.61
	339	CB	LYS	A	61	17.292	90.346	114.400	1.00	57.79
	340	CG	LYS	A	61	16.649	91.109	115.546	1.00	67.28
	341	CD	LYS	A	61	17.530	92.256	116.020	1.00	75.79
	342	CE	LYS	A	61	16.819	93.110	117.071	1.00	78.75
15	343	NZ	LYS	A	61	17.631	94.311	117.454	1.00	81.03
	344	C	LYS	A	61	16.864	89.087	112.301	1.00	53.93
	345	O	LYS	A	61	16.414	89.613	111.287	1.00	58.20
	346	N	LEU	A	62	17.844	88.186	112.283	1.00	51.98
	347	CA	LEU	A	62	18.472	87.758	111.034	1.00	46.07
20	348	CB	LEU	A	62	19.550	86.718	111.314	1.00	49.94
	349	CG	LEU	A	62	20.782	87.190	112.083	1.00	51.21
	350	CD1	LEU	A	62	21.713	86.006	112.341	1.00	53.01
	351	CD2	LEU	A	62	21.491	88.255	111.282	1.00	50.66
	352	C	LEU	A	62	17.489	87.189	110.024	1.00	41.50
25	353	O	LEU	A	62	17.825	87.046	108.853	1.00	43.64
	354	N	GLY	A	63	16.286	86.854	110.483	1.00	39.45
	355	CA	GLY	A	63	15.269	86.303	109.599	1.00	40.08
	356	C	GLY	A	63	14.873	84.837	109.819	1.00	41.98
	357	O	GLY	A	63	14.031	84.290	109.090	1.00	37.96
30	358	N	VAL	A	64	15.461	84.195	110.823	1.00	38.22
	359	CA	VAL	A	64	15.152	82.801	111.104	1.00	31.62
	360	CB	VAL	A	64	16.059	82.262	112.210	1.00	30.82
	361	CG1	VAL	A	64	15.621	80.858	112.599	1.00	28.03
	362	CG2	VAL	A	64	17.517	82.296	111.736	1.00	22.55
35	363	C	VAL	A	64	13.702	82.684	111.523	1.00	33.79
	364	O	VAL	A	64	13.229	83.476	112.323	1.00	39.62
	365	N	LYS	A	65	13.003	81.696	110.967	1.00	31.95
	366	CA	LYS	A	65	11.591	81.461	111.244	1.00	34.02
	367	CB	LYS	A	65	10.927	80.812	110.024	1.00	32.44
40	368	CG	LYS	A	65	10.871	81.681	108.764	1.00	42.92
	369	CD	LYS	A	65	9.713	82.678	108.848	1.00	49.78
	370	CE	LYS	A	65	9.577	83.506	107.585	1.00	53.74
	371	NZ	LYS	A	65	8.520	84.561	107.723	1.00	59.87

	372	C	LYS	A	65	11.326	80.573	112.464	1.00	39.61
	373	O	LYS	A	65	10.357	80.776	113.198	1.00	40.68
	374	N	VAL	A	66	12.175	79.570	112.663	1.00	39.19
	375	CA	VAL	A	66	11.995	78.654	113.761	1.00	30.33
5	376	CB	VAL	A	66	11.257	77.357	113.300	1.00	37.75
	377	CG1	VAL	A	66	11.048	76.410	114.499	1.00	31.00
	378	CG2	VAL	A	66	9.918	77.684	112.654	1.00	24.14
	379	C	VAL	A	66	13.319	78.222	114.365	1.00	33.61
	380	O	VAL	A	66	14.350	78.141	113.688	1.00	34.35
10	381	N	ILE	A	67	13.292	78.001	115.669	1.00	32.90
	382	CA	ILE	A	67	14.434	77.463	116.376	1.00	32.43
	383	CB	ILE	A	67	15.344	78.515	117.056	1.00	34.82
	384	CG2	ILE	A	67	15.968	79.389	116.012	1.00	35.40
	385	CG1	ILE	A	67	14.575	79.331	118.090	1.00	36.83
15	386	CD1	ILE	A	67	15.495	80.199	118.950	1.00	35.47
	387	C	ILE	A	67	13.838	76.535	117.414	1.00	31.59
	388	O	ILE	A	67	12.966	76.925	118.217	1.00	28.43
	389	N	THR	A	68	14.259	75.279	117.324	1.00	30.34
	390	CA	THR	A	68	13.826	74.247	118.238	1.00	27.05
20	391	CB	THR	A	68	13.414	72.998	117.485	1.00	32.54
	392	OG1	THR	A	68	12.301	73.329	116.645	1.00	34.13
	393	CG2	THR	A	68	12.994	71.895	118.444	1.00	23.95
	394	C	THR	A	68	15.055	74.044	119.096	1.00	30.90
	395	O	THR	A	68	16.152	73.725	118.610	1.00	30.17
25	396	N	VAL	A	69	14.867	74.281	120.384	1.00	26.05
	397	CA	VAL	A	69	15.965	74.232	121.310	1.00	31.73
	398	CB	VAL	A	69	16.030	75.624	122.020	1.00	36.66
	399	CG1	VAL	A	69	15.247	75.618	123.317	1.00	36.58
	400	CG2	VAL	A	69	17.451	76.051	122.189	1.00	43.81
30	401	C	VAL	A	69	15.806	73.040	122.249	1.00	34.67
	402	O	VAL	A	69	14.691	72.705	122.673	1.00	33.61
	403	N	TYR	A	70	16.923	72.372	122.531	1.00	35.43
	404	CA	TYR	A	70	16.917	71.183	123.369	1.00	35.78
	405	CB	TYR	A	70	17.140	69.957	122.470	1.00	39.72
35	406	CG	TYR	A	70	16.976	68.602	123.133	1.00	38.18
	407	CD1	TYR	A	70	15.874	68.325	123.938	1.00	38.55
	408	CE1	TYR	A	70	15.718	67.078	124.539	1.00	39.94
	409	CD2	TYR	A	70	17.923	67.590	122.936	1.00	39.38
	410	CE2	TYR	A	70	17.774	66.333	123.521	1.00	43.62
40	411	CZ	TYR	A	70	16.666	66.085	124.327	1.00	48.01
	412	OH	TYR	A	70	16.508	64.850	124.921	1.00	53.21
	413	C	TYR	A	70	17.974	71.263	124.465	1.00	37.56
	414	O	TYR	A	70	19.156	71.441	124.187	1.00	40.77

	415	N	ALA	A	71	17.531	71.151	125.710	1.00	40.93
	416	CA	ALA	A	71	18.425	71.209	126.864	1.00	49.88
	417	CB	ALA	A	71	17.673	71.747	128.054	1.00	54.71
	418	C	ALA	A	71	18.911	69.801	127.151	1.00	52.84
5	419	O	ALA	A	71	18.166	68.998	127.700	1.00	55.15
	420	N	PHE	A	72	20.158	69.502	126.789	1.00	55.42
	421	CA	PHE	A	72	20.692	68.160	126.967	1.00	53.45
	422	CB	PHE	A	72	20.372	67.333	125.726	1.00	58.68
	423	CG	PHE	A	72	20.566	65.859	125.906	1.00	64.09
10	424	CD1	PHE	A	72	19.629	65.104	126.606	1.00	69.96
	425	CD2	PHE	A	72	21.672	65.217	125.357	1.00	66.47
	426	CE1	PHE	A	72	19.785	63.722	126.755	1.00	74.22
	427	CE2	PHE	A	72	21.845	63.840	125.497	1.00	71.85
	428	CZ	PHE	A	72	20.896	63.086	126.198	1.00	75.48
15	429	C	PHE	A	72	22.194	68.149	127.189	1.00	55.50
	430	O	PHE	A	72	22.883	67.237	126.726	1.00	51.11
	431	N	TRP	A	77	29.049	61.597	135.724	0.50	83.76
	432	CA	TRP	A	77	28.116	61.405	136.830	0.50	83.83
	433	CB	TRP	A	77	28.302	62.503	137.881	0.50	83.34
20	434	CG	TRP	A	77	28.029	63.883	137.360	0.50	83.40
	435	CD2	TRP	A	77	26.892	64.702	137.659	0.50	83.20
	436	CE2	TRP	A	77	27.041	65.905	136.934	0.50	82.72
	437	CE3	TRP	A	77	25.762	64.537	138.470	0.50	82.38
	438	CD1	TRP	A	77	28.799	64.602	136.489	0.50	83.99
25	439	NE1	TRP	A	77	28.212	65.818	136.228	0.50	83.46
	440	CZ2	TRP	A	77	26.101	66.936	136.996	0.50	82.40
	441	CZ3	TRP	A	77	24.827	65.565	138.530	0.50	82.13
	442	CH2	TRP	A	77	25.004	66.749	137.797	0.50	80.99
	443	C	TRP	A	77	26.672	61.423	136.339	0.50	83.09
30	444	O	TRP	A	77	26.245	62.363	135.662	0.50	82.20
	445	N	THR	A	78	25.918	60.383	136.682	0.50	80.95
	446	CA	THR	A	78	24.527	60.312	136.268	0.50	80.30
	447	CB	THR	A	78	23.936	58.899	136.474	0.50	81.42
	448	OG1	THR	A	78	24.155	58.476	137.824	0.50	82.99
35	449	CG2	THR	A	78	24.579	57.907	135.517	0.50	82.53
	450	C	THR	A	78	23.684	61.316	137.045	0.50	78.55
	451	O	THR	A	78	23.485	62.445	136.596	0.50	78.80
	452	N	ARG	A	79	23.208	60.909	138.218	0.50	76.29
	453	CA	ARG	A	79	22.364	61.773	139.038	0.50	72.81
40	454	CB	ARG	A	79	23.209	62.841	139.747	0.50	68.91
	455	CG	ARG	A	79	24.137	62.307	140.834	0.50	62.33
	456	CD	ARG	A	79	23.355	61.556	141.897	0.50	51.24
	457	NE	ARG	A	79	22.249	62.351	142.422	0.50	42.31

	458	CZ	ARG	A	79	22.382	63.347	143.291	0.50	38.44
	459	NH1	ARG	A	79	23.581	63.682	143.750	0.50	37.21
	460	NH2	ARG	A	79	21.313	64.015	143.696	0.50	32.45
	461	C	ARG	A	79	21.323	62.445	138.144	0.50	71.51
5	462	O	ARG	A	79	21.067	63.644	138.264	0.50	71.32
	463	N	PRO	A	80	20.705	61.670	137.233	0.50	69.63
	464	CD	PRO	A	80	20.730	60.197	137.163	0.50	69.49
	465	CA	PRO	A	80	19.693	62.207	136.320	0.50	66.79
	466	CB	PRO	A	80	18.969	60.955	135.838	0.50	67.95
10	467	CG	PRO	A	80	20.046	59.927	135.848	0.50	69.28
	468	C	PRO	A	80	18.763	63.157	137.049	0.50	62.86
	469	O	PRO	A	80	18.443	64.238	136.559	0.50	62.46
	470	N	ASP	A	81	18.343	62.734	138.232	0.50	60.06
	471	CA	ASP	A	81	17.446	63.513	139.067	0.50	59.73
15	472	CB	ASP	A	81	17.399	62.916	140.474	0.50	58.87
	473	CG	ASP	A	81	18.718	63.056	141.208	0.50	58.73
	474	OD1	ASP	A	81	19.736	62.507	140.729	0.50	58.80
	475	OD2	ASP	A	81	18.733	63.724	142.264	0.50	56.35
	476	C	ASP	A	81	17.895	64.967	139.153	0.50	57.78
20	477	O	ASP	A	81	17.084	65.887	139.047	0.50	58.30
	478	N	GLN	A	82	19.194	65.163	139.342	0.50	55.16
	479	CA	GLN	A	82	19.753	66.500	139.462	0.50	53.64
	480	CB	GLN	A	82	21.207	66.404	139.915	0.50	54.87
	481	CG	GLN	A	82	21.741	67.668	140.544	0.50	55.73
25	482	CD	GLN	A	82	22.912	67.389	141.460	0.50	56.91
	483	OE1	GLN	A	82	23.965	66.926	141.021	0.50	57.90
	484	NE2	GLN	A	82	22.732	67.663	142.745	0.50	57.60
	485	C	GLN	A	82	19.656	67.251	138.141	0.50	51.84
	486	O	GLN	A	82	19.425	68.457	138.117	0.50	50.08
30	487	N	GLU	A	83	19.825	66.529	137.042	0.50	50.45
	488	CA	GLU	A	83	19.749	67.134	135.723	0.50	50.95
	489	CB	GLU	A	83	20.248	66.153	134.661	0.50	51.97
	490	CG	GLU	A	83	21.714	65.802	134.779	0.50	52.72
	491	CD	GLU	A	83	22.589	67.030	134.864	0.50	54.08
35	492	OE1	GLU	A	83	22.609	67.673	135.930	0.50	55.53
	493	OE2	GLU	A	83	23.249	67.364	133.862	0.50	56.90
	494	C	GLU	A	83	18.324	67.558	135.392	0.50	49.61
	495	O	GLU	A	83	18.084	68.690	134.983	0.50	47.35
	496	N	VAL	A	84	17.380	66.640	135.566	0.50	50.78
40	497	CA	VAL	A	84	15.983	66.936	135.277	0.50	51.40
	498	CB	VAL	A	84	15.108	65.673	135.370	0.50	49.21
	499	CG1	VAL	A	84	15.552	64.662	134.339	0.50	52.02
	500	CG2	VAL	A	84	15.197	65.082	136.757	0.50	50.76



	501	C	VAL A	84	15.462	67.961	136.268	0.50	51.84
	502	O	VAL A	84	14.393	68.529	136.081	0.50	51.41
	503	N	LYS A	85	16.236	68.198	137.319	0.50	52.91
	504	CA	LYS A	85	15.855	69.149	138.349	0.50	53.93
5	505	CB	LYS A	85	16.847	69.087	139.502	0.50	58.82
	506	CG	LYS A	85	16.254	69.391	140.860	0.50	63.20
	507	CD	LYS A	85	15.406	68.227	141.337	0.50	64.80
	508	CE	LYS A	85	15.390	68.153	142.852	0.50	66.73
	509	NZ	LYS A	85	14.554	67.017	143.317	0.50	68.42
10	510	C	LYS A	85	15.825	70.567	137.800	0.50	54.70
	511	O	LYS A	85	14.780	71.214	137.785	0.50	53.35
	512	N	PHE A	86	16.979	71.052	137.352	0.50	55.27
	513	CA	PHE A	86	17.055	72.405	136.828	0.50	57.84
	514	CB	PHE A	86	18.417	73.030	137.153	0.50	62.66
15	515	CG	PHE A	86	18.492	73.609	138.546	0.50	67.86
	516	CD1	PHE A	86	18.481	72.778	139.665	0.50	69.62
	517	CD2	PHE A	86	18.518	74.989	138.741	0.50	69.32
	518	CE1	PHE A	86	18.492	73.312	140.957	0.50	68.23
	519	CE2	PHE A	86	18.528	75.533	140.030	0.50	69.36
20	520	CZ	PHE A	86	18.514	74.692	141.139	0.50	69.26
	521	C	PHE A	86	16.728	72.551	135.349	0.50	56.09
	522	O	PHE A	86	16.941	73.609	134.764	0.50	55.14
	523	N	ILE A	87	16.214	71.486	134.744	0.50	54.04
	524	CA	ILE A	87	15.797	71.545	133.351	0.50	50.81
25	525	CB	ILE A	87	16.149	70.254	132.573	0.50	51.29
	526	CG2	ILE A	87	15.177	70.049	131.413	0.50	50.00
	527	CG1	ILE A	87	17.588	70.348	132.050	0.50	52.13
	528	CD1	ILE A	87	18.015	69.182	131.171	0.50	49.30
	529	C	ILE A	87	14.285	71.722	133.418	0.50	49.18
30	530	O	ILE A	87	13.693	72.436	132.610	0.50	47.41
	531	N	MET A	88	13.677	71.076	134.411	0.50	46.14
	532	CA	MET A	88	12.239	71.156	134.640	0.50	43.21
	533	CB	MET A	88	11.777	70.004	135.525	0.50	44.20
	534	CG	MET A	88	11.716	68.695	134.795	0.50	49.86
35	535	SD	MET A	88	10.473	68.793	133.526	0.50	55.00
	536	CE	MET A	88	9.352	67.531	134.070	0.50	55.18
	537	C	MET A	88	11.914	72.466	135.327	0.50	41.73
	538	O	MET A	88	10.758	72.841	135.463	0.50	39.78
	539	N	ASN A	89	12.951	73.157	135.773	0.50	39.00
40	540	CA	ASN A	89	12.767	74.432	136.434	0.50	34.77
	541	CB	ASN A	89	13.797	74.600	137.546	0.50	31.98
	542	CG	ASN A	89	13.716	75.955	138.201	0.50	33.96
	543	OD1	ASN A	89	12.783	76.233	138.949	0.50	29.01

	544	ND2	ASN	A	89	14.688	76.819	137.909	0.50	32.13
	545	C	ASN	A	89	12.960	75.535	135.406	0.50	33.55
	546	O	ASN	A	89	12.640	76.696	135.654	0.50	33.42
	547	N	LEU	A	90	13.482	75.158	134.245	0.50	32.15
5	548	CA	LEU	A	90	13.759	76.112	133.184	0.50	30.01
	549	CB	LEU	A	90	14.332	75.380	131.965	0.50	29.24
	550	CG	LEU	A	90	14.874	76.252	130.827	0.50	31.79
	551	CD1	LEU	A	90	15.762	75.419	129.932	0.50	30.93
	552	CD2	LEU	A	90	13.732	76.861	130.036	0.50	32.92
10	553	C	LEU	A	90	12.577	76.992	132.770	0.50	30.34
	554	O	LEU	A	90	12.654	78.215	132.875	0.50	28.01
	555	N	PRO	A	91	11.463	76.385	132.322	0.50	29.00
	556	CD	PRO	A	91	11.161	74.945	132.337	0.50	29.81
	557	CA	PRO	A	91	10.285	77.143	131.892	0.50	29.79
15	558	CB	PRO	A	91	9.252	76.055	131.606	0.50	32.55
	559	CG	PRO	A	91	10.085	74.858	131.297	0.50	30.10
	560	C	PRO	A	91	9.784	78.146	132.918	0.50	31.96
	561	O	PRO	A	91	9.346	79.243	132.561	0.50	31.40
	562	N	VAL	A	92	9.849	77.765	134.190	0.50	33.58
20	563	CA	VAL	A	92	9.398	78.634	135.270	0.50	32.46
	564	CB	VAL	A	92	9.427	77.902	136.628	0.50	31.09
	565	CG1	VAL	A	92	9.234	78.886	137.760	0.50	28.29
	566	CG2	VAL	A	92	8.324	76.854	136.668	0.50	33.09
	567	C	VAL	A	92	10.252	79.882	135.350	0.50	34.99
25	568	O	VAL	A	92	9.733	80.998	135.296	0.50	36.96
	569	N	GLU	A	93	11.562	79.704	135.472	0.50	38.79
	570	CA	GLU	A	93	12.453	80.851	135.549	0.50	46.05
	571	CB	GLU	A	93	13.872	80.419	135.909	0.50	47.06
	572	CG	GLU	A	93	14.046	80.055	137.367	0.50	51.46
30	573	CD	GLU	A	93	15.484	80.171	137.810	0.50	54.33
	574	OE1	GLU	A	93	16.039	81.287	137.702	0.50	53.36
	575	OE2	GLU	A	93	16.058	79.154	138.261	0.50	57.38
	576	C	GLU	A	93	12.485	81.626	134.247	0.50	49.99
	577	O	GLU	A	93	12.735	82.831	134.241	0.50	52.42
35	578	N	PHE	A	94	12.230	80.942	133.138	1.00	53.80
	579	CA	PHE	A	94	12.259	81.621	131.855	1.00	57.03
	580	CB	PHE	A	94	12.274	80.630	130.688	1.00	52.58
	581	CG	PHE	A	94	12.969	81.164	129.452	1.00	48.04
	582	CD1	PHE	A	94	14.323	81.513	129.496	1.00	47.20
40	583	CD2	PHE	A	94	12.280	81.329	128.262	1.00	43.90
	584	CE1	PHE	A	94	14.975	82.019	128.372	1.00	43.17
	585	CE2	PHE	A	94	12.922	81.833	127.135	1.00	42.51
	586	CZ	PHE	A	94	14.272	82.179	127.191	1.00	40.41

	587	C	PHE	A	94	11.071	82.545	131.701	1.00	60.02
	588	O	PHE	A	94	11.220	83.665	131.213	1.00	61.99
	589	N	TYR	A	95	9.893	82.085	132.113	1.00	62.56
	590	CA	TYR	A	95	8.696	82.910	131.986	1.00	63.63
5	591	CB	TYR	A	95	7.452	82.147	132.436	1.00	66.64
	592	CG	TYR	A	95	6.174	82.941	132.236	1.00	69.36
	593	CD1	TYR	A	95	5.502	82.926	131.014	1.00	72.07
	594	CE1	TYR	A	95	4.351	83.684	130.813	1.00	72.88
	595	CD2	TYR	A	95	5.661	83.740	133.258	1.00	72.05
10	596	CE2	TYR	A	95	4.512	84.505	133.066	1.00	74.97
	597	CZ	TYR	A	95	3.862	84.470	131.843	1.00	72.08
	598	OH	TYR	A	95	2.722	85.215	131.659	1.00	71.75
	599	C	TYR	A	95	8.776	84.207	132.783	1.00	63.96
	600	O	TYR	A	95	8.193	85.226	132.403	1.00	66.05
15	601	N	ASP	A	96	9.506	84.169	133.888	1.00	62.65
	602	CA	ASP	A	96	9.616	85.332	134.746	1.00	61.40
	603	CB	ASP	A	96	9.912	84.886	136.179	1.00	64.02
	604	CG	ASP	A	96	8.892	83.892	136.697	1.00	67.53
	605	OD1	ASP	A	96	7.691	84.233	136.728	1.00	68.83
20	606	OD2	ASP	A	96	9.289	82.768	137.067	1.00	72.19
	607	C	ASP	A	96	10.655	86.341	134.314	1.00	57.07
	608	O	ASP	A	96	10.399	87.541	134.329	1.00	55.01
	609	N	ASN	A	97	11.814	85.854	133.898	1.00	52.62
	610	CA	ASN	A	97	12.899	86.743	133.535	1.00	54.30
25	611	CB	ASN	A	97	14.180	86.235	134.193	1.00	59.95
	612	CG	ASN	A	97	13.983	85.916	135.663	1.00	66.36
	613	OD1	ASN	A	97	13.512	86.760	136.431	1.00	68.80
	614	ND2	ASN	A	97	14.334	84.694	136.064	1.00	66.73
	615	C	ASN	A	97	13.166	86.988	132.061	1.00	54.27
30	616	O	ASN	A	97	14.024	87.816	131.722	1.00	56.38
	617	N	TYR	A	98	12.449	86.299	131.178	1.00	49.99
	618	CA	TYR	A	98	12.713	86.479	129.754	1.00	46.41
	619	CB	TYR	A	98	13.681	85.400	129.266	1.00	43.30
	620	CG	TYR	A	98	14.992	85.363	130.006	1.00	40.10
35	621	CD1	TYR	A	98	15.179	84.507	131.087	1.00	40.39
	622	CE1	TYR	A	98	16.401	84.448	131.752	1.00	40.34
	623	CD2	TYR	A	98	16.055	86.168	129.614	1.00	36.91
	624	CE2	TYR	A	98	17.275	86.117	130.276	1.00	38.32
	625	CZ	TYR	A	98	17.439	85.253	131.339	1.00	36.57
40	626	OH	TYR	A	98	18.647	85.195	131.987	1.00	44.59
	627	C	TYR	A	98	11.520	86.513	128.809	1.00	43.68
	628	O	TYR	A	98	11.570	87.215	127.799	1.00	43.25
	629	N	VAL	A	99	10.470	85.752	129.107	1.00	40.25

	630	CA	VAL A	99	9.311	85.737	128.227	1.00	46.20
	631	CB	VAL A	99	8.140	84.911	128.822	1.00	47.75
	632	CG1	VAL A	99	6.894	85.045	127.953	1.00	42.95
	633	CG2	VAL A	99	8.538	83.445	128.879	1.00	48.90
5	634	C	VAL A	99	8.868	87.166	127.915	1.00	47.29
	635	O	VAL A	99	8.897	87.581	126.764	1.00	46.51
	636	N	PRO A	100	8.483	87.945	128.934	1.00	47.44
	637	CD	PRO A	100	8.486	87.697	130.380	1.00	48.42
	638	CA	PRO A	100	8.060	89.320	128.652	1.00	47.91
10	639	CB	PRO A	100	8.189	90.020	130.016	1.00	48.71
	640	CG	PRO A	100	8.948	89.017	130.895	1.00	51.10
	641	C	PRO A	100	8.865	90.004	127.546	1.00	43.36
	642	O	PRO A	100	8.292	90.563	126.617	1.00	43.67
	643	N	GLU A	101	10.188	89.966	127.629	1.00	41.37
15	644	CA	GLU A	101	10.971	90.590	126.575	1.00	42.93
	645	CB	GLU A	101	12.448	90.678	126.965	1.00	42.76
	646	CG	GLU A	101	13.294	91.225	125.830	1.00	45.79
	647	CD	GLU A	101	14.706	91.590	126.237	1.00	53.91
	648	OE1	GLU A	101	15.233	91.002	127.211	1.00	56.84
20	649	OE2	GLU A	101	15.299	92.461	125.560	1.00	58.31
	650	C	GLU A	101	10.827	89.845	125.226	1.00	45.93
	651	O	GLU A	101	10.848	90.471	124.170	1.00	45.28
	652	N	LEU A	102	10.675	88.522	125.245	1.00	40.87
	653	CA	LEU A	102	10.525	87.800	123.982	1.00	43.42
25	654	CB	LEU A	102	10.595	86.277	124.181	1.00	35.82
	655	CG	LEU A	102	11.946	85.658	124.560	1.00	41.55
	656	CD1	LEU A	102	11.839	84.143	124.392	1.00	32.70
	657	CD2	LEU A	102	13.076	86.231	123.688	1.00	32.02
	658	C	LEU A	102	9.196	88.158	123.326	1.00	40.10
30	659	O	LEU A	102	9.067	88.129	122.101	1.00	40.19
	660	N	HIS A	103	8.211	88.484	124.150	1.00	36.50
	661	CA	HIS A	103	6.889	88.859	123.659	1.00	39.96
	662	CB	HIS A	103	5.898	88.887	124.810	1.00	36.90
	663	CG	HIS A	103	4.497	89.169	124.386	1.00	41.58
35	664	CD2	HIS A	103	3.618	90.118	124.790	1.00	42.27
	665	ND1	HIS A	103	3.816	88.368	123.496	1.00	40.30
	666	CE1	HIS A	103	2.575	88.804	123.377	1.00	38.88
	667	NE2	HIS A	103	2.429	89.863	124.152	1.00	36.88
	668	C	HIS A	103	6.947	90.235	122.994	1.00	38.23
40	669	O	HIS A	103	6.332	90.470	121.948	1.00	39.67
	670	N	ALA A	104	7.701	91.138	123.601	1.00	33.21
	671	CA	ALA A	104	7.862	92.477	123.050	1.00	41.75
	672	CB	ALA A	104	8.690	93.338	123.998	1.00	34.84

	673	C	ALA A 104	8.559	92.393	121.688	1.00	42.63
	674	O	ALA A 104	8.454	93.311	120.876	1.00	44.45
	675	N	ASN A 105	9.269	91.293	121.441	1.00	39.85
	676	CA	ASN A 105	9.976	91.123	120.179	1.00	41.27
5	677	CB	ASN A 105	11.333	90.444	120.403	1.00	44.70
	678	CG	ASN A 105	12.360	91.378	121.024	1.00	47.75
	679	OD1	ASN A 105	13.381	91.713	120.407	1.00	49.73
	680	ND2	ASN A 105	12.097	91.806	122.250	1.00	49.19
	681	C	ASN A 105	9.153	90.343	119.163	1.00	34.83
10	682	O	ASN A 105	9.652	89.965	118.117	1.00	37.16
	683	N	ASN A 106	7.887	90.113	119.472	1.00	28.28
	684	CA	ASN A 106	6.989	89.409	118.549	1.00	28.61
	685	CB	ASN A 106	6.939	90.162	117.211	1.00	22.32
	686	CG	ASN A 106	5.810	89.706	116.326	1.00	23.45
15	687	OD1	ASN A 106	5.908	89.765	115.097	1.00	38.78
	688	ND2	ASN A 106	4.728	89.256	116.930	1.00	19.52
	689	C	ASN A 106	7.432	87.948	118.313	1.00	33.74
	690	O	ASN A 106	7.267	87.405	117.211	1.00	27.06
	691	N	VAL A 107	8.005	87.339	119.359	1.00	34.88
20	692	CA	VAL A 107	8.473	85.949	119.335	1.00	26.93
	693	CB	VAL A 107	9.746	85.771	120.185	1.00	29.53
	694	CG1	VAL A 107	10.144	84.281	120.245	1.00	26.42
	695	CG2	VAL A 107	10.881	86.628	119.611	1.00	21.95
	696	C	VAL A 107	7.395	85.038	119.894	1.00	27.05
25	697	O	VAL A 107	6.877	85.264	120.986	1.00	28.26
	698	N	LYS A 108	7.042	84.011	119.136	1.00	27.83
	699	CA	LYS A 108	6.032	83.067	119.582	1.00	30.60
	700	CB	LYS A 108	5.269	82.524	118.389	1.00	22.34
	701	CG	LYS A 108	4.153	81.616	118.792	1.00	29.19
30	702	CD	LYS A 108	3.382	81.185	117.589	1.00	27.79
	703	CE	LYS A 108	2.103	80.558	117.998	1.00	29.65
	704	NZ	LYS A 108	1.320	80.375	116.744	1.00	37.79
	705	C	LYS A 108	6.738	81.914	120.302	1.00	32.00
	706	O	LYS A 108	7.779	81.446	119.854	1.00	36.67
35	707	N	ILE A 109	6.172	81.457	121.408	1.00	33.45
	708	CA	ILE A 109	6.769	80.381	122.176	1.00	28.87
	709	CB	ILE A 109	6.975	80.800	123.633	1.00	32.18
	710	CG2	ILE A 109	7.629	79.662	124.410	1.00	33.24
	711	CG1	ILE A 109	7.848	82.055	123.694	1.00	33.34
40	712	CD1	ILE A 109	8.016	82.615	125.091	1.00	36.37
	713	C	ILE A 109	5.907	79.141	122.164	1.00	31.18
	714	O	ILE A 109	4.698	79.221	122.383	1.00	27.52
	715	N	GLN A 110	6.528	77.995	121.896	1.00	28.33

	716	CA	GLN	A	110	5.802	76.719	121.901	1.00	31.13
	717	CB	GLN	A	110	5.408	76.290	120.475	1.00	31.59
	718	CG	GLN	A	110	4.264	77.119	119.898	1.00	44.06
	719	CD	GLN	A	110	3.608	76.504	118.665	1.00	47.03
5	720	OE1	GLN	A	110	4.238	76.351	117.615	1.00	47.46
	721	NE2	GLN	A	110	2.329	76.153	118.791	1.00	47.02
	722	C	GLN	A	110	6.626	75.620	122.570	1.00	29.02
	723	O	GLN	A	110	7.841	75.710	122.680	1.00	27.86
	724	N	MET	A	111	5.957	74.586	123.040	1.00	36.00
10	725	CA	MET	A	111	6.659	73.497	123.698	1.00	38.99
	726	CB	MET	A	111	6.157	73.315	125.139	1.00	44.92
	727	CG	MET	A	111	6.588	71.999	125.808	0.50	50.91
	728	SD	MET	A	111	5.462	70.582	125.540	0.50	62.68
	729	CE	MET	A	111	5.006	70.186	127.271	0.50	54.46
15	730	C	MET	A	111	6.458	72.223	122.915	1.00	38.50
	731	O	MET	A	111	5.359	71.948	122.437	1.00	37.78
	732	N	ILE	A	112	7.543	71.472	122.765	1.00	36.25
	733	CA	ILE	A	112	7.542	70.188	122.073	1.00	36.84
	734	CB	ILE	A	112	8.521	70.251	120.851	1.00	40.49
20	735	CG2	ILE	A	112	9.825	70.894	121.264	1.00	47.77
	736	CG1	ILE	A	112	8.810	68.869	120.286	1.00	46.15
	737	CD1	ILE	A	112	9.996	68.855	119.299	1.00	33.68
	738	C	ILE	A	112	8.017	69.211	123.172	1.00	36.40
	739	O	ILE	A	112	9.023	69.457	123.846	1.00	35.31
25	740	N	GLY	A	113	7.266	68.141	123.395	1.00	35.78
	741	CA	GLY	A	113	7.645	67.197	124.428	1.00	38.24
	742	C	GLY	A	113	6.464	66.554	125.123	1.00	43.62
	743	O	GLY	A	113	5.313	66.725	124.713	1.00	38.13
	744	N	GLU	A	114	6.737	65.802	126.184	1.00	46.42
30	745	CA	GLU	A	114	5.659	65.147	126.898	1.00	51.64
	746	CB	GLU	A	114	6.083	63.723	127.285	1.00	57.67
	747	CG	GLU	A	114	6.008	62.770	126.077	1.00	65.74
	748	CD	GLU	A	114	6.716	61.430	126.276	1.00	72.69
	749	OE1	GLU	A	114	7.944	61.423	126.527	1.00	78.05
35	750	OE2	GLU	A	114	6.045	60.380	126.164	1.00	69.77
	751	C	GLU	A	114	5.180	65.973	128.084	1.00	52.05
	752	O	GLU	A	114	5.928	66.266	129.012	1.00	46.58
	753	N	THR	A	115	3.909	66.362	127.998	1.00	59.26
	754	CA	THR	A	115	3.209	67.197	128.980	1.00	64.51
40	755	CB	THR	A	115	1.944	67.828	128.317	1.00	65.99
	756	OG1	THR	A	115	2.219	69.194	127.988	1.00	68.96
	757	CG2	THR	A	115	0.714	67.746	129.227	1.00	67.11
	758	C	THR	A	115	2.788	66.481	130.252	1.00	66.32

	759	O	THR A 115	3.194	66.850	131.353	1.00	64.20
	760	N	ASP A 116	1.955	65.464	130.068	1.00	70.69
	761	CA	ASP A 116	1.401	64.650	131.140	1.00	73.79
	762	CB	ASP A 116	0.992	63.290	130.558	1.00	71.21
5	763	CG	ASP A 116	0.217	63.426	129.252	0.50	69.22
	764	OD1	ASP A 116	-0.897	63.991	129.266	0.50	65.37
	765	OD2	ASP A 116	0.731	62.974	128.208	0.50	68.02
	766	C	ASP A 116	2.316	64.450	132.361	1.00	76.36
	767	O	ASP A 116	1.864	64.518	133.511	1.00	77.65
10	768	N	ARG A 117	3.600	64.217	132.124	1.00	75.65
	769	CA	ARG A 117	4.508	63.989	133.235	1.00	75.53
	770	CB	ARG A 117	5.417	62.799	132.904	1.00	77.18
	771	CG	ARG A 117	4.658	61.510	132.612	0.00	74.50
	772	CD	ARG A 117	3.712	61.160	133.752	0.00	73.37
15	773	NE	ARG A 117	3.042	59.877	133.554	0.00	71.96
	774	CZ	ARG A 117	2.180	59.624	132.574	0.00	71.32
	775	NH1	ARG A 117	1.876	60.568	131.694	0.00	70.87
	776	NH2	ARG A 117	1.620	58.427	132.476	0.00	70.87
	777	C	ARG A 117	5.342	65.207	133.638	1.00	75.68
20	778	O	ARG A 117	6.545	65.095	133.872	1.00	78.92
	779	N	LEU A 118	4.706	66.371	133.730	1.00	73.23
	780	CA	LEU A 118	5.413	67.592	134.113	1.00	69.41
	781	CB	LEU A 118	5.178	68.698	133.080	1.00	74.56
	782	CG	LEU A 118	5.773	68.609	131.671	1.00	77.14
25	783	CD1	LEU A 118	5.058	69.602	130.751	1.00	79.17
	784	CD2	LEU A 118	7.265	68.902	131.726	1.00	77.77
	785	C	LEU A 118	4.917	68.080	135.462	1.00	66.21
	786	O	LEU A 118	3.809	67.759	135.874	1.00	65.61
	787	N	PRO A 119	5.737	68.864	136.172	1.00	64.49
30	788	CD	PRO A 119	7.173	69.039	135.918	1.00	62.59
	789	CA	PRO A 119	5.375	69.409	137.489	1.00	64.86
	790	CB	PRO A 119	6.711	69.919	138.033	1.00	60.20
	791	CG	PRO A 119	7.720	69.096	137.313	1.00	59.43
	792	C	PRO A 119	4.358	70.548	137.323	1.00	68.00
35	793	O	PRO A 119	4.587	71.466	136.528	1.00	68.35
	794	N	LYS A 120	3.253	70.497	138.070	1.00	66.41
	795	CA	LYS A 120	2.212	71.525	137.976	1.00	66.88
	796	CB	LYS A 120	1.287	71.475	139.196	1.00	64.33
	797	CG	LYS A 120	0.282	72.623	139.226	1.00	62.34
40	798	CD	LYS A 120	-0.443	72.732	140.560	1.00	64.03
	799	CE	LYS A 120	-1.228	74.030	140.643	1.00	62.24
	800	NZ	LYS A 120	-1.772	74.261	142.002	1.00	67.64
	801	C	LYS A 120	2.738	72.954	137.831	1.00	67.39

	802	O	LYS A 120	2.223	73.745	137.039	1.00	66.87
	803	N	GLN A 121	3.764	73.278	138.604	1.00	67.75
	804	CA	GLN A 121	4.345	74.613	138.585	1.00	67.91
	805	CB	GLN A 121	5.404	74.717	139.693	1.00	70.64
5	806	CG	GLN A 121	5.600	76.114	140.259	1.00	72.60
	807	CD	GLN A 121	6.652	76.153	141.353	0.50	72.81
	808	OE1	GLN A 121	7.815	75.813	141.126	0.50	71.84
	809	NE2	GLN A 121	6.247	76.567	142.547	0.50	71.62
	810	C	GLN A 121	4.964	74.929	137.222	1.00	66.48
10	811	O	GLN A 121	4.915	76.065	136.749	1.00	68.61
	812	N	THR A 122	5.540	73.918	136.584	1.00	64.63
	813	CA	THR A 122	6.168	74.114	135.288	1.00	61.07
	814	CB	THR A 122	7.289	73.071	135.056	1.00	64.34
	815	OG1	THR A 122	6.721	71.774	134.834	1.00	70.06
15	816	CG2	THR A 122	8.190	73.013	136.272	1.00	65.26
	817	C	THR A 122	5.165	74.067	134.134	1.00	54.52
	818	O	THR A 122	5.269	74.849	133.203	1.00	48.44
	819	N	PHE A 123	4.203	73.153	134.194	1.00	51.91
	820	CA	PHE A 123	3.195	73.047	133.150	1.00	51.08
20	821	CB	PHE A 123	2.165	71.987	133.524	1.00	52.11
	822	CG	PHE A 123	1.017	71.860	132.558	1.00	49.86
	823	CD1	PHE A 123	1.088	70.987	131.484	1.00	51.07
	824	CD2	PHE A 123	-0.169	72.570	132.767	1.00	53.79
	825	CE1	PHE A 123	-0.007	70.809	130.631	1.00	53.43
25	826	CE2	PHE A 123	-1.274	72.400	131.918	1.00	52.90
	827	CZ	PHE A 123	-1.191	71.517	130.850	1.00	49.77
	828	C	PHE A 123	2.525	74.408	133.055	1.00	52.04
	829	O	PHE A 123	2.141	74.849	131.975	1.00	54.62
	830	N	GLU A 124	2.404	75.078	134.195	1.00	51.24
30	831	CA	GLU A 124	1.777	76.390	134.233	1.00	51.49
	832	CB	GLU A 124	1.321	76.716	135.661	1.00	50.26
	833	CG	GLU A 124	0.162	75.842	136.143	1.00	57.84
	834	CD	GLU A 124	-0.300	76.162	137.570	1.00	66.06
	835	OE1	GLU A 124	-1.262	75.515	138.037	1.00	65.15
35	836	OE2	GLU A 124	0.292	77.053	138.223	1.00	69.81
	837	C	GLU A 124	2.678	77.500	133.689	1.00	48.89
	838	O	GLU A 124	2.199	78.441	133.064	1.00	51.84
	839	N	ALA A 125	3.980	77.405	133.916	1.00	46.10
	840	CA	ALA A 125	4.874	78.436	133.400	1.00	46.86
40	841	CB	ALA A 125	6.283	78.272	133.980	1.00	47.53
	842	C	ALA A 125	4.927	78.353	131.875	1.00	46.75
	843	O	ALA A 125	5.079	79.374	131.197	1.00	47.56
	844	N	LEU A 126	4.804	77.133	131.352	1.00	43.97



	845	CA	LEU	A	126	4.842	76.889	129.914	1.00	44.55
	846	CB	LEU	A	126	5.027	75.396	129.588	1.00	46.39
	847	CG	LEU	A	126	6.388	74.693	129.706	1.00	49.76
	848	CD1	LEU	A	126	6.191	73.192	129.515	1.00	48.17
5	849	CD2	LEU	A	126	7.358	75.230	128.671	1.00	47.92
	850	C	LEU	A	126	3.560	77.358	129.263	1.00	43.19
	851	O	LEU	A	126	3.610	78.140	128.319	1.00	40.93
	852	N	THR	A	127	2.419	76.878	129.754	1.00	40.32
	853	CA	THR	A	127	1.153	77.275	129.163	1.00	44.09
10	854	CB	THR	A	127	-0.047	76.626	129.876	1.00	45.80
	855	OG1	THR	A	127	-0.159	77.156	131.199	1.00	60.56
	856	CG2	THR	A	127	0.122	75.112	129.945	1.00	41.64
	857	C	THR	A	127	0.978	78.803	129.157	1.00	42.36
	858	O	THR	A	127	0.462	79.360	128.191	1.00	40.22
15	859	N	LYS	A	128	1.430	79.480	130.210	1.00	38.62
	860	CA	LYS	A	128	1.304	80.932	130.273	1.00	40.36
	861	CB	LYS	A	128	1.694	81.456	131.657	1.00	39.22
	862	CG	LYS	A	128	0.538	81.527	132.650	1.00	45.17
	863	CD	LYS	A	128	1.031	81.487	134.104	1.00	50.00
20	864	CE	LYS	A	128	2.002	82.625	134.433	1.00	52.36
	865	NZ	LYS	A	128	2.497	82.547	135.843	1.00	54.40
	866	C	LYS	A	128	2.153	81.633	129.230	1.00	40.74
	867	O	LYS	A	128	1.730	82.635	128.650	1.00	40.80
	868	N	ALA	A	129	3.359	81.122	129.007	1.00	39.05
25	869	CA	ALA	A	129	4.265	81.722	128.032	1.00	35.75
	870	CB	ALA	A	129	5.635	81.117	128.154	1.00	33.65
	871	C	ALA	A	129	3.717	81.492	126.635	1.00	32.92
	872	O	ALA	A	129	3.922	82.296	125.734	1.00	33.79
	873	N	GLU	A	130	3.009	80.389	126.473	1.00	27.60
30	874	CA	GLU	A	130	2.419	80.042	125.199	1.00	31.86
	875	CB	GLU	A	130	1.920	78.608	125.230	1.00	30.48
	876	CG	GLU	A	130	2.764	77.660	124.441	1.00	41.19
	877	CD	GLU	A	130	2.318	76.228	124.610	1.00	48.03
	878	OE1	GLU	A	130	1.103	75.951	124.456	1.00	52.16
35	879	OE2	GLU	A	130	3.190	75.381	124.897	1.00	52.75
	880	C	GLU	A	130	1.250	80.959	124.897	1.00	35.57
	881	O	GLU	A	130	1.238	81.640	123.869	1.00	37.96
	882	N	GLU	A	131	0.272	80.962	125.800	1.00	34.48
	883	CA	GLU	A	131	-0.931	81.779	125.660	1.00	39.03
40	884	CB	GLU	A	131	-1.850	81.573	126.856	1.00	38.20
	885	CG	GLU	A	131	-2.330	80.144	126.956	1.00	45.95
	886	CD	GLU	A	131	-3.202	79.907	128.163	1.00	51.07
	887	OE1	GLU	A	131	-3.008	80.628	129.172	1.00	50.65

	888	OE2	GLU	A	131	-4.063	78.994	128.105	1.00	47.59
	889	C	GLU	A	131	-0.592	83.244	125.515	1.00	37.43
	890	O	GLU	A	131	-1.276	83.985	124.812	1.00	39.28
	891	N	LEU	A	132	0.481	83.659	126.166	1.00	30.90
5	892	CA	LEU	A	132	0.895	85.037	126.066	1.00	32.78
	893	CB	LEU	A	132	2.075	85.299	126.980	1.00	28.29
	894	CG	LEU	A	132	2.719	86.663	126.772	1.00	29.65
	895	CD1	LEU	A	132	1.723	87.767	127.177	1.00	31.20
	896	CD2	LEU	A	132	3.985	86.738	127.607	1.00	28.05
10	897	C	LEU	A	132	1.319	85.409	124.650	1.00	37.71
	898	O	LEU	A	132	0.908	86.439	124.123	1.00	41.43
	899	N	THR	A	133	2.148	84.560	124.052	1.00	35.51
	900	CA	THR	A	133	2.713	84.807	122.731	1.00	30.52
	901	CB	THR	A	133	4.196	84.378	122.726	1.00	31.37
15	902	OG1	THR	A	133	4.270	82.967	122.957	1.00	33.04
	903	CG2	THR	A	133	4.959	85.060	123.810	1.00	24.29
	904	C	THR	A	133	2.036	84.104	121.551	1.00	25.25
	905	O	THR	A	133	2.576	84.100	120.447	1.00	28.45
	906	N	LYS	A	134	0.864	83.524	121.753	1.00	23.90
20	907	CA	LYS	A	134	0.239	82.774	120.668	1.00	27.92
	908	CB	LYS	A	134	-0.919	81.951	121.210	1.00	29.08
	909	CG	LYS	A	134	-2.141	82.768	121.557	1.00	31.47
	910	CD	LYS	A	134	-3.352	81.862	121.663	1.00	34.96
	911	CE	LYS	A	134	-4.642	82.638	121.452	1.00	44.12
25	912	NZ	LYS	A	134	-5.841	81.807	121.810	1.00	48.78
	913	C	LYS	A	134	-0.244	83.524	119.430	1.00	34.37
	914	O	LYS	A	134	-0.791	82.911	118.509	1.00	36.07
	915	N	ASN	A	135	-0.071	84.839	119.398	1.00	37.45
	916	CA	ASN	A	135	-0.509	85.615	118.245	1.00	33.67
30	917	CB	ASN	A	135	-1.433	86.763	118.675	1.00	30.92
	918	CG	ASN	A	135	-2.730	86.278	119.287	1.00	35.48
	919	OD1	ASN	A	135	-3.424	85.427	118.715	1.00	28.13
	920	ND2	ASN	A	135	-3.080	86.831	120.453	1.00	29.80
	921	C	ASN	A	135	0.717	86.200	117.583	1.00	33.52
35	922	O	ASN	A	135	0.635	86.744	116.481	1.00	32.65
	923	N	ASN	A	136	1.858	86.103	118.257	1.00	30.11
	924	CA	ASN	A	136	3.069	86.681	117.704	1.00	31.38
	925	CB	ASN	A	136	4.213	86.527	118.700	1.00	33.22
	926	CG	ASN	A	136	3.912	87.239	120.030	1.00	43.19
40	927	OD1	ASN	A	136	2.777	87.671	120.268	1.00	42.46
	928	ND2	ASN	A	136	4.917	87.356	120.897	1.00	41.77
	929	C	ASN	A	136	3.353	86.086	116.328	1.00	36.21
	930	O	ASN	A	136	3.032	84.924	116.049	1.00	34.01

	931	N	THR A 137	3.914	86.916	115.457	1.00	34.83
	932	CA	THR A 137	4.164	86.531	114.082	1.00	32.66
	933	CB	THR A 137	3.425	87.488	113.125	1.00	34.49
	934	OG1	THR A 137	3.912	88.821	113.330	1.00	31.41
5	935	CG2	THR A 137	1.924	87.445	113.371	1.00	24.50
	936	C	THR A 137	5.636	86.559	113.725	1.00	30.65
	937	O	THR A 137	5.995	86.504	112.555	1.00	35.55
	938	N	GLY A 138	6.493	86.684	114.723	1.00	27.91
	939	CA	GLY A 138	7.912	86.677	114.427	1.00	28.89
10	940	C	GLY A 138	8.433	85.247	114.576	1.00	31.45
	941	O	GLY A 138	7.697	84.272	114.371	1.00	26.45
	942	N	LEU A 139	9.701	85.125	114.947	1.00	30.47
	943	CA	LEU A 139	10.339	83.829	115.155	1.00	31.01
	944	CB	LEU A 139	11.727	84.053	115.733	1.00	29.82
15	945	CG	LEU A 139	12.369	82.797	116.284	1.00	34.12
	946	CD1	LEU A 139	12.839	81.940	115.126	1.00	36.64
	947	CD2	LEU A 139	13.526	83.186	117.171	1.00	32.20
	948	C	LEU A 139	9.547	82.924	116.100	1.00	32.43
	949	O	LEU A 139	8.911	83.397	117.043	1.00	33.74
20	950	N	ILE A 140	9.571	81.621	115.836	1.00	34.27
	951	CA	ILE A 140	8.879	80.666	116.695	1.00	33.52
	952	CB	ILE A 140	8.106	79.641	115.871	1.00	35.87
	953	CG2	ILE A 140	7.543	78.560	116.770	1.00	32.19
	954	CG1	ILE A 140	6.958	80.323	115.143	1.00	36.10
25	955	CD1	ILE A 140	6.059	79.349	114.456	1.00	31.48
	956	C	ILE A 140	9.919	79.928	117.546	1.00	36.26
	957	O	ILE A 140	10.693	79.144	117.014	1.00	43.67
	958	N	LEU A 141	9.970	80.210	118.849	1.00	35.75
	959	CA	LEU A 141	10.918	79.540	119.750	1.00	33.85
30	960	CB	LEU A 141	11.317	80.451	120.912	1.00	33.19
	961	CG	LEU A 141	12.165	79.852	122.042	1.00	40.29
	962	CD1	LEU A 141	13.501	79.370	121.509	1.00	39.07
	963	CD2	LEU A 141	12.399	80.901	123.128	1.00	35.45
	964	C	LEU A 141	10.241	78.277	120.272	1.00	35.36
35	965	O	LEU A 141	9.261	78.331	121.030	1.00	36.02
	966	N	ASN A 142	10.785	77.145	119.828	1.00	35.99
	967	CA	ASN A 142	10.305	75.808	120.147	1.00	32.73
	968	CB	ASN A 142	10.344	74.984	118.864	1.00	39.58
	969	CG	ASN A 142	9.130	74.138	118.688	1.00	42.67
40	970	OD1	ASN A 142	8.018	74.645	118.630	1.00	52.35
	971	ND2	ASN A 142	9.327	72.833	118.595	1.00	51.43
	972	C	ASN A 142	11.155	75.120	121.235	1.00	31.91
	973	O	ASN A 142	12.283	74.699	120.975	1.00	31.49

	974	N	PHE A 143	10.593	75.005	122.436	1.00	25.73
	975	CA	PHE A 143	11.246	74.387	123.593	1.00	31.11
	976	CB	PHE A 143	10.689	74.941	124.898	1.00	37.34
	977	CG	PHE A 143	11.432	76.101	125.423	1.00	33.79
5	978	CD1	PHE A 143	10.882	77.380	125.349	1.00	38.95
	979	CD2	PHE A 143	12.678	75.924	126.005	1.00	36.66
	980	CE1	PHE A 143	11.571	78.490	125.854	1.00	40.06
	981	CE2	PHE A 143	13.387	77.012	126.516	1.00	42.21
	982	CZ	PHE A 143	12.832	78.305	126.441	1.00	45.28
10	983	C	PHE A 143	11.010	72.908	123.656	1.00	31.33
	984	O	PHE A 143	9.875	72.487	123.854	1.00	33.93
	985	N	ALA A 144	12.062	72.111	123.502	1.00	28.70
	986	CA	ALA A 144	11.889	70.672	123.579	1.00	28.31
	987	CB	ALA A 144	12.799	69.973	122.570	1.00	26.41
15	988	C	ALA A 144	12.214	70.227	125.004	1.00	32.80
	989	O	ALA A 144	13.381	70.102	125.365	1.00	40.95
	990	N	LEU A 145	11.180	69.993	125.809	1.00	32.64
	991	CA	LEU A 145	11.357	69.569	127.196	1.00	34.62
	992	CB	LEU A 145	10.674	70.537	128.143	1.00	40.24
20	993	CG	LEU A 145	11.195	71.952	128.085	1.00	47.75
	994	CD1	LEU A 145	10.306	72.789	128.971	1.00	55.49
	995	CD2	LEU A 145	12.650	72.007	128.531	1.00	48.97
	996	C	LEU A 145	10.738	68.212	127.412	1.00	35.42
	997	O	LEU A 145	9.648	67.940	126.899	1.00	33.86
25	998	N	ASN A 146	11.405	67.361	128.191	1.00	34.76
	999	CA	ASN A 146	10.856	66.039	128.422	1.00	33.39
	1000	CB	ASN A 146	9.525	66.186	129.141	1.00	41.62
	1001	CG	ASN A 146	9.261	65.065	130.094	1.00	52.62
	1002	OD1	ASN A 146	10.146	64.674	130.857	1.00	58.30
30	1003	ND2	ASN A 146	8.033	64.538	130.073	1.00	56.39
	1004	C	ASN A 146	10.643	65.452	127.030	1.00	27.95
	1005	O	ASN A 146	9.646	64.780	126.757	1.00	27.11
	1006	N	TYR A 147	11.605	65.726	126.154	1.00	25.89
	1007	CA	TYR A 147	11.536	65.290	124.765	1.00	30.30
35	1008	CB	TYR A 147	11.819	66.482	123.820	1.00	26.33
	1009	CG	TYR A 147	11.923	66.085	122.363	1.00	26.35
	1010	CD1	TYR A 147	10.787	66.063	121.541	1.00	25.42
	1011	CE1	TYR A 147	10.862	65.627	120.222	1.00	22.93
	1012	CD2	TYR A 147	13.142	65.662	121.819	1.00	20.87
40	1013	CE2	TYR A 147	13.226	65.223	120.507	1.00	21.80
	1014	CZ	TYR A 147	12.080	65.206	119.712	1.00	24.13
	1015	OH	TYR A 147	12.145	64.755	118.412	1.00	25.17
	1016	C	TYR A 147	12.507	64.163	124.423	1.00	29.45

	1017	O	TYR A 147	13.646	64.136	124.892	1.00	21.27
	1018	N	GLY A 148	12.029	63.256	123.578	1.00	26.00
	1019	CA	GLY A 148	12.834	62.151	123.108	1.00	25.84
	1020	C	GLY A 148	12.331	61.801	121.722	1.00	24.44
5	1021	O	GLY A 148	11.140	61.562	121.539	1.00	28.46
	1022	N	GLY A 149	13.231	61.770	120.749	1.00	23.59
	1023	CA	GLY A 149	12.838	61.454	119.388	1.00	24.54
	1024	C	GLY A 149	12.055	60.168	119.218	1.00	20.46
	1025	O	GLY A 149	10.991	60.147	118.609	1.00	19.79
10	1026	N	ARG A 150	12.583	59.074	119.744	1.00	21.38
	1027	CA	ARG A 150	11.892	57.808	119.606	1.00	19.50
	1028	CB	ARG A 150	12.776	56.699	120.127	1.00	21.91
	1029	CG	ARG A 150	14.073	56.510	119.349	1.00	24.57
	1030	CD	ARG A 150	14.826	55.343	119.957	1.00	17.07
15	1031	NE	ARG A 150	16.030	55.025	119.212	1.00	28.22
	1032	CZ	ARG A 150	16.898	54.081	119.564	1.00	32.10
	1033	NH1	ARG A 150	16.685	53.361	120.654	1.00	33.58
	1034	NH2	ARG A 150	17.987	53.860	118.836	1.00	29.63
	1035	C	ARG A 150	10.549	57.817	120.340	1.00	22.37
20	1036	O	ARG A 150	9.568	57.214	119.892	1.00	24.29
	1037	N	ALA A 151	10.497	58.511	121.465	1.00	19.13
	1038	CA	ALA A 151	9.263	58.575	122.229	1.00	22.35
	1039	CB	ALA A 151	9.511	59.266	123.572	1.00	16.87
	1040	C	ALA A 151	8.237	59.346	121.402	1.00	26.47
25	1041	O	ALA A 151	7.085	58.934	121.299	1.00	29.47
	1042	N	GLU A 152	8.658	60.459	120.809	1.00	23.96
	1043	CA	GLU A 152	7.765	61.252	119.961	1.00	29.53
	1044	CB	GLU A 152	8.508	62.458	119.387	1.00	28.51
	1045	CG	GLU A 152	7.819	63.101	118.202	1.00	23.64
30	1046	CD	GLU A 152	8.621	64.239	117.612	1.00	30.04
	1047	OE1	GLU A 152	9.846	64.081	117.397	1.00	27.57
	1048	OE2	GLU A 152	8.021	65.299	117.354	1.00	29.98
	1049	C	GLU A 152	7.191	60.411	118.813	1.00	29.21
	1050	O	GLU A 152	6.000	60.477	118.513	1.00	33.94
35	1051	N	ILE A 153	8.032	59.610	118.177	1.00	30.06
	1052	CA	ILE A 153	7.577	58.760	117.075	1.00	27.84
	1053	CB	ILE A 153	8.779	58.143	116.355	1.00	24.38
	1054	CG2	ILE A 153	8.319	57.131	115.356	1.00	20.92
	1055	CG1	ILE A 153	9.624	59.268	115.750	1.00	22.68
40	1056	CD1	ILE A 153	10.886	58.816	115.109	1.00	23.49
	1057	C	ILE A 153	6.651	57.660	117.576	1.00	27.70
	1058	O	ILE A 153	5.673	57.300	116.915	1.00	32.24
	1059	N	THR A 154	6.965	57.117	118.743	1.00	30.25

	1060	CA	THR A 154	6.137	56.076	119.350	1.00	28.49
	1061	CB	THR A 154	6.845	55.484	120.592	1.00	23.50
	1062	OG1	THR A 154	8.071	54.863	120.183	1.00	34.63
	1063	CG2	THR A 154	5.989	54.431	121.261	1.00	27.71
5	1064	C	THR A 154	4.774	56.672	119.738	1.00	28.18
	1065	O	THR A 154	3.733	56.063	119.522	1.00	31.16
	1066	N	GLN A 155	4.777	57.870	120.296	1.00	29.63
	1067	CA	GLN A 155	3.530	58.521	120.673	1.00	36.38
	1068	CB	GLN A 155	3.822	59.821	121.429	1.00	39.77
10	1069	CG	GLN A 155	2.592	60.661	121.753	1.00	51.92
	1070	CD	GLN A 155	2.343	61.773	120.736	0.50	53.92
	1071	OE1	GLN A 155	1.322	62.457	120.795	0.50	57.58
	1072	NE2	GLN A 155	3.281	61.961	119.806	0.50	54.97
	1073	C	GLN A 155	2.691	58.813	119.427	1.00	41.21
15	1074	O	GLN A 155	1.466	58.710	119.462	1.00	44.14
	1075	N	ALA A 156	3.345	59.175	118.325	1.00	42.25
	1076	CA	ALA A 156	2.625	59.457	117.087	1.00	40.59
	1077	CB	ALA A 156	3.578	59.921	116.016	1.00	34.98
	1078	C	ALA A 156	1.900	58.200	116.629	1.00	42.14
20	1079	O	ALA A 156	0.743	58.262	116.221	1.00	41.76
	1080	N	LEU A 157	2.579	57.060	116.698	1.00	41.36
	1081	CA	LEU A 157	1.975	55.791	116.300	1.00	42.90
	1082	CB	LEU A 157	3.003	54.671	116.412	1.00	40.99
	1083	CG	LEU A 157	2.454	53.258	116.217	1.00	41.50
25	1084	CD1	LEU A 157	1.617	53.179	114.935	1.00	36.67
	1085	CD2	LEU A 157	3.627	52.282	116.172	1.00	42.66
	1086	C	LEU A 157	0.754	55.437	117.163	1.00	47.07
	1087	O	LEU A 157	-0.301	55.047	116.662	1.00	45.03
	1088	N	LYS A 158	0.908	55.559	118.472	1.00	47.38
30	1089	CA	LYS A 158	-0.187	55.260	119.373	1.00	52.29
	1090	CB	LYS A 158	0.207	55.655	120.806	1.00	53.87
	1091	CG	LYS A 158	-0.117	54.597	121.840	1.00	62.16
	1092	CD	LYS A 158	0.454	54.931	123.219	1.00	66.75
	1093	CE	LYS A 158	1.927	54.565	123.328	1.00	70.99
35	1094	NZ	LYS A 158	2.406	54.522	124.746	1.00	69.14
	1095	C	LYS A 158	-1.439	56.029	118.896	1.00	49.70
	1096	O	LYS A 158	-2.505	55.440	118.739	1.00	51.07
	1097	N	LEU A 159	-1.297	57.332	118.649	1.00	44.47
	1098	CA	LEU A 159	-2.404	58.162	118.177	1.00	42.31
40	1099	CB	LEU A 159	-1.965	59.619	118.038	1.00	39.23
	1100	CG	LEU A 159	-1.513	60.315	119.323	1.00	43.99
	1101	CD1	LEU A 159	-0.914	61.680	119.040	1.00	43.55
	1102	CD2	LEU A 159	-2.714	60.452	120.230	1.00	50.23

	1103	C	LEU A 159	-2.897	57.655	116.822	1.00	46.83
	1104	O	LEU A 159	-4.100	57.451	116.627	1.00	45.36
	1105	N	ILE A 160	-1.966	57.446	115.892	1.00	45.12
	1106	CA	ILE A 160	-2.318	56.961	114.560	1.00	44.34
5	1107	CB	ILE A 160	-1.064	56.792	113.652	1.00	39.75
	1108	CG2	ILE A 160	-1.430	56.073	112.381	1.00	28.98
	1109	CG1	ILE A 160	-0.476	58.165	113.283	1.00	41.04
	1110	CD1	ILE A 160	0.885	58.066	112.546	1.00	31.10
	1111	C	ILE A 160	-3.091	55.642	114.580	1.00	44.99
10	1112	O	ILE A 160	-4.079	55.506	113.858	1.00	46.48
	1113	N	SER A 161	-2.659	54.678	115.395	1.00	48.88
	1114	CA	SER A 161	-3.344	53.381	115.461	1.00	49.81
	1115	CB	SER A 161	-2.504	52.351	116.214	1.00	49.04
	1116	OG	SER A 161	-2.802	52.377	117.599	1.00	54.96
15	1117	C	SER A 161	-4.705	53.543	116.150	1.00	52.95
	1118	O	SER A 161	-5.656	52.830	115.836	1.00	54.24
	1119	N	GLN A 162	-4.800	54.478	117.091	1.00	54.23
	1120	CA	GLN A 162	-6.075	54.716	117.745	1.00	57.67
	1121	CB	GLN A 162	-5.952	55.791	118.821	1.00	60.93
20	1122	CG	GLN A 162	-7.255	56.043	119.589	1.00	69.51
	1123	CD	GLN A 162	-7.744	54.809	120.334	1.00	73.81
	1124	OE1	GLN A 162	-8.125	53.802	119.725	1.00	76.11
	1125	NE2	GLN A 162	-7.726	54.880	121.663	1.00	77.75
	1126	C	GLN A 162	-7.011	55.202	116.639	1.00	60.30
25	1127	O	GLN A 162	-8.100	54.656	116.461	1.00	63.21
	1128	N	ASP A 163	-6.575	56.224	115.897	1.00	58.05
	1129	CA	ASP A 163	-7.362	56.761	114.794	1.00	56.08
	1130	CB	ASP A 163	-6.612	57.891	114.102	1.00	53.75
	1131	CG	ASP A 163	-6.708	59.190	114.863	1.00	56.70
30	1132	OD1	ASP A 163	-6.833	59.126	116.100	1.00	63.97
	1133	OD2	ASP A 163	-6.650	60.268	114.241	1.00	56.05
	1134	C	ASP A 163	-7.727	55.678	113.785	1.00	57.17
	1135	O	ASP A 163	-8.771	55.766	113.142	1.00	58.59
	1136	N	VAL A 164	-6.884	54.657	113.646	1.00	53.74
35	1137	CA	VAL A 164	-7.191	53.574	112.727	1.00	53.29
	1138	CB	VAL A 164	-5.983	52.656	112.505	1.00	51.29
	1139	CG1	VAL A 164	-6.418	51.368	111.819	1.00	49.71
	1140	CG2	VAL A 164	-4.956	53.367	111.656	1.00	52.69
	1141	C	VAL A 164	-8.349	52.759	113.304	1.00	58.94
40	1142	O	VAL A 164	-9.245	52.339	112.569	1.00	62.76
	1143	N	LEU A 165	-8.337	52.533	114.616	1.00	58.01
	1144	CA	LEU A 165	-9.421	51.783	115.249	1.00	60.34
	1145	CB	LEU A 165	-9.121	51.512	116.724	1.00	58.51

	1146	CG	LEU A 165	-8.157	50.362	117.022	1.00	56.47
	1147	CD1	LEU A 165	-8.023	50.201	118.528	1.00	50.87
	1148	CD2	LEU A 165	-8.665	49.075	116.380	1.00	52.53
	1149	C	LEU A 165	-10.699	52.598	115.130	1.00	61.56
5	1150	O	LEU A 165	-11.683	52.127	114.569	1.00	64.25
	1151	N	ASP A 166	-10.667	53.824	115.653	1.00	60.25
	1152	CA	ASP A 166	-11.805	54.743	115.595	1.00	63.16
	1153	CB	ASP A 166	-11.405	56.125	116.131	1.00	64.19
	1154	CG	ASP A 166	-11.284	56.162	117.650	1.00	69.25
10	1155	OD1	ASP A 166	-10.899	55.133	118.249	1.00	68.14
	1156	OD2	ASP A 166	-11.564	57.231	118.240	1.00	69.18
	1157	C	ASP A 166	-12.311	54.900	114.161	1.00	64.36
	1158	O	ASP A 166	-13.318	55.571	113.922	1.00	66.24
	1159	N	ALA A 167	-11.595	54.287	113.219	1.00	63.52
15	1160	CA	ALA A 167	-11.923	54.326	111.796	1.00	61.19
	1161	CB	ALA A 167	-13.289	53.701	111.554	1.00	63.47
	1162	C	ALA A 167	-11.870	55.727	111.187	1.00	58.29
	1163	O	ALA A 167	-12.507	55.993	110.172	1.00	58.01
	1164	N	LYS A 168	-11.118	56.623	111.810	1.00	55.00
20	1165	CA	LYS A 168	-10.982	57.969	111.276	1.00	56.83
	1166	CB	LYS A 168	-10.387	58.911	112.323	1.00	60.06
	1167	CG	LYS A 168	-11.383	59.474	113.325	1.00	65.21
	1168	CD	LYS A 168	-10.749	60.634	114.095	1.00	70.32
	1169	CE	LYS A 168	-11.789	61.625	114.598	1.00	71.98
25	1170	NZ	LYS A 168	-11.156	62.821	115.231	1.00	76.79
	1171	C	LYS A 168	-10.075	57.936	110.043	1.00	56.13
	1172	O	LYS A 168	-10.131	58.826	109.197	1.00	55.29
	1173	N	ILE A 169	-9.239	56.904	109.953	1.00	56.46
	1174	CA	ILE A 169	-8.317	56.731	108.832	1.00	56.72
30	1175	CB	AILE A 169	-6.946	57.424	109.084	0.50	56.13
	7701	CB	BILE A 169	-6.992	57.513	109.093	0.50	57.59
	1176	CG2AILE	A 169	-7.127	58.937	109.176	0.50	55.73
	7702	CG2BILE	A 169	-5.816	56.845	108.392	0.50	58.25
	1177	CG1AILE	A 169	-6.287	56.848	110.346	0.50	52.21
35	7703	CG1BILE	A 169	-7.166	58.972	108.643	0.50	54.53
	1178	CD1AILE	A 169	-4.909	57.422	110.646	0.50	46.70
	7704	CD1BILE	A 169	-5.966	59.863	108.898	0.50	52.01
	1179	C	ILE A 169	-8.048	55.244	108.630	1.00	58.60
	1180	O	ILE A 169	-8.383	54.429	109.489	1.00	62.18
40	1181	N	ASN A 170	-7.463	54.895	107.489	1.00	58.23
	1182	CA	ASN A 170	-7.136	53.507	107.177	1.00	58.09
	1183	CB	ASN A 170	-7.691	53.138	105.790	1.00	59.63
	1184	CG	ASN A 170	-7.364	51.706	105.383	0.50	61.62



	1185	OD1	ASN	A	170	-6.232	51.395	105.011	0.50	60.27
	1186	ND2	ASN	A	170	-8.360	50.826	105.456	0.50	62.86
	1187	C	ASN	A	170	-5.611	53.383	107.188	1.00	58.37
	1188	O	ASN	A	170	-4.904	54.347	106.903	1.00	51.00
5	1189	N	PRO	A	171	-5.083	52.199	107.539	1.00	59.71
	1190	CD	PRO	A	171	-5.743	50.961	107.991	1.00	61.83
	1191	CA	PRO	A	171	-3.626	52.046	107.557	1.00	59.45
	1192	CB	PRO	A	171	-3.429	50.601	108.043	1.00	57.48
	1193	CG	PRO	A	171	-4.700	49.920	107.665	1.00	59.99
10	1194	C	PRO	A	171	-2.977	52.329	106.200	1.00	58.58
	1195	O	PRO	A	171	-1.784	52.640	106.125	1.00	60.74
	1196	N	GLY	A	172	-3.765	52.230	105.133	1.00	57.99
	1197	CA	GLY	A	172	-3.248	52.506	103.802	1.00	53.09
	1198	C	GLY	A	172	-2.934	53.986	103.676	1.00	51.16
15	1199	O	GLY	A	172	-2.130	54.403	102.834	1.00	50.47
	1200	N	ASP	A	173	-3.574	54.779	104.534	1.00	49.06
	1201	CA	ASP	A	173	-3.382	56.223	104.563	1.00	51.49
	1202	CB	ASP	A	173	-4.571	56.903	105.238	1.00	60.24
	1203	CG	ASP	A	173	-5.852	56.735	104.461	1.00	67.87
20	1204	OD1	ASP	A	173	-6.311	55.581	104.299	1.00	76.27
	1205	OD2	ASP	A	173	-6.396	57.764	104.007	1.00	73.57
	1206	C	ASP	A	173	-2.101	56.640	105.283	1.00	48.17
	1207	O	ASP	A	173	-1.712	57.806	105.214	1.00	46.24
	1208	N	ILE	A	174	-1.471	55.688	105.977	1.00	47.18
25	1209	CA	ILE	A	174	-0.220	55.918	106.715	1.00	45.26
	1210	CB	ILE	A	174	0.069	54.764	107.720	1.00	46.67
	1211	CG2	ILE	A	174	1.479	54.898	108.279	1.00	45.07
	1212	CG1	ILE	A	174	-0.956	54.788	108.867	1.00	42.99
	1213	CD1	ILE	A	174	-0.811	53.638	109.844	1.00	34.24
30	1214	C	ILE	A	174	0.954	56.048	105.738	1.00	41.85
	1215	O	ILE	A	174	1.427	55.079	105.150	1.00	41.06
	1216	N	THR	A	175	1.405	57.280	105.582	1.00	40.68
	1217	CA	THR	A	175	2.490	57.624	104.682	1.00	39.32
	1218	CB	THR	A	175	1.944	58.339	103.466	1.00	38.50
35	1219	OG1	THR	A	175	1.375	59.584	103.894	1.00	34.69
	1220	CG2	THR	A	175	0.855	57.499	102.807	1.00	34.01
	1221	C	THR	A	175	3.379	58.612	105.416	1.00	35.87
	1222	O	THR	A	175	3.014	59.113	106.486	1.00	36.32
	1223	N	GLU	A	176	4.532	58.909	104.834	1.00	34.88
40	1224	CA	GLU	A	176	5.454	59.849	105.442	1.00	30.79
	1225	CB	GLU	A	176	6.616	60.078	104.514	1.00	31.95
	1226	CG	GLU	A	176	7.571	58.921	104.509	1.00	30.89
	1227	CD	GLU	A	176	8.787	59.222	103.686	1.00	31.86

	1228	OE1	GLU	A	176	9.185	60.405	103.680	1.00	36.98
	1229	OE2	GLU	A	176	9.343	58.295	103.061	1.00	33.39
	1230	C	GLU	A	176	4.824	61.175	105.819	1.00	33.02
	1231	O	GLU	A	176	5.027	61.671	106.928	1.00	34.02
5	1232	N	GLU	A	177	4.049	61.756	104.914	1.00	33.79
	1233	CA	GLU	A	177	3.412	63.032	105.218	1.00	40.89
	1234	CB	GLU	A	177	2.760	63.623	103.968	1.00	45.59
	1235	CG	GLU	A	177	2.632	62.652	102.787	1.00	58.96
	1236	CD	GLU	A	177	3.978	62.211	102.185	1.00	61.04
10	1237	OE1	GLU	A	177	4.833	63.087	101.893	1.00	67.66
	1238	OE2	GLU	A	177	4.169	60.987	101.988	1.00	54.76
	1239	C	GLU	A	177	2.378	62.917	106.341	1.00	42.80
	1240	O	GLU	A	177	2.219	63.838	107.138	1.00	42.88
	1241	N	LEU	A	178	1.678	61.787	106.409	1.00	41.31
15	1242	CA	LEU	A	178	0.682	61.590	107.457	1.00	42.26
	1243	CB	LEU	A	178	-0.032	60.245	107.303	1.00	40.52
	1244	CG	LEU	A	178	-1.020	60.016	108.447	1.00	46.79
	1245	CD1	LEU	A	178	-2.142	61.038	108.336	1.00	46.47
	1246	CD2	LEU	A	178	-1.582	58.613	108.399	1.00	49.79
20	1247	C	LEU	A	178	1.369	61.616	108.811	1.00	41.43
	1248	O	LEU	A	178	0.966	62.354	109.711	1.00	36.61
	1249	N	ILE	A	179	2.413	60.801	108.939	1.00	40.34
	1250	CA	ILE	A	179	3.163	60.709	110.177	1.00	35.81
	1251	CB	ILE	A	179	4.344	59.751	110.011	1.00	30.64
25	1252	CG2	ILE	A	179	5.327	59.907	111.165	1.00	26.56
	1253	CG1	ILE	A	179	3.803	58.325	109.923	1.00	21.96
	1254	CD1	ILE	A	179	4.805	57.294	109.483	1.00	21.42
	1255	C	ILE	A	179	3.637	62.075	110.643	1.00	37.49
	1256	O	ILE	A	179	3.552	62.393	111.832	1.00	38.37
30	1257	N	GLY	A	180	4.107	62.894	109.711	1.00	36.42
	1258	CA	GLY	A	180	4.562	64.221	110.079	1.00	35.57
	1259	C	GLY	A	180	3.480	65.062	110.742	1.00	41.87
	1260	O	GLY	A	180	3.783	65.994	111.490	1.00	42.41
	1261	N	ASN	A	181	2.212	64.756	110.474	1.00	42.75
35	1262	CA	ASN	A	181	1.126	65.522	111.078	1.00	43.17
	1263	CB	ASN	A	181	-0.158	65.396	110.252	1.00	44.11
	1264	CG	ASN	A	181	-0.052	66.081	108.899	1.00	41.60
	1265	OD1	ASN	A	181	0.314	67.250	108.813	1.00	46.90
	1266	ND2	ASN	A	181	-0.375	65.355	107.840	1.00	39.46
40	1267	C	ASN	A	181	0.865	65.095	112.511	1.00	42.08
	1268	O	ASN	A	181	0.240	65.833	113.276	1.00	45.36
	1269	N	TYR	A	182	1.348	63.912	112.879	1.00	39.97
	1270	CA	TYR	A	182	1.166	63.411	114.237	1.00	38.67

	1271	CB	TYR A 182	0.794	61.928	114.220	1.00	43.17
	1272	CG	TYR A 182	-0.618	61.630	113.738	1.00	50.86
	1273	CD1	TYR A 182	-0.922	61.588	112.374	1.00	53.96
	1274	CE1	TYR A 182	-2.215	61.262	111.920	1.00	53.67
5	1275	CD2	TYR A 182	-1.645	61.354	114.647	1.00	50.20
	1276	CE2	TYR A 182	-2.936	61.031	114.208	1.00	53.31
	1277	CZ	TYR A 182	-3.212	60.981	112.842	1.00	54.11
	1278	OH	TYR A 182	-4.455	60.592	112.400	1.00	50.32
	1279	C	TYR A 182	2.373	63.615	115.162	1.00	39.20
10	1280	O	TYR A 182	2.325	63.254	116.337	1.00	39.06
	1281	N	LEU A 183	3.452	64.192	114.645	1.00	36.72
	1282	CA	LEU A 183	4.635	64.422	115.468	1.00	33.95
	1283	CB	LEU A 183	5.894	64.501	114.591	1.00	27.37
	1284	CG	LEU A 183	6.233	63.224	113.810	1.00	26.13
15	1285	CD1	LEU A 183	7.356	63.499	112.846	1.00	21.71
	1286	CD2	LEU A 183	6.614	62.103	114.769	1.00	25.23
	1287	C	LEU A 183	4.454	65.710	116.261	1.00	34.92
	1288	O	LEU A 183	3.576	66.512	115.957	1.00	35.87
	1289	N	PHE A 184	5.292	65.918	117.270	1.00	32.97
20	1290	CA	PHE A 184	5.178	67.103	118.109	1.00	32.95
	1291	CB	PHE A 184	6.192	67.051	119.256	1.00	33.14
	1292	CG	PHE A 184	5.978	65.907	120.208	1.00	31.94
	1293	CD1	PHE A 184	7.022	65.444	120.995	1.00	29.81
	1294	CD2	PHE A 184	4.721	65.330	120.360	1.00	34.12
25	1295	CE1	PHE A 184	6.824	64.428	121.923	1.00	31.12
	1296	CE2	PHE A 184	4.513	64.308	121.292	1.00	37.64
	1297	CZ	PHE A 184	5.573	63.862	122.073	1.00	36.11
	1298	C	PHE A 184	5.365	68.395	117.348	1.00	33.85
	1299	O	PHE A 184	5.032	69.459	117.848	1.00	42.18
30	1300	N	THR A 185	5.900	68.311	116.141	1.00	32.75
	1301	CA	THR A 185	6.141	69.508	115.352	1.00	29.41
	1302	CB	THR A 185	7.484	69.386	114.637	1.00	30.00
	1303	OG1	THR A 185	7.545	68.113	113.991	1.00	24.04
	1304	CG2	THR A 185	8.643	69.497	115.642	1.00	22.45
35	1305	C	THR A 185	5.033	69.814	114.338	1.00	29.02
	1306	O	THR A 185	5.181	70.686	113.498	1.00	27.43
	1307	N	GLN A 186	3.934	69.072	114.409	1.00	33.84
	1308	CA	GLN A 186	2.794	69.289	113.521	1.00	41.75
	1309	CB	GLN A 186	1.646	68.344	113.892	1.00	41.00
40	1310	CG	GLN A 186	1.157	68.529	115.332	1.00	49.89
	1311	CD	GLN A 186	0.158	67.471	115.776	1.00	56.99
	1312	OE1	GLN A 186	-0.987	67.444	115.316	1.00	62.44
	1313	NE2	GLN A 186	0.588	66.592	116.678	1.00	54.20

	1314	C	GLN A 186	2.341	70.725	113.745	1.00	48.38
	1315	O	GLN A 186	1.892	71.403	112.824	1.00	48.39
	1316	N	HIS A 187	2.495	71.178	114.987	1.00	54.46
	1317	CA	HIS A 187	2.094	72.516	115.406	1.00	60.71
5	1318	CB	HIS A 187	2.189	72.633	116.935	1.00	68.73
	1319	CG	HIS A 187	1.423	71.573	117.675	1.00	75.60
	1320	CD2	HIS A 187	1.795	70.738	118.677	1.00	77.36
	1321	ND1	HIS A 187	0.095	71.293	117.420	1.00	76.34
	1322	CE1	HIS A 187	-0.316	70.334	118.232	1.00	77.87
10	1323	NE2	HIS A 187	0.696	69.979	119.005	1.00	78.08
	1324	C	HIS A 187	2.887	73.640	114.756	1.00	59.30
	1325	O	HIS A 187	2.764	74.794	115.144	1.00	61.90
	1326	N	LEU A 188	3.713	73.304	113.774	1.00	57.82
	1327	CA	LEU A 188	4.492	74.311	113.067	1.00	52.51
15	1328	CB	LEU A 188	5.977	73.963	113.042	1.00	49.73
	1329	CG	LEU A 188	6.877	73.870	114.272	1.00	49.29
	1330	CD1	LEU A 188	8.283	73.511	113.801	1.00	40.12
	1331	CD2	LEU A 188	6.899	75.190	115.031	1.00	48.66
	1332	C	LEU A 188	3.997	74.303	111.639	1.00	53.88
20	1333	O	LEU A 188	3.414	73.322	111.186	1.00	55.99
	1334	N	PRO A 189	4.198	75.405	110.912	1.00	56.13
	1335	CD	PRO A 189	4.530	76.766	111.367	1.00	55.62
	1336	CA	PRO A 189	3.733	75.404	109.521	1.00	56.18
	1337	CB	PRO A 189	4.091	76.812	109.022	1.00	58.65
25	1338	CG	PRO A 189	5.013	77.395	110.104	1.00	57.80
	1339	C	PRO A 189	4.422	74.287	108.736	1.00	56.90
	1340	O	PRO A 189	5.629	74.082	108.864	1.00	58.22
	1341	N	LYS A 190	3.649	73.567	107.928	1.00	55.53
	1342	CA	LYS A 190	4.171	72.445	107.158	1.00	53.05
30	1343	CB	LYS A 190	3.123	71.956	106.150	1.00	57.09
	1344	CG	LYS A 190	1.916	71.317	106.813	1.00	63.79
	1345	CD	LYS A 190	1.164	70.356	105.900	1.00	64.18
	1346	CE	LYS A 190	-0.028	69.745	106.652	1.00	65.71
	1347	NZ	LYS A 190	-0.910	68.906	105.785	1.00	64.57
35	1348	C	LYS A 190	5.494	72.631	106.437	1.00	50.65
	1349	O	LYS A 190	6.258	71.676	106.289	1.00	51.90
	1350	N	ASP A 191	5.780	73.849	105.999	1.00	47.91
	1351	CA	ASP A 191	7.010	74.119	105.251	1.00	45.70
	1352	CB	ASP A 191	6.793	75.330	104.324	1.00	49.06
40	1353	CG	ASP A 191	6.235	76.551	105.069	0.50	51.88
	1354	OD1	ASP A 191	5.131	76.456	105.655	0.50	51.16
	1355	OD2	ASP A 191	6.902	77.608	105.072	0.50	53.71
	1356	C	ASP A 191	8.234	74.364	106.120	1.00	43.08

	1357	O	ASP A 191	9.358	74.456	105.612	1.00	43.34
	1358	N	LEU A 192	8.014	74.469	107.427	1.00	40.39
	1359	CA	LEU A 192	9.092	74.746	108.367	1.00	36.65
	1360	CB	LEU A 192	8.834	76.106	109.038	1.00	41.31
5	1361	CG	LEU A 192	8.851	77.390	108.192	1.00	38.59
	1362	CD1	LEU A 192	8.059	78.473	108.888	1.00	33.65
	1363	CD2	LEU A 192	10.284	77.841	107.959	1.00	30.35
	1364	C	LEU A 192	9.245	73.671	109.450	1.00	34.59
	1365	O	LEU A 192	10.043	73.827	110.365	1.00	35.53
10	1366	N	ARG A 193	8.486	72.586	109.343	1.00	31.49
	1367	CA	ARG A 193	8.527	71.525	110.346	1.00	33.84
	1368	CB	ARG A 193	7.484	70.458	110.010	1.00	32.16
	1369	CG	ARG A 193	6.056	70.868	110.303	1.00	36.84
	1370	CD	ARG A 193	5.107	69.885	109.661	1.00	35.27
15	1371	NE	ARG A 193	3.737	70.028	110.133	1.00	38.84
	1372	CZ	ARG A 193	2.733	69.248	109.740	1.00	47.21
	1373	NH1	ARG A 193	2.952	68.267	108.859	1.00	45.69
	1374	NH2	ARG A 193	1.515	69.429	110.246	1.00	41.23
	1375	C	ARG A 193	9.893	70.857	110.555	1.00	34.23
20	1376	O	ARG A 193	10.215	70.428	111.665	1.00	32.64
	1377	N	ASP A 194	10.691	70.769	109.498	1.00	33.12
	1378	CA	ASP A 194	11.995	70.126	109.591	1.00	33.80
	1379	CB	ASP A 194	12.193	69.151	108.425	1.00	33.56
	1380	CG	ASP A 194	11.072	68.150	108.308	1.00	34.25
25	1381	OD1	ASP A 194	10.427	67.824	109.336	1.00	26.30
	1382	OD2	ASP A 194	10.847	67.680	107.172	1.00	36.29
	1383	C	ASP A 194	13.149	71.112	109.603	1.00	29.22
	1384	O	ASP A 194	13.238	71.961	108.736	1.00	30.26
	1385	N	PRO A 195	14.062	70.994	110.586	1.00	29.58
30	1386	CD	PRO A 195	14.116	69.924	111.595	1.00	23.81
	1387	CA	PRO A 195	15.225	71.884	110.707	1.00	25.87
	1388	CB	PRO A 195	15.975	71.322	111.920	1.00	30.04
	1389	CG	PRO A 195	14.935	70.561	112.680	1.00	30.61
	1390	C	PRO A 195	16.105	71.811	109.454	1.00	29.31
35	1391	O	PRO A 195	16.320	70.732	108.905	1.00	29.35
	1392	N	ASP A 196	16.631	72.947	109.018	1.00	29.28
	1393	CA	ASP A 196	17.497	72.972	107.847	1.00	28.26
	1394	CB	ASP A 196	17.429	74.332	107.140	1.00	30.74
	1395	CG	ASP A 196	16.055	74.633	106.596	1.00	34.65
40	1396	OD1	ASP A 196	15.198	75.192	107.333	1.00	33.66
	1397	OD2	ASP A 196	15.828	74.286	105.423	1.00	39.73
	1398	C	ASP A 196	18.890	72.780	108.385	1.00	30.42
	1399	O	ASP A 196	19.795	72.351	107.680	1.00	29.11

	1400	N	LEU A 197	19.042	73.113	109.658	1.00	26.44
	1401	CA	LEU A 197	20.320	73.026	110.326	1.00	26.28
	1402	CB	LEU A 197	21.035	74.380	110.216	1.00	28.09
	1403	CG	LEU A 197	22.302	74.625	111.043	1.00	26.61
5	1404	CD1	LEU A 197	23.433	73.785	110.504	1.00	32.33
	1405	CD2	LEU A 197	22.680	76.107	111.004	1.00	29.44
	1406	C	LEU A 197	20.143	72.647	111.797	1.00	30.02
	1407	O	LEU A 197	19.195	73.088	112.455	1.00	31.79
	1408	N	ILE A 198	21.051	71.813	112.301	1.00	30.09
10	1409	CA	ILE A 198	21.038	71.410	113.701	1.00	27.96
	1410	CB	ILE A 198	20.722	69.918	113.864	1.00	28.79
	1411	CG2	ILE A 198	20.884	69.508	115.314	1.00	28.75
	1412	CG1	ILE A 198	19.272	69.653	113.445	1.00	26.24
	1413	CD1	ILE A 198	18.860	68.197	113.540	1.00	20.85
15	1414	C	ILE A 198	22.433	71.735	114.211	1.00	26.43
	1415	O	ILE A 198	23.431	71.405	113.578	1.00	28.65
	1416	N	ILE A 199	22.489	72.426	115.341	1.00	28.97
	1417	CA	ILE A 199	23.745	72.855	115.943	1.00	24.85
	1418	CB	ILE A 199	23.744	74.382	116.277	1.00	29.70
20	1419	CG2	ILE A 199	24.954	74.735	117.101	1.00	25.35
	1420	CG1	ILE A 199	23.737	75.226	115.009	1.00	31.67
	1421	CD1	ILE A 199	23.580	76.686	115.299	1.00	34.68
	1422	C	ILE A 199	23.912	72.175	117.269	1.00	22.40
	1423	O	ILE A 199	22.961	72.088	118.040	1.00	21.21
25	1424	N	ARG A 200	25.108	71.677	117.548	1.00	25.04
	1425	CA	ARG A 200	25.329	71.109	118.861	1.00	27.33
	1426	CB	ARG A 200	25.442	69.596	118.844	1.00	29.53
	1427	CG	ARG A 200	25.553	69.098	120.272	1.00	35.88
	1428	CD	ARG A 200	25.255	67.635	120.458	1.00	36.27
30	1429	NE	ARG A 200	25.423	67.299	121.866	1.00	37.85
	1430	CZ	ARG A 200	24.985	66.179	122.416	1.00	36.79
	1431	NH1	ARG A 200	24.349	65.293	121.670	1.00	42.33
	1432	NH2	ARG A 200	25.189	65.945	123.702	1.00	38.15
	1433	C	ARG A 200	26.589	71.720	119.427	1.00	28.20
35	1434	O	ARG A 200	27.575	71.861	118.720	1.00	32.58
	1435	N	THR A 201	26.525	72.119	120.691	1.00	27.92
	1436	CA	THR A 201	27.649	72.721	121.389	1.00	29.95
	1437	CB	THR A 201	27.202	74.006	122.149	1.00	32.38
	1438	OG1	THR A 201	26.076	73.714	122.991	1.00	34.33
40	1439	CG2	THR A 201	26.807	75.096	121.164	1.00	30.66
	1440	C	THR A 201	28.301	71.751	122.392	1.00	32.49
	1441	O	THR A 201	27.811	70.648	122.627	1.00	33.65
	1442	N	SER A 202	29.425	72.183	122.959	1.00	36.87

	1443	CA	SER A 202	30.185	71.432	123.945	1.00	34.07
	1444	CB	SER A 202	29.267	70.908	125.046	1.00	39.41
	1445	OG	SER A 202	29.974	70.810	126.274	1.00	47.53
	1446	C	SER A 202	31.006	70.290	123.385	1.00	37.19
5	1447	O	SER A 202	31.374	69.381	124.115	1.00	40.03
	1448	N	GLY A 203	31.279	70.329	122.086	1.00	35.57
	1449	CA	GLY A 203	32.112	69.313	121.464	1.00	32.57
	1450	C	GLY A 203	31.619	67.885	121.295	1.00	36.02
	1451	O	GLY A 203	32.364	67.037	120.815	1.00	31.58
10	1452	N	GLU A 204	30.386	67.596	121.680	1.00	34.34
	1453	CA	GLU A 204	29.881	66.247	121.543	1.00	37.88
	1454	CB	GLU A 204	28.752	66.020	122.546	1.00	43.74
	1455	CG	GLU A 204	29.204	66.139	123.994	1.00	46.98
	1456	CD	GLU A 204	30.434	65.294	124.288	1.00	51.17
15	1457	OE1	GLU A 204	30.419	64.083	123.967	1.00	50.63
	1458	OE2	GLU A 204	31.416	65.844	124.841	1.00	58.26
	1459	C	GLU A 204	29.405	65.950	120.118	1.00	39.94
	1460	O	GLU A 204	28.549	66.651	119.578	1.00	42.35
	1461	N	LEU A 205	29.972	64.906	119.515	1.00	38.98
20	1462	CA	LEU A 205	29.621	64.513	118.161	1.00	38.39
	1463	CB	LEU A 205	30.860	64.030	117.410	1.00	44.77
	1464	CG	LEU A 205	31.646	65.097	116.646	1.00	47.12
	1465	CD1	LEU A 205	32.812	64.455	115.905	1.00	50.00
	1466	CD2	LEU A 205	30.725	65.755	115.656	1.00	44.90
25	1467	C	LEU A 205	28.565	63.426	118.149	1.00	38.17
	1468	O	LEU A 205	28.862	62.266	117.858	1.00	39.87
	1469	N	ARG A 206	27.333	63.812	118.467	1.00	36.54
	1470	CA	ARG A 206	26.216	62.884	118.496	1.00	36.16
	1471	CB	ARG A 206	26.366	61.929	119.688	1.00	33.75
30	1472	CG	ARG A 206	26.196	62.543	121.047	1.00	43.22
	1473	CD	ARG A 206	26.076	61.466	122.134	1.00	42.89
	1474	NE	ARG A 206	27.376	61.091	122.668	1.00	51.11
	1475	CZ	ARG A 206	28.045	61.809	123.567	1.00	55.74
	1476	NH1	ARG A 206	27.522	62.935	124.035	1.00	57.07
35	1477	NH2	ARG A 206	29.245	61.418	123.984	1.00	52.11
	1478	C	ARG A 206	24.901	63.675	118.539	1.00	37.36
	1479	O	ARG A 206	24.880	64.863	118.892	1.00	35.99
	1480	N	LEU A 207	23.798	63.038	118.161	1.00	37.49
	1481	CA	LEU A 207	22.519	63.753	118.131	1.00	34.07
40	1482	CB	LEU A 207	21.733	63.342	116.881	1.00	38.49
	1483	CG	LEU A 207	22.465	63.806	115.609	1.00	35.25
	1484	CD1	LEU A 207	21.841	63.185	114.391	1.00	38.43
	1485	CD2	LEU A 207	22.404	65.337	115.521	1.00	41.16

	1486	C	LEU A 207	21.662	63.625	119.383	1.00	33.23
	1487	O	LEU A 207	20.817	64.477	119.664	1.00	37.93
	1488	N	SER A 208	21.877	62.565	120.140	1.00	28.66
	1489	CA	SER A 208	21.142	62.382	121.373	1.00	22.25
5	1490	CB	SER A 208	21.509	63.473	122.377	1.00	28.70
	1491	OG	SER A 208	22.849	63.328	122.815	1.00	33.59
	1492	C	SER A 208	19.644	62.329	121.246	1.00	22.21
	1493	O	SER A 208	18.946	62.911	122.059	1.00	22.32
	1494	N	ASN A 209	19.147	61.635	120.228	1.00	22.69
10	1495	CA	ASN A 209	17.710	61.456	120.088	1.00	24.65
	1496	CB	ASN A 209	17.202	60.723	121.339	1.00	19.61
	1497	CG	ASN A 209	15.868	60.058	121.129	1.00	22.39
	1498	OD1	ASN A 209	15.495	59.721	120.010	1.00	15.96
	1499	ND2	ASN A 209	15.141	59.844	122.220	1.00	25.04
15	1500	C	ASN A 209	16.923	62.754	119.865	1.00	24.40
	1501	O	ASN A 209	15.772	62.864	120.270	1.00	23.22
	1502	N	PHE A 210	17.552	63.724	119.214	1.00	21.21
	1503	CA	PHE A 210	16.916	65.001	118.901	1.00	23.62
	1504	CB	PHE A 210	17.932	66.137	119.093	1.00	21.89
20	1505	CG	PHE A 210	17.347	67.505	118.941	1.00	23.88
	1506	CD1	PHE A 210	16.228	67.881	119.679	1.00	24.80
	1507	CD2	PHE A 210	17.889	68.413	118.039	1.00	24.87
	1508	CE1	PHE A 210	15.646	69.152	119.516	1.00	25.12
	1509	CE2	PHE A 210	17.321	69.686	117.868	1.00	25.18
25	1510	CZ	PHE A 210	16.193	70.050	118.611	1.00	22.12
	1511	C	PHE A 210	16.341	65.052	117.460	1.00	22.68
	1512	O	PHE A 210	17.077	65.025	116.493	1.00	25.08
	1513	N	LEU A 211	15.016	65.127	117.330	1.00	26.44
	1514	CA	LEU A 211	14.352	65.206	116.024	1.00	20.62
30	1515	CB	LEU A 211	14.491	66.627	115.470	1.00	18.71
	1516	CG	LEU A 211	14.089	67.779	116.404	1.00	16.62
	1517	CD1	LEU A 211	14.443	69.101	115.738	1.00	20.19
	1518	CD2	LEU A 211	12.582	67.720	116.741	1.00	16.06
	1519	C	LEU A 211	14.889	64.209	114.988	1.00	22.65
35	1520	O	LEU A 211	15.240	64.591	113.870	1.00	19.02
	1521	N	PRO A 212	14.968	62.919	115.345	1.00	21.39
	1522	CD	PRO A 212	14.572	62.262	116.600	1.00	17.19
	1523	CA	PRO A 212	15.483	61.944	114.375	1.00	21.14
	1524	CB	PRO A 212	15.385	60.607	115.130	1.00	16.65
40	1525	CG	PRO A 212	14.290	60.855	116.135	1.00	16.28
	1526	C	PRO A 212	14.730	61.945	113.045	1.00	19.18
	1527	O	PRO A 212	15.340	61.885	111.986	1.00	18.17
	1528	N	TRP A 213	13.406	62.015	113.096	1.00	19.16



	1529	CA	TRP	A	213	12.621	62.046	111.868	1.00	18.47
	1530	CB	TRP	A	213	11.140	61.818	112.182	1.00	20.17
	1531	CG	TRP	A	213	10.222	61.926	110.996	1.00	25.14
	1532	CD2	TRP	A	213	9.526	60.854	110.331	1.00	21.22
5	1533	CE2	TRP	A	213	8.789	61.430	109.275	1.00	21.08
	1534	CE3	TRP	A	213	9.459	59.474	110.523	1.00	19.67
	1535	CD1	TRP	A	213	9.881	63.068	110.330	1.00	24.56
	1536	NE1	TRP	A	213	9.025	62.778	109.302	1.00	23.34
	1537	CZ2	TRP	A	213	7.991	60.671	108.414	1.00	22.18
10	1538	CZ3	TRP	A	213	8.664	58.713	109.663	1.00	26.13
	1539	CH2	TRP	A	213	7.939	59.314	108.623	1.00	20.43
	1540	C	TRP	A	213	12.791	63.374	111.143	1.00	21.16
	1541	O	TRP	A	213	13.253	63.421	109.994	1.00	21.23
	1542	N	GLN	A	214	12.434	64.456	111.825	1.00	17.95
15	1543	CA	GLN	A	214	12.500	65.782	111.231	1.00	19.49
	1544	CB	GLN	A	214	11.937	66.836	112.195	1.00	15.54
	1545	CG	GLN	A	214	10.538	66.542	112.725	1.00	16.53
	1546	CD	GLN	A	214	10.563	65.812	114.044	1.00	21.67
	1547	OE1	GLN	A	214	9.675	65.994	114.879	1.00	29.84
20	1548	NE2	GLN	A	214	11.575	64.974	114.244	1.00	17.11
	1549	C	GLN	A	214	13.874	66.229	110.747	1.00	19.14
	1550	O	GLN	A	214	13.963	66.888	109.716	1.00	20.78
	1551	N	GLY	A	215	14.937	65.878	111.467	1.00	19.90
	1552	CA	GLY	A	215	16.270	66.295	111.056	1.00	15.98
25	1553	C	GLY	A	215	17.000	65.266	110.201	1.00	20.21
	1554	O	GLY	A	215	18.220	65.311	110.079	1.00	20.17
	1555	N	ALA	A	216	16.256	64.347	109.593	1.00	19.60
	1556	CA	ALA	A	216	16.852	63.281	108.774	1.00	22.16
	1557	CB	ALA	A	216	15.742	62.395	108.157	1.00	21.51
30	1558	C	ALA	A	216	17.773	63.791	107.683	1.00	26.02
	1559	O	ALA	A	216	18.763	63.136	107.356	1.00	28.48
	1560	N	TYR	A	217	17.464	64.966	107.136	1.00	26.30
	1561	CA	TYR	A	217	18.259	65.544	106.054	1.00	26.28
	1562	CB	TYR	A	217	17.386	65.846	104.823	1.00	25.48
35	1563	CG	TYR	A	217	16.745	64.653	104.165	1.00	25.26
	1564	CD1	TYR	A	217	15.476	64.244	104.519	1.00	23.97
	1565	CE1	TYR	A	217	14.873	63.160	103.904	1.00	33.81
	1566	CD2	TYR	A	217	17.411	63.946	103.181	1.00	26.91
	1567	CE2	TYR	A	217	16.824	62.848	102.560	1.00	29.87
40	1568	CZ	TYR	A	217	15.557	62.463	102.920	1.00	35.95
	1569	OH	TYR	A	217	14.959	61.401	102.275	1.00	34.87
	1570	C	TYR	A	217	18.945	66.842	106.425	1.00	30.05
	1571	O	TYR	A	217	19.423	67.552	105.541	1.00	31.35

	1572	N	SER A 218	18.990	67.161	107.710	1.00	29.76
	1573	CA	SER A 218	19.586	68.413	108.155	1.00	28.20
	1574	CB	SER A 218	19.244	68.685	109.631	1.00	27.28
	1575	OG	SER A 218	17.856	68.741	109.832	1.00	32.03
5	1576	C	SER A 218	21.086	68.493	108.034	1.00	29.01
	1577	O	SER A 218	21.783	67.473	108.103	1.00	28.50
	1578	N	GLU A 219	21.568	69.725	107.888	1.00	24.41
	1579	CA	GLU A 219	22.995	70.002	107.849	1.00	24.84
	1580	CB	GLU A 219	23.279	71.385	107.276	1.00	27.05
10	1581	CG	GLU A 219	23.117	71.507	105.780	1.00	27.48
	1582	CD	GLU A 219	24.090	70.627	105.015	1.00	29.56
	1583	OE1	GLU A 219	25.281	70.577	105.392	1.00	25.20
	1584	OE2	GLU A 219	23.659	69.997	104.026	1.00	31.20
	1585	C	GLU A 219	23.358	70.013	109.322	1.00	28.01
15	1586	O	GLU A 219	22.576	70.482	110.149	1.00	25.81
	1587	N	LEU A 220	24.527	69.485	109.654	1.00	25.13
	1588	CA	LEU A 220	24.967	69.444	111.037	1.00	22.61
	1589	CB	LEU A 220	25.400	68.022	111.416	1.00	19.00
	1590	CG	LEU A 220	24.368	66.922	111.122	1.00	21.72
20	1591	CD1	LEU A 220	24.993	65.577	111.293	1.00	20.51
	1592	CD2	LEU A 220	23.164	67.067	112.025	1.00	16.40
	1593	C	LEU A 220	26.136	70.414	111.240	1.00	27.53
	1594	O	LEU A 220	26.953	70.624	110.346	1.00	23.67
	1595	N	TYR A 221	26.186	71.011	112.423	1.00	27.06
25	1596	CA	TYR A 221	27.249	71.936	112.779	1.00	28.31
	1597	CB	TYR A 221	26.757	73.380	112.646	1.00	27.87
	1598	CG	TYR A 221	27.793	74.390	113.056	1.00	30.52
	1599	CD1	TYR A 221	28.911	74.622	112.273	1.00	30.21
	1600	CE1	TYR A 221	29.909	75.511	112.685	1.00	35.33
30	1601	CD2	TYR A 221	27.688	75.071	114.268	1.00	32.58
	1602	CE2	TYR A 221	28.677	75.952	114.687	1.00	34.90
	1603	CZ	TYR A 221	29.781	76.165	113.888	1.00	34.41
	1604	OH	TYR A 221	30.750	77.040	114.296	1.00	37.37
	1605	C	TYR A 221	27.655	71.657	114.229	1.00	30.14
35	1606	O	TYR A 221	26.850	71.809	115.148	1.00	33.38
	1607	N	PHE A 222	28.892	71.228	114.443	1.00	29.06
	1608	CA	PHE A 222	29.343	70.963	115.803	1.00	31.74
	1609	CB	PHE A 222	29.928	69.542	115.922	1.00	28.53
	1610	CG	PHE A 222	28.985	68.444	115.476	1.00	30.68
40	1611	CD1	PHE A 222	28.917	68.060	114.135	1.00	30.93
	1612	CD2	PHE A 222	28.158	67.805	116.392	1.00	28.45
	1613	CE1	PHE A 222	28.041	67.060	113.724	1.00	28.21
	1614	CE2	PHE A 222	27.280	66.804	115.985	1.00	25.33

	1615	CZ	PHE A 222	27.226	66.435	114.654	1.00	24.35
	1616	C	PHE A 222	30.398	71.985	116.230	1.00	33.17
	1617	O	PHE A 222	31.284	72.335	115.459	1.00	34.89
	1618	N	THR A 223	30.290	72.482	117.452	1.00	30.10
5	1619	CA	THR A 223	31.275	73.425	117.944	1.00	34.76
	1620	CB	THR A 223	30.735	74.873	118.032	1.00	38.89
	1621	OG1	THR A 223	31.783	75.722	118.492	1.00	36.14
	1622	CG2	THR A 223	29.579	74.987	119.018	1.00	28.79
	1623	C	THR A 223	31.709	73.012	119.331	1.00	38.68
10	1624	O	THR A 223	30.930	72.428	120.096	1.00	37.75
	1625	N	ASP A 224	32.951	73.330	119.663	1.00	39.83
	1626	CA	ASP A 224	33.480	72.991	120.972	1.00	42.25
	1627	CB	ASP A 224	35.016	72.934	120.939	1.00	45.40
	1628	CG	ASP A 224	35.549	71.599	120.439	1.00	50.54
15	1629	OD1	ASP A 224	36.782	71.483	120.266	1.00	54.69
	1630	OD2	ASP A 224	34.747	70.664	120.225	1.00	53.06
	1631	C	ASP A 224	33.038	73.995	122.031	1.00	40.13
	1632	O	ASP A 224	33.102	73.700	123.225	1.00	43.38
	1633	N	THR A 225	32.573	75.168	121.613	1.00	38.16
20	1634	CA	THR A 225	32.194	76.159	122.609	1.00	38.25
	1635	CB	THR A 225	31.999	77.584	121.963	1.00	38.63
	1636	OG1	THR A 225	30.709	78.119	122.292	1.00	42.27
	1637	CG2	THR A 225	32.202	77.539	120.476	1.00	30.63
	1638	C	THR A 225	30.988	75.739	123.460	1.00	41.88
25	1639	O	THR A 225	30.023	75.156	122.959	1.00	40.64
	1640	N	LEU A 226	31.077	76.010	124.762	1.00	40.31
	1641	CA	LEU A 226	30.022	75.666	125.706	1.00	33.69
	1642	CB	LEU A 226	30.526	75.864	127.130	1.00	33.90
	1643	CG	LEU A 226	31.928	75.307	127.396	1.00	30.39
30	1644	CD1	LEU A 226	32.235	75.416	128.878	1.00	29.14
	1645	CD2	LEU A 226	32.011	73.842	126.935	1.00	35.55
	1646	C	LEU A 226	28.824	76.546	125.441	1.00	34.85
	1647	O	LEU A 226	28.984	77.700	125.066	1.00	38.93
	1648	N	TRP A 227	27.619	76.018	125.650	1.00	35.17
35	1649	CA	TRP A 227	26.404	76.786	125.378	1.00	34.56
	1650	CB	TRP A 227	25.168	76.007	125.838	1.00	32.61
	1651	CG	TRP A 227	23.869	76.744	125.633	1.00	29.95
	1652	CD2	TRP A 227	23.344	77.255	124.394	1.00	28.20
	1653	CE2	TRP A 227	22.151	77.952	124.700	1.00	29.98
40	1654	CE3	TRP A 227	23.768	77.201	123.061	1.00	22.52
	1655	CD1	TRP A 227	22.988	77.129	126.606	1.00	34.57
	1656	NE1	TRP A 227	21.954	77.857	126.052	1.00	30.03
	1657	CZ2	TRP A 227	21.383	78.592	123.716	1.00	28.42

	1658	CZ3	TRP	A	227	23.006	77.835	122.085	1.00	23.22
	1659	CH2	TRP	A	227	21.830	78.521	122.416	1.00	26.65
	1660	C	TRP	A	227	26.365	78.199	125.959	1.00	35.73
	1661	O	TRP	A	227	25.911	79.125	125.301	1.00	35.52
5	1662	N	PRO	A	228	26.826	78.387	127.206	1.00	41.61
	1663	CD	PRO	A	228	27.109	77.382	128.246	1.00	39.80
	1664	CA	PRO	A	228	26.795	79.736	127.788	1.00	41.13
	1665	CB	PRO	A	228	27.338	79.511	129.197	1.00	41.91
	1666	CG	PRO	A	228	26.803	78.141	129.520	1.00	40.55
10	1667	C	PRO	A	228	27.599	80.777	127.005	1.00	41.05
	1668	O	PRO	A	228	27.387	81.981	127.155	1.00	39.39
	1669	N	ASP	A	229	28.525	80.317	126.174	1.00	41.40
	1670	CA	ASP	A	229	29.322	81.241	125.379	1.00	41.11
	1671	CB	ASP	A	229	30.768	80.759	125.264	1.00	36.19
15	1672	CG	ASP	A	229	31.462	80.661	126.611	1.00	38.63
	1673	OD1	ASP	A	229	31.235	81.535	127.479	1.00	45.31
	1674	OD2	ASP	A	229	32.258	79.720	126.801	1.00	42.02
	1675	C	ASP	A	229	28.735	81.400	123.982	1.00	42.40
	1676	O	ASP	A	229	29.193	82.225	123.197	1.00	43.97
20	1677	N	PHE	A	230	27.711	80.617	123.666	1.00	41.17
	1678	CA	PHE	A	230	27.125	80.710	122.338	1.00	39.63
	1679	CB	PHE	A	230	26.237	79.498	122.040	1.00	39.07
	1680	CG	PHE	A	230	26.107	79.193	120.579	1.00	33.54
	1681	CD1	PHE	A	230	27.072	78.431	119.930	1.00	34.65
25	1682	CD2	PHE	A	230	25.032	79.694	119.842	1.00	33.73
	1683	CE1	PHE	A	230	26.968	78.172	118.563	1.00	34.41
	1684	CE2	PHE	A	230	24.914	79.442	118.479	1.00	26.96
	1685	CZ	PHE	A	230	25.883	78.680	117.836	1.00	34.43
	1686	C	PHE	A	230	26.305	81.978	122.258	1.00	37.29
30	1687	O	PHE	A	230	25.295	82.128	122.932	1.00	35.31
	1688	N	ASP	A	231	26.748	82.897	121.426	1.00	42.64
	1689	CA	ASP	A	231	26.048	84.156	121.272	1.00	46.45
	1690	CB	ASP	A	231	26.910	85.291	121.809	1.00	48.20
	1691	CG	ASP	A	231	28.300	85.265	121.232	1.00	47.99
35	1692	OD1	ASP	A	231	28.431	84.832	120.072	1.00	47.41
	1693	OD2	ASP	A	231	29.251	85.675	121.927	1.00	48.67
	1694	C	ASP	A	231	25.763	84.403	119.805	1.00	48.56
	1695	O	ASP	A	231	26.067	83.568	118.952	1.00	50.79
	1696	N	GLU	A	232	25.191	85.568	119.522	1.00	48.23
40	1697	CA	GLU	A	232	24.860	85.953	118.166	1.00	48.82
	1698	CB	GLU	A	232	24.416	87.415	118.157	1.00	49.67
	1699	CG	GLU	A	232	24.245	88.019	116.788	1.00	53.58
	1700	CD	GLU	A	232	23.650	89.410	116.854	1.00	60.09

	1701	OE1	GLU	A	232	24.042	90.184	117.759	1.00	62.24
	1702	OE2	GLU	A	232	22.793	89.731	115.998	1.00	64.38
	1703	C	GLU	A	232	26.025	85.716	117.198	1.00	48.14
	1704	O	GLU	A	232	25.825	85.192	116.098	1.00	50.25
5	1705	N	ALA	A	233	27.237	86.074	117.605	1.00	43.03
	1706	CA	ALA	A	233	28.407	85.886	116.746	1.00	45.37
	1707	CB	ALA	A	233	29.660	86.354	117.462	1.00	49.45
	1708	C	ALA	A	233	28.565	84.427	116.351	1.00	48.31
	1709	O	ALA	A	233	28.785	84.102	115.182	1.00	51.31
10	1710	N	ALA	A	234	28.470	83.548	117.344	1.00	48.64
	1711	CA	ALA	A	234	28.587	82.117	117.115	1.00	43.18
	1712	CB	ALA	A	234	28.559	81.371	118.443	1.00	41.91
	1713	C	ALA	A	234	27.435	81.667	116.231	1.00	42.29
	1714	O	ALA	A	234	27.604	80.800	115.388	1.00	46.39
15	1715	N	LEU	A	235	26.263	82.263	116.427	1.00	38.94
	1716	CA	LEU	A	235	25.097	81.918	115.631	1.00	42.54
	1717	CB	LEU	A	235	23.904	82.790	116.016	1.00	35.04
	1718	CG	LEU	A	235	22.495	82.227	115.827	1.00	38.29
	1719	CD1	LEU	A	235	21.565	83.310	115.287	1.00	30.02
20	1720	CD2	LEU	A	235	22.526	81.042	114.891	1.00	34.57
	1721	C	LEU	A	235	25.422	82.166	114.162	1.00	47.47
	1722	O	LEU	A	235	25.160	81.323	113.303	1.00	52.12
	1723	N	GLN	A	236	26.001	83.331	113.887	1.00	46.82
	1724	CA	GLN	A	236	26.340	83.720	112.528	1.00	45.55
25	1725	CB	GLN	A	236	26.746	85.200	112.500	1.00	48.25
	1726	CG	GLN	A	236	25.566	86.135	112.769	1.00	48.05
	1727	CD	GLN	A	236	25.959	87.598	112.857	0.50	48.03
	1728	OE1	GLN	A	236	26.729	88.000	113.732	0.50	44.57
	1729	NE2	GLN	A	236	25.424	88.405	111.949	0.50	48.83
30	1730	C	GLN	A	236	27.414	82.848	111.909	1.00	43.76
	1731	O	GLN	A	236	27.323	82.503	110.728	1.00	42.54
	1732	N	GLU	A	237	28.427	82.483	112.692	1.00	43.99
	1733	CA	GLU	A	237	29.485	81.619	112.170	1.00	42.47
	1734	CB	GLU	A	237	30.617	81.449	113.191	1.00	40.15
35	1735	CG	GLU	A	237	31.749	80.539	112.714	0.50	43.35
	1736	CD	GLU	A	237	32.938	80.501	113.667	0.50	47.72
	1737	OE1	GLU	A	237	32.718	80.412	114.895	0.50	47.71
	1738	OE2	GLU	A	237	34.095	80.547	113.186	0.50	49.90
	1739	C	GLU	A	237	28.886	80.252	111.812	1.00	44.42
40	1740	O	GLU	A	237	29.422	79.529	110.966	1.00	45.94
	1741	N	ALA	A	238	27.770	79.904	112.450	1.00	41.53
	1742	CA	ALA	A	238	27.111	78.638	112.164	1.00	41.95
	1743	CB	ALA	A	238	26.160	78.256	113.285	1.00	41.28

	1744	C	ALA A 238	26.346	78.801	110.861	1.00	41.75
	1745	O	ALA A 238	26.445	77.955	109.972	1.00	42.38
	1746	N	ILE A 239	25.585	79.889	110.745	1.00	38.68
	1747	CA	ILE A 239	24.830	80.142	109.530	1.00	38.23
5	1748	CB	ILE A 239	23.983	81.418	109.636	1.00	39.14
	1749	CG2	ILE A 239	23.382	81.767	108.267	1.00	29.23
	1750	CG1	ILE A 239	22.890	81.217	110.678	1.00	38.28
	1751	CD1	ILE A 239	22.090	82.445	110.970	1.00	33.97
	1752	C	ILE A 239	25.815	80.297	108.370	1.00	43.17
10	1753	O	ILE A 239	25.509	79.948	107.236	1.00	42.00
	1754	N	LEU A 240	27.001	80.815	108.660	1.00	43.84
	1755	CA	LEU A 240	28.004	80.979	107.617	1.00	48.64
	1756	CB	LEU A 240	29.229	81.723	108.152	1.00	49.65
	1757	CG	LEU A 240	30.324	81.858	107.096	1.00	54.49
15	1758	CD1	LEU A 240	29.865	82.857	106.028	1.00	54.05
	1759	CD2	LEU A 240	31.629	82.300	107.745	1.00	55.41
	1760	C	LEU A 240	28.433	79.601	107.112	1.00	49.30
	1761	O	LEU A 240	28.392	79.330	105.901	1.00	43.27
	1762	N	ALA A 241	28.853	78.741	108.047	1.00	46.41
20	1763	CA	ALA A 241	29.274	77.382	107.708	1.00	44.99
	1764	CB	ALA A 241	29.588	76.585	108.979	1.00	39.83
	1765	C	ALA A 241	28.155	76.702	106.917	1.00	43.77
	1766	O	ALA A 241	28.418	75.999	105.945	1.00	45.25
	1767	N	TYR A 242	26.910	76.927	107.337	1.00	41.14
25	1768	CA	TYR A 242	25.752	76.363	106.660	1.00	43.59
	1769	CB	TYR A 242	24.464	76.848	107.329	1.00	37.06
	1770	CG	TYR A 242	23.190	76.504	106.570	1.00	35.60
	1771	CD1	TYR A 242	22.661	75.220	106.597	1.00	37.73
	1772	CE1	TYR A 242	21.473	74.903	105.910	1.00	36.54
30	1773	CD2	TYR A 242	22.509	77.472	105.834	1.00	40.36
	1774	CE2	TYR A 242	21.323	77.172	105.144	1.00	37.10
	1775	CZ	TYR A 242	20.807	75.886	105.186	1.00	40.18
	1776	OH	TYR A 242	19.628	75.585	104.520	1.00	35.96
	1777	C	TYR A 242	25.753	76.799	105.192	1.00	50.36
35	1778	O	TYR A 242	25.612	75.975	104.290	1.00	54.54
	1779	N	ASN A 243	25.902	78.100	104.953	1.00	53.90
	1780	CA	ASN A 243	25.907	78.614	103.591	1.00	58.86
	1781	CB	ASN A 243	25.865	80.137	103.584	1.00	62.00
	1782	CG	ASN A 243	24.482	80.668	103.833	1.00	61.17
40	1783	OD1	ASN A 243	24.022	80.702	104.962	1.00	66.12
	1784	ND2	ASN A 243	23.799	81.069	102.768	1.00	70.22
	1785	C	ASN A 243	27.100	78.134	102.794	1.00	60.03
	1786	O	ASN A 243	27.054	78.099	101.571	1.00	58.37

	1787	N	ARG A 244	28.170	77.775	103.492	1.00	67.00
	1788	CA	ARG A 244	29.359	77.260	102.831	1.00	71.47
	1789	CB	ARG A 244	30.537	77.223	103.808	1.00	75.63
	1790	CG	ARG A 244	31.416	78.464	103.773	1.00	82.45
5	1791	CD	ARG A 244	30.639	79.736	104.103	1.00	90.60
	1792	NE	ARG A 244	31.467	80.938	103.973	1.00	96.09
	1793	CZ	ARG A 244	32.592	81.160	104.650	1.00	97.67
	1794	NH1	ARG A 244	33.037	80.261	105.521	1.00	99.15
	1795	NH2	ARG A 244	33.281	82.279	104.450	1.00	97.56
10	1796	C	ARG A 244	29.083	75.854	102.288	1.00	71.89
	1797	O	ARG A 244	29.885	75.309	101.536	1.00	72.97
	1798	N	ARG A 245	27.949	75.267	102.671	1.00	71.85
	1799	CA	ARG A 245	27.587	73.931	102.194	1.00	74.97
	1800	CB	ARG A 245	26.580	73.251	103.131	1.00	70.19
15	1801	CG	ARG A 245	26.946	73.255	104.612	1.00	65.86
	1802	CD	ARG A 245	28.230	72.508	104.916	1.00	56.38
	1803	NE	ARG A 245	28.580	72.585	106.335	1.00	50.77
	1804	CZ	ARG A 245	27.920	71.975	107.320	1.00	50.64
	1805	NH1	ARG A 245	26.855	71.224	107.059	1.00	50.99
20	1806	NH2	ARG A 245	28.332	72.115	108.579	1.00	46.38
	1807	C	ARG A 245	26.946	74.082	100.820	1.00	79.51
	1808	O	ARG A 245	27.103	73.224	99.951	1.00	79.02
	1809	N	HIS A 246	26.214	75.181	100.643	1.00	85.07
	1810	CA	HIS A 246	25.539	75.488	99.386	1.00	88.50
25	1811	CB	HIS A 246	24.709	76.769	99.535	0.00	87.41
	1812	CG	HIS A 246	23.856	77.084	98.344	0.00	86.33
	1813	CD2	HIS A 246	22.512	77.081	98.186	0.00	85.87
	1814	ND1	HIS A 246	24.384	77.449	97.124	0.00	85.87
	1815	CE1	HIS A 246	23.402	77.656	96.265	0.00	85.55
30	1816	NE2	HIS A 246	22.255	77.440	96.884	0.00	85.55
	1817	C	HIS A 246	26.581	75.661	98.283	1.00	92.71
	1818	O	HIS A 246	26.232	75.875	97.120	1.00	94.85
	1819	N	ARG A 247	27.859	75.570	98.660	1.00	95.25
	1820	CA	ARG A 247	28.973	75.685	97.712	1.00	97.19
35	1821	CB	ARG A 247	30.224	76.216	98.416	0.00	95.62
	1822	CG	ARG A 247	30.335	77.732	98.430	0.00	93.93
	1823	CD	ARG A 247	29.193	78.382	99.192	0.00	92.37
	1824	NE	ARG A 247	29.233	79.838	99.085	0.00	91.00
	1825	CZ	ARG A 247	30.259	80.591	99.468	0.00	90.30
40	1826	NH1	ARG A 247	31.342	80.030	99.990	0.00	89.86
	1827	NH2	ARG A 247	30.204	81.908	99.328	0.00	89.86
	1828	C	ARG A 247	29.292	74.337	97.053	1.00	99.05
	1829	O	ARG A 247	29.440	74.251	95.829	1.00	99.58

	1830	N	ARG A 248	29.402	73.290	97.868	1.00	99.42
	1831	CA	ARG A 248	29.689	71.951	97.361	1.00	99.65
	1832	CB	ARG A 248	31.025	71.443	97.911	0.00	98.33
	1833	CG	ARG A 248	32.236	72.079	97.248	0.00	96.73
5	1834	CD	ARG A 248	32.201	71.862	95.740	0.00	95.24
	1835	NE	ARG A 248	33.343	72.467	95.061	0.00	93.87
	1836	CZ	ARG A 248	34.603	72.077	95.221	0.00	93.16
	1837	NH1	ARG A 248	34.892	71.077	96.042	0.00	92.69
	1838	NH2	ARG A 248	35.577	72.688	94.560	0.00	92.69
10	1839	C	ARG A 248	28.576	70.961	97.698	1.00	100.00
	1840	O	ARG A 248	27.465	71.423	98.044	1.00	100.00
	1841	OT	ARG A 248	28.821	69.738	97.593	1.00	100.00
	1842	CB	THR B 17	40.998	52.015	122.655	0.00	81.97
	1843	OG1	THR B 17	41.941	51.570	121.674	0.00	81.40
15	1844	CG2	THR B 17	41.583	53.196	123.416	0.00	81.40
	1845	C	THR B 17	40.063	49.703	122.817	1.00	82.60
	1846	O	THR B 17	40.773	48.987	122.097	1.00	81.20
	1847	N	THR B 17	41.897	50.435	124.363	1.00	83.66
	1848	CA	THR B 17	40.676	50.860	123.621	1.00	82.07
20	1849	N	GLN B 18	38.745	49.528	122.939	1.00	80.50
	1850	CA	GLN B 18	38.044	48.461	122.227	1.00	76.85
	1851	CB	GLN B 18	37.041	47.768	123.145	1.00	82.95
	1852	CG	GLN B 18	37.670	46.629	123.926	1.00	92.02
	1853	CD	GLN B 18	36.647	45.645	124.460	1.00	97.09
25	1854	OE1	GLN B 18	35.720	45.247	123.748	1.00	97.89
	1855	NE2	GLN B 18	36.820	45.232	125.714	1.00	98.51
	1856	C	GLN B 18	37.357	48.868	120.926	1.00	68.92
	1857	O	GLN B 18	37.500	50.000	120.464	1.00	68.81
	1858	N	VAL B 19	36.594	47.933	120.361	1.00	55.51
30	1859	CA	VAL B 19	35.926	48.125	119.076	1.00	49.30
	1860	CB	VAL B 19	36.293	46.967	118.123	1.00	51.82
	1861	CG1	VAL B 19	35.671	47.195	116.759	1.00	54.87
	1862	CG2	VAL B 19	37.805	46.830	118.027	1.00	52.28
	1863	C	VAL B 19	34.402	48.230	119.071	1.00	41.83
35	1864	O	VAL B 19	33.712	47.411	119.668	1.00	40.78
	1865	N	PRO B 20	33.856	49.234	118.372	1.00	34.04
	1866	CD	PRO B 20	34.501	50.283	117.575	1.00	32.05
	1867	CA	PRO B 20	32.397	49.371	118.323	1.00	30.87
	1868	CB	PRO B 20	32.204	50.640	117.501	1.00	31.44
40	1869	CG	PRO B 20	33.399	50.643	116.616	1.00	31.78
	1870	C	PRO B 20	31.807	48.131	117.644	1.00	29.11
	1871	O	PRO B 20	32.248	47.738	116.566	1.00	30.64
	1872	N	ALA B 21	30.811	47.515	118.272	1.00	24.00



	1873	CA	ALA	B	21	30.197	46.311	117.730	1.00	21.61
	1874	CB	ALA	B	21	29.237	45.708	118.761	1.00	20.34
	1875	C	ALA	B	21	29.482	46.522	116.395	1.00	24.20
	1876	O	ALA	B	21	29.598	45.691	115.499	1.00	25.73
5	1877	N	HIS	B	22	28.744	47.627	116.264	1.00	21.72
	1878	CA	HIS	B	22	28.024	47.929	115.031	1.00	23.31
	1879	CB	HIS	B	22	26.509	47.871	115.291	1.00	23.24
	1880	CG	HIS	B	22	25.665	48.102	114.073	1.00	21.21
	1881	CD2	HIS	B	22	25.991	48.496	112.816	1.00	19.25
10	1882	ND1	HIS	B	22	24.298	47.901	114.067	1.00	19.64
	1883	CE1	HIS	B	22	23.821	48.154	112.860	1.00	18.87
	1884	NE2	HIS	B	22	24.826	48.516	112.081	1.00	21.92
	1885	C	HIS	B	22	28.419	49.304	114.467	1.00	26.58
	1886	O	HIS	B	22	28.287	50.322	115.143	1.00	26.93
15	1887	N	ILE	B	23	28.908	49.322	113.228	1.00	25.49
	1888	CA	ILE	B	23	29.321	50.566	112.565	1.00	21.21
	1889	CB	ILE	B	23	30.786	50.499	112.078	1.00	22.12
	1890	CG2	ILE	B	23	31.232	51.852	111.574	1.00	17.21
	1891	CG1	ILE	B	23	31.704	50.067	113.209	1.00	22.28
20	1892	CD1	ILE	B	23	33.136	50.010	112.784	1.00	23.31
	1893	C	ILE	B	23	28.471	50.828	111.327	1.00	20.60
	1894	O	ILE	B	23	28.322	49.953	110.461	1.00	22.96
	1895	N	GLY	B	24	27.904	52.028	111.241	1.00	22.85
	1896	CA	GLY	B	24	27.106	52.377	110.076	1.00	19.72
25	1897	C	GLY	B	24	28.026	53.215	109.210	1.00	17.39
	1898	O	GLY	B	24	28.793	54.014	109.744	1.00	16.37
	1899	N	ILE	B	25	27.962	53.045	107.895	1.00	21.07
	1900	CA	ILE	B	25	28.829	53.809	107.008	1.00	22.11
	1901	CB	ILE	B	25	30.042	52.976	106.511	1.00	27.19
30	1902	CG2	ILE	B	25	30.953	53.883	105.659	1.00	19.14
	1903	CG1	ILE	B	25	30.809	52.361	107.703	1.00	26.65
	1904	CD1	ILE	B	25	31.945	51.388	107.309	1.00	23.85
	1905	C	ILE	B	25	28.164	54.357	105.766	1.00	21.65
	1906	O	ILE	B	25	27.594	53.614	104.974	1.00	21.38
35	1907	N	ILE	B	26	28.253	55.665	105.594	1.00	19.40
	1908	CA	ILE	B	26	27.700	56.298	104.418	1.00	23.14
	1909	CB	ILE	B	26	27.011	57.651	104.791	1.00	23.25
	1910	CG2	ILE	B	26	26.340	58.245	103.577	1.00	18.01
	1911	CG1	ILE	B	26	25.903	57.406	105.819	1.00	24.31
40	1912	CD1	ILE	B	26	25.429	58.663	106.507	1.00	24.75
	1913	C	ILE	B	26	28.887	56.488	103.443	1.00	22.93
	1914	O	ILE	B	26	29.729	57.377	103.616	1.00	17.21
	1915	N	MET	B	27	28.938	55.617	102.436	1.00	24.95

	1916	CA	MET	B	27	30.010	55.575	101.431	1.00	24.93
	1917	CB	MET	B	27	29.996	54.205	100.747	1.00	23.61
	1918	CG	MET	B	27	30.210	53.055	101.727	1.00	26.80
	1919	SD	MET	B	27	30.045	51.390	101.018	1.00	35.62
5	1920	CE	MET	B	27	28.440	51.571	100.090	1.00	27.74
	1921	C	MET	B	27	29.879	56.679	100.402	1.00	31.10
	1922	O	MET	B	27	29.393	56.459	99.294	1.00	40.09
	1923	N	ASP	B	28	30.335	57.867	100.783	1.00	27.37
	1924	CA	ASP	B	28	30.256	59.058	99.949	1.00	29.73
10	1925	CB	ASP	B	28	29.855	60.213	100.858	1.00	36.16
	1926	CG	ASP	B	28	28.832	61.112	100.254	1.00	39.96
	1927	OD1	ASP	B	28	29.147	61.814	99.281	1.00	48.57
	1928	OD2	ASP	B	28	27.702	61.120	100.773	1.00	48.14
	1929	C	ASP	B	28	31.610	59.389	99.280	1.00	32.14
15	1930	O	ASP	B	28	32.663	59.136	99.859	1.00	28.74
	1931	N	GLY	B	29	31.585	59.953	98.075	1.00	30.73
	1932	CA	GLY	B	29	32.838	60.324	97.429	1.00	34.78
	1933	C	GLY	B	29	33.340	59.550	96.221	1.00	35.30
	1934	O	GLY	B	29	34.378	59.913	95.662	1.00	34.25
20	1935	N	ASN	B	30	32.643	58.492	95.808	1.00	30.13
	1936	CA	ASN	B	30	33.094	57.744	94.648	1.00	30.50
	1937	CB	ASN	B	30	32.148	56.595	94.349	1.00	26.69
	1938	CG	ASN	B	30	32.111	55.590	95.456	1.00	26.88
	1939	OD1	ASN	B	30	31.364	54.615	95.412	1.00	35.61
25	1940	ND2	ASN	B	30	32.916	55.821	96.465	1.00	27.99
	1941	C	ASN	B	30	33.213	58.627	93.408	1.00	35.56
	1942	O	ASN	B	30	34.133	58.450	92.613	1.00	36.55
	1943	N	GLY	B	31	32.276	59.565	93.242	1.00	35.25
	1944	CA	GLY	B	31	32.282	60.450	92.089	1.00	28.98
30	1945	C	GLY	B	31	33.435	61.433	92.071	1.00	31.68
	1946	O	GLY	B	31	34.141	61.525	91.068	1.00	33.76
	1947	N	ARG	B	32	33.615	62.179	93.159	1.00	30.19
	1948	CA	ARG	B	32	34.718	63.126	93.260	1.00	36.83
	1949	CB	ARG	B	32	34.744	63.795	94.640	1.00	34.40
35	1950	CG	ARG	B	32	33.892	65.061	94.762	1.00	45.79
	1951	CD	ARG	B	32	33.763	65.523	96.220	1.00	51.82
	1952	NE	ARG	B	32	35.034	65.912	96.840	1.00	58.74
	1953	CZ	ARG	B	32	35.233	65.982	98.159	1.00	64.83
	1954	NH1	ARG	B	32	34.249	65.685	99.002	1.00	67.57
40	1955	NH2	ARG	B	32	36.411	66.358	98.645	1.00	69.76
	1956	C	ARG	B	32	36.041	62.389	93.038	1.00	36.48
	1957	O	ARG	B	32	36.959	62.932	92.433	1.00	37.31
	1958	N	TRP	B	33	36.123	61.150	93.531	1.00	34.59

	1959	CA	TRP	B	33	37.324	60.328	93.399	1.00	33.53
	1960	CB	TRP	B	33	37.138	59.017	94.148	1.00	28.04
	1961	CG	TRP	B	33	38.386	58.166	94.265	1.00	28.47
	1962	CD2	TRP	B	33	38.796	57.122	93.376	1.00	20.64
5	1963	CE2	TRP	B	33	39.950	56.528	93.937	1.00	20.29
	1964	CE3	TRP	B	33	38.298	56.628	92.156	1.00	19.24
	1965	CD1	TRP	B	33	39.295	58.174	95.294	1.00	27.06
	1966	NE1	TRP	B	33	40.229	57.191	95.103	1.00	23.78
	1967	CZ2	TRP	B	33	40.618	55.454	93.327	1.00	20.40
10	1968	CZ3	TRP	B	33	38.961	55.563	91.541	1.00	22.66
	1969	CH2	TRP	B	33	40.107	54.987	92.129	1.00	24.51
	1970	C	TRP	B	33	37.629	60.028	91.926	1.00	37.07
	1971	O	TRP	B	33	38.741	60.291	91.442	1.00	32.97
	1972	N	ALA	B	34	36.647	59.471	91.217	1.00	32.56
15	1973	CA	ALA	B	34	36.840	59.167	89.815	1.00	32.39
	1974	CB	ALA	B	34	35.572	58.538	89.218	1.00	31.79
	1975	C	ALA	B	34	37.214	60.474	89.089	1.00	35.38
	1976	O	ALA	B	34	38.046	60.463	88.186	1.00	35.71
	1977	N	LYS	B	35	36.642	61.603	89.506	1.00	34.28
20	1978	CA	LYS	B	35	36.979	62.874	88.861	1.00	33.69
	1979	CB	LYS	B	35	36.031	63.985	89.304	1.00	36.65
	1980	CG	LYS	B	35	36.181	65.269	88.488	1.00	50.72
	1981	CD	LYS	B	35	35.161	66.327	88.904	1.00	63.85
	1982	CE	LYS	B	35	35.263	67.597	88.054	1.00	68.91
25	1983	NZ	LYS	B	35	34.178	68.591	88.381	1.00	72.03
	1984	C	LYS	B	35	38.440	63.313	89.097	1.00	31.98
	1985	O	LYS	B	35	39.081	63.806	88.176	1.00	33.90
	1986	N	LYS	B	36	38.961	63.158	90.312	1.00	27.77
	1987	CA	LYS	B	36	40.355	63.522	90.584	1.00	35.52
30	1988	CB	LYS	B	36	40.670	63.359	92.069	1.00	37.11
	1989	CG	LYS	B	36	40.309	64.540	92.905	1.00	54.70
	1990	CD	LYS	B	36	40.708	64.341	94.360	1.00	60.66
	1991	CE	LYS	B	36	40.273	65.546	95.207	1.00	67.91
	1992	NZ	LYS	B	36	40.420	65.314	96.681	1.00	75.16
35	1993	C	LYS	B	36	41.341	62.653	89.767	1.00	34.92
	1994	O	LYS	B	36	42.348	63.148	89.280	1.00	35.27
	1995	N	ARG	B	37	41.037	61.360	89.641	1.00	35.16
	1996	CA	ARG	B	37	41.859	60.406	88.884	1.00	35.62
	1997	CB	ARG	B	37	41.508	58.950	89.269	1.00	39.51
40	1998	CG	ARG	B	37	41.976	58.447	90.634	1.00	38.37
	1999	CD	ARG	B	37	42.879	57.226	90.460	1.00	45.86
	2000	NE	ARG	B	37	43.246	56.566	91.715	1.00	42.83
	2001	CZ	ARG	B	37	43.493	57.196	92.856	1.00	35.81

	2002	NH1	ARG	B	37	43.412	58.512	92.934	1.00	42.43
	2003	NH2	ARG	B	37	43.836	56.507	93.925	1.00	39.69
	2004	C	ARG	B	37	41.556	60.571	87.386	1.00	34.97
	2005	O	ARG	B	37	42.055	59.811	86.561	1.00	28.07
5	2006	N	MET	B	38	40.712	61.548	87.057	1.00	35.33
	2007	CA	MET	B	38	40.308	61.818	85.681	1.00	37.27
	2008	CB	MET	B	38	41.471	62.395	84.874	1.00	38.26
	2009	CG	MET	B	38	41.874	63.792	85.305	1.00	43.26
	2010	SD	MET	B	38	43.320	64.442	84.413	1.00	50.85
10	2011	CE	MET	B	38	42.639	64.685	82.741	1.00	42.32
	2012	C	MET	B	38	39.774	60.581	84.983	1.00	41.75
	2013	O	MET	B	38	40.097	60.322	83.828	1.00	44.59
	2014	N	GLN	B	39	38.968	59.808	85.694	1.00	38.24
	2015	CA	GLN	B	39	38.368	58.614	85.128	1.00	39.36
15	2016	CB	GLN	B	39	38.766	57.364	85.937	1.00	40.98
	2017	CG	GLN	B	39	40.240	56.980	85.829	1.00	43.52
	2018	CD	GLN	B	39	40.588	55.705	86.589	0.50	43.10
	2019	OE1	GLN	B	39	40.396	55.611	87.803	0.50	39.90
	2020	NE2	GLN	B	39	41.112	54.718	85.870	0.50	44.08
20	2021	C	GLN	B	39	36.858	58.812	85.203	1.00	40.23
	2022	O	GLN	B	39	36.375	59.639	85.969	1.00	34.98
	2023	N	PRO	B	40	36.092	58.072	84.391	1.00	42.21
	2024	CD	PRO	B	40	36.495	57.164	83.304	1.00	48.07
	2025	CA	PRO	B	40	34.637	58.230	84.443	1.00	45.23
25	2026	CB	PRO	B	40	34.154	57.388	83.258	1.00	47.19
	2027	CG	PRO	B	40	35.238	56.369	83.076	1.00	50.59
	2028	C	PRO	B	40	34.067	57.766	85.798	1.00	44.28
	2029	O	PRO	B	40	34.635	56.881	86.441	1.00	38.91
	2030	N	ARG	B	41	32.959	58.376	86.222	1.00	44.37
30	2031	CA	ARG	B	41	32.319	58.058	87.504	1.00	49.09
	2032	CB	ARG	B	41	30.968	58.777	87.608	1.00	51.36
	2033	CG	ARG	B	41	30.302	58.631	88.975	1.00	63.60
	2034	CD	ARG	B	41	29.289	59.748	89.264	1.00	66.85
	2035	NE	ARG	B	41	28.693	59.591	90.588	1.00	67.64
35	2036	CZ	ARG	B	41	28.506	60.590	91.445	1.00	71.31
	2037	NH1	ARG	B	41	28.869	61.826	91.117	1.00	71.73
	2038	NH2	ARG	B	41	27.973	60.351	92.637	1.00	72.69
	2039	C	ARG	B	41	32.137	56.563	87.768	1.00	44.94
	2040	O	ARG	B	41	32.172	56.114	88.908	1.00	44.70
40	2041	N	VAL	B	42	31.946	55.799	86.705	1.00	45.95
	2042	CA	VAL	B	42	31.782	54.356	86.806	1.00	48.03
	2043	CB	VAL	B	42	31.646	53.729	85.402	1.00	52.94
	2044	CG1	VAL	B	42	31.015	52.363	85.518	1.00	55.31

	2045	CG2	VAL	B	42	30.839	54.657	84.478	1.00	50.44
	2046	C	VAL	B	42	32.991	53.714	87.510	1.00	48.86
	2047	O	VAL	B	42	32.835	52.778	88.302	1.00	49.43
	2048	N	PHE	B	43	34.194	54.205	87.208	1.00	45.00
5	2049	CA	PHE	B	43	35.413	53.691	87.823	1.00	42.02
	2050	CB	PHE	B	43	36.643	54.331	87.174	1.00	48.39
	2051	CG	PHE	B	43	36.997	53.724	85.838	1.00	60.42
	2052	CD1	PHE	B	43	36.068	53.711	84.791	1.00	64.41
	2053	CD2	PHE	B	43	38.240	53.127	85.632	1.00	63.92
10	2054	CE1	PHE	B	43	36.365	53.111	83.556	1.00	61.84
	2055	CE2	PHE	B	43	38.550	52.522	84.394	1.00	67.46
	2056	CZ	PHE	B	43	37.605	52.516	83.358	1.00	64.18
	2057	C	PHE	B	43	35.412	53.945	89.329	1.00	38.71
	2058	O	PHE	B	43	35.980	53.167	90.106	1.00	38.95
15	2059	N	GLY	B	44	34.755	55.026	89.738	1.00	33.04
	2060	CA	GLY	B	44	34.673	55.363	91.150	1.00	27.83
	2061	C	GLY	B	44	33.871	54.338	91.933	1.00	27.02
	2062	O	GLY	B	44	34.266	53.957	93.028	1.00	28.51
	2063	N	HIS	B	45	32.755	53.870	91.382	1.00	24.46
20	2064	CA	HIS	B	45	31.950	52.895	92.107	1.00	32.87
	2065	CB	HIS	B	45	30.559	52.789	91.475	1.00	33.20
	2066	CG	HIS	B	45	29.792	54.072	91.554	1.00	43.34
	2067	CD2	HIS	B	45	29.450	54.838	92.620	1.00	45.47
	2068	ND1	HIS	B	45	29.387	54.772	90.437	1.00	46.02
25	2069	CE1	HIS	B	45	28.838	55.916	90.809	1.00	49.17
	2070	NE2	HIS	B	45	28.865	55.982	92.129	1.00	49.30
	2071	C	HIS	B	45	32.662	51.560	92.179	1.00	30.87
	2072	O	HIS	B	45	32.569	50.854	93.168	1.00	35.86
	2073	N	LYS	B	46	33.406	51.225	91.137	1.00	34.28
30	2074	CA	LYS	B	46	34.168	49.982	91.140	1.00	28.34
	2075	CB	LYS	B	46	34.901	49.816	89.811	1.00	31.70
	2076	CG	LYS	B	46	34.759	48.442	89.191	1.00	42.06
	2077	CD	LYS	B	46	34.412	48.551	87.698	1.00	47.89
	2078	CE	LYS	B	46	34.046	47.188	87.107	1.00	48.64
35	2079	NZ	LYS	B	46	33.475	47.323	85.743	1.00	52.00
	2080	C	LYS	B	46	35.181	50.027	92.281	1.00	26.85
	2081	O	LYS	B	46	35.295	49.062	93.038	1.00	30.29
	2082	N	ALA	B	47	35.912	51.148	92.396	1.00	24.69
	2083	CA	ALA	B	47	36.915	51.329	93.444	1.00	25.46
40	2084	CB	ALA	B	47	37.685	52.655	93.237	1.00	22.07
	2085	C	ALA	B	47	36.216	51.327	94.813	1.00	25.59
	2086	O	ALA	B	47	36.773	50.851	95.806	1.00	23.45
	2087	N	GLY	B	48	35.001	51.867	94.851	1.00	20.99

	2088	CA	GLY	B	48	34.244	51.882	96.087	1.00	23.47
	2089	C	GLY	B	48	33.988	50.455	96.519	1.00	24.50
	2090	O	GLY	B	48	34.029	50.164	97.719	1.00	24.94
	2091	N	MET	B	49	33.744	49.559	95.554	1.00	24.06
5	2092	CA	MET	B	49	33.517	48.144	95.869	1.00	28.88
	2093	CB	MET	B	49	33.130	47.331	94.621	1.00	31.04
	2094	CG	MET	B	49	31.635	47.133	94.381	1.00	39.52
	2095	SD	MET	B	49	31.234	45.702	93.276	0.50	35.36
	2096	CE	MET	B	49	31.697	46.395	91.762	1.00	37.74
10	2097	C	MET	B	49	34.793	47.551	96.477	1.00	30.80
	2098	O	MET	B	49	34.734	46.752	97.413	1.00	35.99
	2099	N	GLU	B	50	35.950	47.940	95.952	1.00	33.55
	2100	CA	GLU	B	50	37.221	47.426	96.480	1.00	31.25
	2101	CB	GLU	B	50	38.417	47.919	95.649	1.00	32.09
15	2102	CG	GLU	B	50	38.554	47.294	94.256	1.00	38.13
	2103	CD	GLU	B	50	38.789	45.789	94.313	1.00	47.32
	2104	OE1	GLU	B	50	39.537	45.337	95.217	1.00	47.00
	2105	OE2	GLU	B	50	38.232	45.061	93.456	1.00	42.37
	2106	C	GLU	B	50	37.384	47.898	97.905	1.00	30.84
20	2107	O	GLU	B	50	37.708	47.110	98.796	1.00	31.48
	2108	N	ALA	B	51	37.156	49.193	98.120	1.00	30.50
	2109	CA	ALA	B	51	37.286	49.768	99.453	1.00	32.09
	2110	CB	ALA	B	51	36.911	51.262	99.426	1.00	32.81
	2111	C	ALA	B	51	36.395	49.008	100.436	1.00	27.96
25	2112	O	ALA	B	51	36.814	48.700	101.548	1.00	30.77
	2113	N	LEU	B	52	35.173	48.686	100.016	1.00	29.85
	2114	CA	LEU	B	52	34.257	47.957	100.891	1.00	25.95
	2115	CB	LEU	B	52	32.848	47.823	100.274	1.00	26.02
	2116	CG	LEU	B	52	31.809	47.122	101.177	1.00	26.29
30	2117	CD1	LEU	B	52	31.723	47.839	102.524	1.00	18.74
	2118	CD2	LEU	B	52	30.432	47.111	100.508	1.00	24.68
	2119	C	LEU	B	52	34.831	46.581	101.182	1.00	27.37
	2120	O	LEU	B	52	34.856	46.154	102.332	1.00	23.49
	2121	N	GLN	B	53	35.307	45.892	100.150	1.00	26.27
35	2122	CA	GLN	B	53	35.886	44.574	100.374	1.00	32.31
	2123	CB	GLN	B	53	36.462	43.988	99.083	1.00	34.86
	2124	CG	GLN	B	53	36.905	42.525	99.236	1.00	39.18
	2125	CD	GLN	B	53	35.767	41.559	98.947	1.00	45.30
	2126	OE1	GLN	B	53	34.594	41.928	99.057	1.00	37.18
40	2127	NE2	GLN	B	53	36.105	40.319	98.580	1.00	38.63
	2128	C	GLN	B	53	37.002	44.627	101.428	1.00	33.06
	2129	O	GLN	B	53	37.005	43.815	102.356	1.00	31.91
	2130	N	THR	B	54	37.938	45.578	101.313	1.00	31.58

	2131	CA	THR	B	54	39.016	45.628	102.297	1.00	30.94
	2132	CB	THR	B	54	40.269	46.420	101.782	1.00	31.07
	2133	OG1	THR	B	54	40.611	47.472	102.692	1.00	35.99
	2134	CG2	THR	B	54	40.034	46.962	100.420	1.00	31.12
5	2135	C	THR	B	54	38.568	46.138	103.658	1.00	31.94
	2136	O	THR	B	54	39.111	45.717	104.684	1.00	31.66
	2137	N	VAL	B	55	37.566	47.015	103.697	1.00	30.46
	2138	CA	VAL	B	55	37.094	47.482	104.995	1.00	22.29
	2139	CB	VAL	B	55	36.265	48.805	104.886	1.00	26.98
10	2140	CG1	VAL	B	55	35.531	49.106	106.212	1.00	20.70
	2141	CG2	VAL	B	55	37.197	49.958	104.558	1.00	25.40
	2142	C	VAL	B	55	36.274	46.393	105.696	1.00	23.87
	2143	O	VAL	B	55	36.387	46.243	106.910	1.00	23.56
	2144	N	THR	B	56	35.458	45.609	104.988	1.00	20.73
15	2145	CA	THR	B	56	34.725	44.609	105.766	1.00	27.78
	2146	CB	THR	B	56	33.415	44.089	105.058	1.00	30.51
	2147	OG1	THR	B	56	33.512	42.685	104.783	1.00	30.99
	2148	CG2	THR	B	56	33.121	44.863	103.809	1.00	19.24
	2149	C	THR	B	56	35.632	43.448	106.235	1.00	31.52
20	2150	O	THR	B	56	35.380	42.847	107.284	1.00	26.30
	2151	N	LYS	B	57	36.698	43.150	105.486	1.00	31.59
	2152	CA	LYS	B	57	37.649	42.102	105.903	1.00	31.17
	2153	CB	LYS	B	57	38.657	41.787	104.790	1.00	32.89
	2154	CG	LYS	B	57	38.101	40.919	103.652	1.00	32.46
25	2155	CD	LYS	B	57	39.028	40.925	102.445	1.00	41.21
	2156	CE	LYS	B	57	40.406	40.359	102.778	1.00	43.46
	2157	NZ	LYS	B	57	41.295	40.449	101.587	1.00	49.50
	2158	C	LYS	B	57	38.401	42.597	107.134	1.00	29.97
	2159	O	LYS	B	57	38.564	41.865	108.110	1.00	30.87
30	2160	N	ALA	B	58	38.848	43.850	107.095	1.00	30.19
	2161	CA	ALA	B	58	39.569	44.425	108.228	1.00	33.34
	2162	CB	ALA	B	58	40.115	45.810	107.857	1.00	28.83
	2163	C	ALA	B	58	38.682	44.528	109.479	1.00	36.20
	2164	O	ALA	B	58	39.129	44.240	110.594	1.00	44.51
35	2165	N	ALA	B	59	37.425	44.935	109.305	1.00	33.36
	2166	CA	ALA	B	59	36.533	45.070	110.451	1.00	28.78
	2167	CB	ALA	B	59	35.239	45.790	110.048	1.00	21.85
	2168	C	ALA	B	59	36.228	43.694	111.021	1.00	25.10
	2169	O	ALA	B	59	36.154	43.522	112.225	1.00	27.28
40	2170	N	ASN	B	60	36.054	42.708	110.153	1.00	26.74
	2171	CA	ASN	B	60	35.765	41.362	110.613	1.00	29.35
	2172	CB	ASN	B	60	35.548	40.428	109.423	1.00	33.41
	2173	CG	ASN	B	60	35.201	39.011	109.854	1.00	34.54

	2174	OD1	ASN	B	60	34.329	38.802	110.708	1.00	29.13
	2175	ND2	ASN	B	60	35.881	38.029	109.260	1.00	30.88
	2176	C	ASN	B	60	36.900	40.842	111.482	1.00	32.70
	2177	O	ASN	B	60	36.667	40.269	112.546	1.00	30.17
5	2178	N	LYS	B	61	38.131	41.060	111.032	1.00	34.45
	2179	CA	LYS	B	61	39.296	40.615	111.792	1.00	40.30
	2180	CB	LYS	B	61	40.584	40.779	110.962	1.00	47.00
	2181	CG	LYS	B	61	40.760	39.665	109.917	1.00	58.47
	2182	CD	LYS	B	61	41.822	39.980	108.860	1.00	63.94
10	2183	CE	LYS	B	61	41.827	38.916	107.756	1.00	63.09
	2184	NZ	LYS	B	61	42.537	39.364	106.524	1.00	61.07
	2185	C	LYS	B	61	39.419	41.357	113.112	1.00	34.14
	2186	O	LYS	B	61	39.792	40.757	114.115	1.00	31.31
	2187	N	LEU	B	62	39.086	42.649	113.114	1.00	35.44
15	2188	CA	LEU	B	62	39.162	43.473	114.333	1.00	33.84
	2189	CB	LEU	B	62	39.119	44.957	113.970	1.00	34.78
	2190	CG	LEU	B	62	40.407	45.570	113.411	1.00	37.52
	2191	CD1	LEU	B	62	40.170	47.000	112.942	1.00	37.58
	2192	CD2	LEU	B	62	41.442	45.559	114.507	1.00	36.63
20	2193	C	LEU	B	62	38.081	43.182	115.382	1.00	33.41
	2194	O	LEU	B	62	38.157	43.671	116.510	1.00	35.10
	2195	N	GLY	B	63	37.076	42.387	115.023	1.00	33.78
	2196	CA	GLY	B	63	36.027	42.083	115.984	1.00	33.21
	2197	C	GLY	B	63	34.728	42.892	115.894	1.00	34.60
25	2198	O	GLY	B	63	33.911	42.820	116.814	1.00	34.52
	2199	N	VAL	B	64	34.531	43.665	114.820	1.00	30.55
	2200	CA	VAL	B	64	33.293	44.439	114.637	1.00	21.10
	2201	CB	VAL	B	64	33.423	45.395	113.433	1.00	25.13
	2202	CG1	VAL	B	64	32.107	46.082	113.173	1.00	25.41
30	2203	CG2	VAL	B	64	34.537	46.407	113.683	1.00	20.22
	2204	C	VAL	B	64	32.246	43.376	114.318	1.00	26.49
	2205	O	VAL	B	64	32.522	42.462	113.533	1.00	28.36
	2206	N	LYS	B	65	31.059	43.461	114.910	1.00	21.50
	2207	CA	LYS	B	65	30.039	42.437	114.656	1.00	18.25
35	2208	CB	LYS	B	65	29.163	42.188	115.906	1.00	23.24
	2209	CG	LYS	B	65	29.896	41.769	117.197	1.00	21.33
	2210	CD	LYS	B	65	30.711	40.490	116.998	1.00	27.99
	2211	CE	LYS	B	65	31.510	40.128	118.244	0.50	28.62
	2212	NZ	LYS	B	65	32.655	39.219	117.910	0.50	25.61
40	2213	C	LYS	B	65	29.122	42.777	113.504	1.00	18.18
	2214	O	LYS	B	65	28.527	41.901	112.885	1.00	18.90
	2215	N	VAL	B	66	28.987	44.060	113.216	1.00	21.30
	2216	CA	VAL	B	66	28.104	44.448	112.144	1.00	17.27



	2217	CB	VAL	B	66	26.646	44.711	112.679	1.00	18.01
	2218	CG1	VAL	B	66	25.763	45.233	111.562	1.00	15.39
	2219	CG2	VAL	B	66	26.040	43.442	113.291	1.00	13.76
	2220	C	VAL	B	66	28.534	45.727	111.472	1.00	20.59
5	2221	O	VAL	B	66	29.005	46.655	112.131	1.00	21.20
	2222	N	ILE	B	67	28.407	45.764	110.152	1.00	18.71
	2223	CA	ILE	B	67	28.601	47.023	109.452	1.00	21.79
	2224	CB	AILE	B	67	29.858	47.000	108.555	0.50	20.55
	7705	CB	BILE	B	67	29.956	47.150	108.685	0.50	23.04
10	2225	CG2AILE	B	67	29.930	48.263	107.726	0.50	16.82	
	7706	CG2BILE	B	67	31.113	46.972	109.662	0.50	21.74	
	2226	CG1AILE	B	67	31.118	46.875	109.401	0.50	19.77	
	7707	CG1BILE	B	67	30.038	46.174	107.525	0.50	18.17	
	2227	CD1AILE	B	67	32.334	46.678	108.555	0.50	11.80	
15	7708	CD1BILE	B	67	31.310	46.364	106.725	0.50	26.05	
	2228	C	ILE	B	67	27.387	47.189	108.524	1.00	20.18
	2229	O	ILE	B	67	27.009	46.267	107.767	1.00	17.55
	2230	N	THR	B	68	26.722	48.338	108.652	1.00	18.83
	2231	CA	THR	B	68	25.580	48.638	107.789	1.00	22.11
20	2232	CB	THR	B	68	24.351	49.122	108.562	1.00	18.94
	2233	OG1	THR	B	68	23.957	48.112	109.498	1.00	29.44
	2234	CG2	THR	B	68	23.197	49.374	107.595	1.00	15.84
	2235	C	THR	B	68	26.064	49.752	106.872	1.00	23.35
	2236	O	THR	B	68	26.415	50.829	107.347	1.00	22.03
25	2237	N	VAL	B	69	26.098	49.468	105.568	1.00	22.76
	2238	CA	VAL	B	69	26.594	50.414	104.595	1.00	22.98
	2239	CB	AVAL	B	69	27.751	49.799	103.777	0.50	24.68
	7709	CB	BVAL	B	69	27.752	49.795	103.780	0.50	24.64
	2240	CG1AVAL	B	69	28.854	49.370	104.712	0.50	23.61	
30	7710	CG1BVAL	B	69	28.828	49.312	104.725	0.50	23.24	
	2241	CG2AVAL	B	69	27.253	48.610	102.972	0.50	20.54	
	7711	CG2BVAL	B	69	27.242	48.642	102.930	0.50	20.73	
	2242	C	VAL	B	69	25.521	50.912	103.657	1.00	26.29
	2243	O	VAL	B	69	24.708	50.151	103.148	1.00	26.43
35	2244	N	TYR	B	70	25.556	52.220	103.427	1.00	29.36
	2245	CA	TYR	B	70	24.595	52.929	102.599	1.00	29.39
	2246	CB	TYR	B	70	24.008	54.036	103.454	1.00	27.15
	2247	CG	TYR	B	70	22.862	54.822	102.883	1.00	25.96
	2248	CD1	TYR	B	70	21.829	54.193	102.195	1.00	27.79
40	2249	CE1	TYR	B	70	20.666	54.887	101.839	1.00	32.19
	2250	CD2	TYR	B	70	22.719	56.173	103.187	1.00	24.54
	2251	CE2	TYR	B	70	21.575	56.864	102.843	1.00	34.82
	2252	CZ	TYR	B	70	20.548	56.215	102.178	1.00	32.74

	2253	OH	TYR	B	70	19.386	56.882	101.909	1.00	43.33
	2254	C	TYR	B	70	25.285	53.523	101.383	1.00	35.91
	2255	O	TYR	B	70	26.228	54.312	101.528	1.00	37.18
	2256	N	ALA	B	71	24.820	53.163	100.200	1.00	39.15
5	2257	CA	ALA	B	71	25.388	53.675	98.954	1.00	50.72
	2258	CB	ALA	B	71	24.844	52.879	97.783	1.00	51.20
	2259	C	ALA	B	71	25.098	55.181	98.738	1.00	58.46
	2260	O	ALA	B	71	23.988	55.541	98.331	1.00	58.45
	2261	N	PHE	B	72	26.101	56.028	99.017	1.00	63.98
10	2262	CA	PHE	B	72	25.996	57.485	98.850	1.00	64.38
	2263	CB	PHE	B	72	26.363	57.864	97.407	0.00	63.09
	2264	CG	PHE	B	72	26.425	59.349	97.158	0.00	61.25
	2265	CD1	PHE	B	72	27.615	60.047	97.313	0.00	60.50
	2266	CD2	PHE	B	72	25.293	60.043	96.757	0.00	60.50
15	2267	CE1	PHE	B	72	27.673	61.421	97.061	0.00	59.87
	2268	CE2	PHE	B	72	25.346	61.416	96.509	0.00	59.87
	2269	CZ	PHE	B	72	26.536	62.101	96.661	0.00	59.69
	2270	C	PHE	B	72	24.589	57.985	99.163	1.00	67.12
	2271	O	PHE	B	72	24.386	58.852	100.010	1.00	71.18
20	2272	N	ARG	B	79	21.453	60.062	86.391	1.00	98.48
	2273	CA	ARG	B	79	21.443	59.714	84.973	1.00	99.65
	2274	CB	ARG	B	79	22.698	60.270	84.293	1.00	99.37
	2275	CG	ARG	B	79	23.990	60.014	85.046	1.00	100.00
	2276	CD	ARG	B	79	25.186	60.551	84.273	1.00	100.00
25	2277	NE	ARG	B	79	25.372	59.857	83.000	1.00	100.00
	2278	CZ	ARG	B	79	26.289	60.183	82.091	1.00	100.00
	2279	NH1	ARG	B	79	27.115	61.203	82.307	1.00	100.00
	2280	NH2	ARG	B	79	26.382	59.486	80.962	1.00	100.00
	2281	C	ARG	B	79	21.331	58.200	84.731	1.00	99.87
30	2282	O	ARG	B	79	22.125	57.418	85.254	1.00	99.98
	2283	N	PRO	B	80	20.342	57.775	83.918	1.00	100.00
	2284	CD	PRO	B	80	19.376	58.690	83.280	1.00	100.00
	2285	CA	PRO	B	80	20.037	56.385	83.548	1.00	100.00
	2286	CB	PRO	B	80	19.017	56.548	82.426	1.00	99.48
35	2287	CG	PRO	B	80	18.260	57.748	82.867	1.00	100.00
	2288	C	PRO	B	80	21.185	55.466	83.141	1.00	99.89
	2289	O	PRO	B	80	21.150	54.272	83.442	1.00	98.69
	2290	N	ASP	B	81	22.192	55.998	82.453	1.00	100.00
	2291	CA	ASP	B	81	23.305	55.159	82.024	1.00	100.00
40	2292	CB	ASP	B	81	24.022	55.775	80.822	1.00	100.00
	2293	CG	ASP	B	81	24.599	54.720	79.890	1.00	100.00
	2294	OD1	ASP	B	81	23.795	53.965	79.291	1.00	99.35
	2295	OD2	ASP	B	81	25.844	54.638	79.768	1.00	98.37

	2296	C	ASP	B	81	24.292	54.917	83.162	1.00	99.36
	2297	O	ASP	B	81	25.319	54.260	82.990	1.00	99.22
	2298	N	GLN	B	82	23.969	55.458	84.328	1.00	98.43
	2299	CA	GLN	B	82	24.800	55.284	85.505	1.00	98.86
5	2300	CB	GLN	B	82	25.355	56.630	85.979	1.00	98.97
	2301	CG	GLN	B	82	26.328	56.526	87.151	1.00	98.76
	2302	CD	GLN	B	82	26.671	57.879	87.755	1.00	98.93
	2303	OE1	GLN	B	82	27.055	58.809	87.041	1.00	98.73
	2304	NE2	GLN	B	82	26.539	57.994	89.077	1.00	96.05
10	2305	C	GLN	B	82	23.906	54.677	86.585	1.00	99.75
	2306	O	GLN	B	82	24.310	53.753	87.293	1.00	100.00
	2307	N	GLU	B	83	22.683	55.204	86.689	1.00	100.00
	2308	CA	GLU	B	83	21.697	54.743	87.665	1.00	98.86
	2309	CB	GLU	B	83	20.397	55.543	87.519	0.00	99.32
15	2310	CG	GLU	B	83	20.554	57.043	87.717	0.00	99.30
	2311	CD	GLU	B	83	21.051	57.409	89.104	0.00	99.42
	2312	OE1	GLU	B	83	21.267	58.612	89.362	0.00	99.48
	2313	OE2	GLU	B	83	21.225	56.495	89.938	0.00	99.48
	2314	C	GLU	B	83	21.407	53.252	87.498	1.00	99.34
20	2315	O	GLU	B	83	22.299	52.418	87.668	1.00	98.62
	2316	N	VAL	B	84	20.163	52.920	87.156	1.00	100.00
	2317	CA	VAL	B	84	19.747	51.521	86.978	1.00	100.00
	2318	CB	VAL	B	84	18.263	51.420	86.471	1.00	100.00
	2319	CG1	VAL	B	84	17.268	51.796	87.589	1.00	99.23
25	2320	CG2	VAL	B	84	18.076	52.328	85.269	1.00	100.00
	2321	C	VAL	B	84	20.645	50.721	86.012	1.00	100.00
	2322	O	VAL	B	84	20.416	49.518	85.793	1.00	100.00
	2323	N	LYS	B	85	21.667	51.379	85.454	1.00	96.27
	2324	CA	LYS	B	85	22.564	50.722	84.514	1.00	91.89
30	2325	CB	LYS	B	85	23.052	51.715	83.457	1.00	92.14
	2326	CG	LYS	B	85	23.655	51.051	82.243	0.00	91.98
	2327	CD	LYS	B	85	24.401	52.034	81.339	0.00	91.89
	2328	CE	LYS	B	85	25.031	51.302	80.154	0.00	91.77
	2329	NZ	LYS	B	85	25.878	52.209	79.338	0.00	91.53
35	2330	C	LYS	B	85	23.759	50.084	85.215	1.00	90.19
	2331	O	LYS	B	85	23.699	48.911	85.616	1.00	86.89
	2332	N	PHE	B	86	24.837	50.852	85.377	1.00	89.52
	2333	CA	PHE	B	86	26.035	50.321	86.019	1.00	88.74
	2334	CB	PHE	B	86	27.275	51.138	85.641	1.00	92.15
40	2335	CG	PHE	B	86	27.777	50.850	84.253	1.00	98.73
	2336	CD1	PHE	B	86	27.403	51.658	83.178	1.00	99.74
	2337	CD2	PHE	B	86	28.594	49.744	84.009	1.00	100.00
	2338	CE1	PHE	B	86	27.834	51.370	81.872	1.00	100.00

	2339	CE2	PHE	B	86	29.031	49.442	82.709	1.00	100.00
	2340	CZ	PHE	B	86	28.649	50.259	81.637	1.00	100.00
	2341	C	PHE	B	86	25.988	50.127	87.534	1.00	85.29
	2342	O	PHE	B	86	26.644	49.219	88.051	1.00	84.94
5	2343	N	ILE	B	87	25.232	50.955	88.252	1.00	80.15
	2344	CA	ILE	B	87	25.134	50.789	89.701	1.00	75.10
	2345	CB	ILE	B	87	24.651	52.075	90.395	1.00	73.06
	2346	CG2	ILE	B	87	24.352	51.792	91.873	1.00	72.58
	2347	CG1	ILE	B	87	25.724	53.160	90.271	1.00	71.73
10	2348	CD1	ILE	B	87	25.436	54.404	91.090	1.00	70.71
	2349	C	ILE	B	87	24.199	49.632	90.084	1.00	72.87
	2350	O	ILE	B	87	24.378	49.010	91.132	1.00	73.21
	2351	N	MET	B	88	23.203	49.343	89.250	1.00	70.19
	2352	CA	MET	B	88	22.297	48.233	89.537	1.00	68.05
15	2353	CB	MET	B	88	20.942	48.432	88.854	1.00	68.28
	2354	CG	MET	B	88	20.012	49.364	89.626	1.00	66.92
	2355	SD	MET	B	88	19.619	48.738	91.273	0.50	59.10
	2356	CE	MET	B	88	18.028	49.538	91.593	1.00	67.20
	2357	C	MET	B	88	22.913	46.913	89.101	1.00	66.04
20	2358	O	MET	B	88	22.416	45.844	89.444	1.00	68.71
	2359	N	ASN	B	89	24.002	46.997	88.347	1.00	64.44
	2360	CA	ASN	B	89	24.719	45.817	87.884	1.00	62.80
	2361	CB	ASN	B	89	25.225	46.019	86.456	1.00	70.00
	2362	CG	ASN	B	89	24.345	45.342	85.425	1.00	80.14
25	2363	OD1	ASN	B	89	23.142	45.618	85.326	1.00	85.25
	2364	ND2	ASN	B	89	24.942	44.444	84.647	1.00	83.00
	2365	C	ASN	B	89	25.905	45.523	88.798	1.00	60.13
	2366	O	ASN	B	89	26.618	44.537	88.592	1.00	57.81
	2367	N	LEU	B	90	26.121	46.379	89.800	1.00	53.28
30	2368	CA	LEU	B	90	27.229	46.185	90.743	1.00	50.44
	2369	CB	LEU	B	90	27.522	47.473	91.534	1.00	48.07
	2370	CG	LEU	B	90	28.133	48.680	90.792	1.00	51.30
	2371	CD1	LEU	B	90	28.202	49.877	91.723	1.00	47.19
	2372	CD2	LEU	B	90	29.517	48.346	90.261	1.00	47.85
35	2373	C	LEU	B	90	26.941	45.040	91.710	1.00	46.83
	2374	O	LEU	B	90	27.834	44.256	92.032	1.00	44.52
	2375	N	PRO	B	91	25.691	44.929	92.196	1.00	46.91
	2376	CD	PRO	B	91	24.537	45.840	92.097	1.00	45.81
	2377	CA	PRO	B	91	25.400	43.834	93.121	1.00	44.29
40	2378	CB	PRO	B	91	23.910	43.997	93.377	1.00	47.92
	2379	CG	PRO	B	91	23.748	45.491	93.342	1.00	45.72
	2380	C	PRO	B	91	25.733	42.522	92.438	1.00	45.05
	2381	O	PRO	B	91	26.161	41.555	93.073	1.00	42.25

	2382	N	VAL	B	92	25.544	42.504	91.126	1.00	42.78
	2383	CA	VAL	B	92	25.834	41.315	90.349	1.00	42.62
	2384	CB	VAL	B	92	25.253	41.425	88.921	1.00	38.76
	2385	CG1	VAL	B	92	25.575	40.184	88.136	1.00	33.84
5	2386	CG2	VAL	B	92	23.734	41.642	88.994	1.00	38.66
	2387	C	VAL	B	92	27.343	41.120	90.293	1.00	45.92
	2388	O	VAL	B	92	27.836	40.015	90.530	1.00	50.14
	2389	N	GLU	B	93	28.077	42.193	90.001	1.00	46.79
	2390	CA	GLU	B	93	29.534	42.127	89.921	1.00	46.04
10	2391	CB	GLU	B	93	30.099	43.477	89.486	1.00	54.15
	2392	CG	GLU	B	93	31.616	43.579	89.523	1.00	62.65
	2393	CD	GLU	B	93	32.180	44.336	88.322	1.00	72.41
	2394	OE1	GLU	B	93	31.566	45.346	87.889	1.00	69.66
	2395	OE2	GLU	B	93	33.248	43.916	87.817	1.00	78.42
15	2396	C	GLU	B	93	30.087	41.750	91.278	1.00	42.44
	2397	O	GLU	B	93	31.066	41.002	91.389	1.00	40.90
	2398	N	PHE	B	94	29.440	42.274	92.310	1.00	41.10
	2399	CA	PHE	B	94	29.823	42.001	93.687	1.00	40.89
	2400	CB	PHE	B	94	28.867	42.740	94.633	1.00	39.94
20	2401	CG	PHE	B	94	29.188	42.577	96.101	1.00	38.23
	2402	CD1	PHE	B	94	30.364	43.106	96.647	1.00	28.87
	2403	CD2	PHE	B	94	28.289	41.927	96.948	1.00	37.14
	2404	CE1	PHE	B	94	30.627	42.991	98.005	1.00	29.32
	2405	CE2	PHE	B	94	28.553	41.811	98.309	1.00	35.79
25	2406	CZ	PHE	B	94	29.731	42.349	98.839	1.00	31.62
	2407	C	PHE	B	94	29.768	40.497	93.946	1.00	38.73
	2408	O	PHE	B	94	30.760	39.896	94.352	1.00	41.46
	2409	N	TYR	B	95	28.606	39.897	93.690	1.00	43.75
	2410	CA	TYR	B	95	28.394	38.466	93.905	1.00	44.84
30	2411	CB	TYR	B	95	26.978	38.053	93.482	1.00	46.83
	2412	CG	TYR	B	95	26.728	36.571	93.658	1.00	50.09
	2413	CD1	TYR	B	95	26.525	36.019	94.930	1.00	47.10
	2414	CE1	TYR	B	95	26.371	34.642	95.103	1.00	50.61
	2415	CD2	TYR	B	95	26.763	35.706	92.563	1.00	53.25
35	2416	CE2	TYR	B	95	26.610	34.322	92.728	1.00	53.76
	2417	CZ	TYR	B	95	26.417	33.799	93.998	1.00	52.79
	2418	OH	TYR	B	95	26.281	32.433	94.155	1.00	55.30
	2419	C	TYR	B	95	29.382	37.601	93.146	1.00	47.75
	2420	O	TYR	B	95	29.701	36.488	93.569	1.00	49.84
40	2421	N	ASP	B	96	29.851	38.098	92.009	1.00	48.97
	2422	CA	ASP	B	96	30.793	37.331	91.209	1.00	49.83
	2423	CB	ASP	B	96	30.660	37.692	89.721	1.00	53.72
	2424	CG	ASP	B	96	29.377	37.148	89.090	1.00	59.27

	2425	OD1	ASP	B	96	29.084	35.941	89.268	1.00	60.23
	2426	OD2	ASP	B	96	28.669	37.925	88.408	1.00	60.91
	2427	C	ASP	B	96	32.250	37.475	91.635	1.00	44.71
	2428	O	ASP	B	96	32.946	36.479	91.792	1.00	44.14
5	2429	N	ASN	B	97	32.705	38.703	91.853	1.00	40.89
	2430	CA	ASN	B	97	34.104	38.916	92.198	1.00	41.98
	2431	CB	ASN	B	97	34.705	39.992	91.286	1.00	48.28
	2432	CG	ASN	B	97	34.306	39.814	89.832	1.00	50.29
	2433	OD1	ASN	B	97	34.302	38.698	89.309	1.00	49.16
10	2434	ND2	ASN	B	97	33.966	40.918	89.172	1.00	53.76
	2435	C	ASN	B	97	34.431	39.280	93.628	1.00	39.66
	2436	O	ASN	B	97	35.603	39.516	93.935	1.00	43.46
	2437	N	TYR	B	98	33.429	39.341	94.504	1.00	33.14
	2438	CA	TYR	B	98	33.689	39.695	95.905	1.00	30.70
15	2439	CB	TYR	B	98	33.265	41.146	96.165	1.00	31.81
	2440	CG	TYR	B	98	33.956	42.147	95.263	1.00	34.60
	2441	CD1	TYR	B	98	33.521	42.353	93.954	1.00	30.38
	2442	CE1	TYR	B	98	34.174	43.239	93.115	1.00	35.19
	2443	CD2	TYR	B	98	35.067	42.860	95.710	1.00	36.60
20	2444	CE2	TYR	B	98	35.729	43.757	94.876	1.00	43.15
	2445	CZ	TYR	B	98	35.276	43.939	93.583	1.00	41.47
	2446	OH	TYR	B	98	35.923	44.826	92.760	1.00	45.95
	2447	C	TYR	B	98	33.055	38.799	96.973	1.00	25.72
	2448	O	TYR	B	98	33.661	38.534	98.006	1.00	24.75
25	2449	N	VAL	B	99	31.835	38.340	96.736	1.00	21.53
	2450	CA	VAL	B	99	31.167	37.516	97.723	1.00	22.09
	2451	CB	VAL	B	99	29.700	37.256	97.305	1.00	25.80
	2452	CG1	VAL	B	99	29.091	36.151	98.128	1.00	24.07
	2453	CG2	VAL	B	99	28.888	38.551	97.501	1.00	22.03
30	2454	C	VAL	B	99	31.906	36.219	98.024	1.00	23.91
	2455	O	VAL	B	99	31.945	35.776	99.182	1.00	22.47
	2456	N	PRO	B	100	32.523	35.591	97.004	1.00	23.57
	2457	CD	PRO	B	100	32.417	35.724	95.539	1.00	23.04
	2458	CA	PRO	B	100	33.215	34.349	97.380	1.00	22.71
35	2459	CB	PRO	B	100	33.743	33.821	96.036	1.00	24.86
	2460	CG	PRO	B	100	32.660	34.273	95.049	1.00	22.36
	2461	C	PRO	B	100	34.319	34.578	98.432	1.00	24.06
	2462	O	PRO	B	100	34.437	33.811	99.395	1.00	23.65
	2463	N	GLU	B	101	35.096	35.651	98.289	1.00	23.03
40	2464	CA	GLU	B	101	36.158	35.902	99.252	1.00	25.09
	2465	CB	GLU	B	101	37.101	36.990	98.736	1.00	21.53
	2466	CG	GLU	B	101	38.097	37.427	99.803	1.00	31.97
	2467	CD	GLU	B	101	39.104	38.469	99.321	1.00	35.51

	2468	OE1	GLU	B	101	38.760	39.275	98.427	1.00	34.38
	2469	OE2	GLU	B	101	40.238	38.493	99.865	1.00	37.80
	2470	C	GLU	B	101	35.593	36.286	100.628	1.00	26.50
	2471	O	GLU	B	101	36.148	35.927	101.671	1.00	26.24
5	2472	N	LEU	B	102	34.481	37.008	100.634	1.00	24.48
	2473	CA	LEU	B	102	33.884	37.411	101.909	1.00	26.54
	2474	CB	LEU	B	102	32.786	38.466	101.692	1.00	22.48
	2475	CG	LEU	B	102	33.202	39.845	101.174	1.00	25.30
	2476	CD1	LEU	B	102	31.957	40.717	101.009	1.00	23.40
10	2477	CD2	LEU	B	102	34.189	40.489	102.140	1.00	21.50
	2478	C	LEU	B	102	33.296	36.183	102.615	1.00	23.51
	2479	O	LEU	B	102	33.366	36.056	103.853	1.00	20.23
	2480	N	HIS	B	103	32.720	35.285	101.824	1.00	20.02
	2481	CA	HIS	B	103	32.143	34.058	102.366	1.00	24.30
15	2482	CB	HIS	B	103	31.430	33.276	101.259	1.00	23.28
	2483	CG	HIS	B	103	31.016	31.905	101.673	1.00	25.55
	2484	CD2	HIS	B	103	31.221	30.697	101.095	1.00	25.14
	2485	ND1	HIS	B	103	30.300	31.665	102.825	1.00	20.38
	2486	CE1	HIS	B	103	30.081	30.368	102.941	1.00	25.01
20	2487	NE2	HIS	B	103	30.629	29.757	101.904	1.00	22.67
	2488	C	HIS	B	103	33.275	33.225	102.976	1.00	22.44
	2489	O	HIS	B	103	33.135	32.646	104.053	1.00	25.90
	2490	N	ALA	B	104	34.412	33.204	102.296	1.00	20.95
	2491	CA	ALA	B	104	35.580	32.486	102.786	1.00	24.16
25	2492	CB	ALA	B	104	36.682	32.454	101.699	1.00	23.79
	2493	C	ALA	B	104	36.095	33.149	104.077	1.00	27.52
	2494	O	ALA	B	104	36.784	32.500	104.876	1.00	28.23
	2495	N	ASN	B	105	35.759	34.428	104.293	1.00	26.50
	2496	CA	ASN	B	105	36.172	35.131	105.522	1.00	25.94
30	2497	CB	ASN	B	105	36.449	36.614	105.238	1.00	30.61
	2498	CG	ASN	B	105	37.854	36.860	104.750	1.00	31.73
	2499	OD1	ASN	B	105	38.728	37.238	105.525	1.00	34.08
	2500	ND2	ASN	B	105	38.085	36.637	103.464	1.00	29.92
	2501	C	ASN	B	105	35.125	35.016	106.652	1.00	25.24
35	2502	O	ASN	B	105	35.192	35.726	107.655	1.00	23.15
	2503	N	ASN	B	106	34.163	34.118	106.474	1.00	20.70
	2504	CA	ASN	B	106	33.109	33.878	107.456	1.00	23.39
	2505	CB	ASN	B	106	33.718	33.428	108.810	1.00	13.37
	2506	CG	ASN	B	106	32.672	32.805	109.740	1.00	15.95
40	2507	OD1	ASN	B	106	32.817	32.804	110.964	1.00	27.21
	2508	ND2	ASN	B	106	31.612	32.279	109.156	1.00	8.31
	2509	C	ASN	B	106	32.162	35.086	107.670	1.00	25.07
	2510	O	ASN	B	106	31.604	35.249	108.759	1.00	25.05

	2511	N	VAL B 107	31.977	35.898	106.621	1.00	26.55
	2512	CA	VAL B 107	31.119	37.087	106.645	1.00	18.84
	2513	CB	VAL B 107	31.680	38.215	105.746	1.00	22.56
	2514	CG1	VAL B 107	30.713	39.398	105.733	1.00	20.58
5	2515	CG2	VAL B 107	33.048	38.673	106.261	1.00	14.96
	2516	C	VAL B 107	29.697	36.778	106.178	1.00	22.54
	2517	O	VAL B 107	29.478	36.172	105.109	1.00	20.17
	2518	N	LYS B 108	28.724	37.194	106.985	1.00	14.90
	2519	CA	LYS B 108	27.331	36.962	106.643	1.00	16.80
10	2520	CB	LYS B 108	26.509	36.697	107.906	1.00	17.89
	2521	CG	LYS B 108	25.054	36.236	107.652	1.00	24.01
	2522	CD	LYS B 108	24.371	35.904	108.986	1.00	23.26
	2523	CE	LYS B 108	23.064	35.175	108.815	1.00	32.06
	2524	NZ	LYS B 108	22.471	34.831	110.164	1.00	35.43
15	2525	C	LYS B 108	26.812	38.201	105.926	1.00	19.58
	2526	O	LYS B 108	26.987	39.330	106.399	1.00	24.59
	2527	N	ILE B 109	26.176	37.996	104.785	1.00	15.32
	2528	CA	ILE B 109	25.652	39.117	104.026	1.00	20.76
	2529	CB	ILE B 109	26.109	39.000	102.551	1.00	21.13
20	2530	CG2	ILE B 109	25.414	40.068	101.666	1.00	22.20
	2531	CG1	ILE B 109	27.641	39.155	102.511	1.00	23.32
	2532	CD1	ILE B 109	28.287	38.898	101.156	1.00	19.26
	2533	C	ILE B 109	24.125	39.234	104.123	1.00	21.80
	2534	O	ILE B 109	23.400	38.265	103.934	1.00	23.83
25	2535	N	GLN B 110	23.645	40.427	104.441	1.00	22.66
	2536	CA	GLN B 110	22.205	40.683	104.532	1.00	25.26
	2537	CB	GLN B 110	21.742	40.698	105.995	1.00	23.45
	2538	CG	GLN B 110	22.171	39.432	106.769	1.00	29.81
	2539	CD	GLN B 110	21.437	39.217	108.099	1.00	35.24
30	2540	OE1	GLN B 110	21.145	40.164	108.839	1.00	41.06
	2541	NE2	GLN B 110	21.152	37.958	108.411	1.00	38.90
	2542	C	GLN B 110	21.910	42.028	103.885	1.00	24.97
	2543	O	GLN B 110	22.814	42.808	103.611	1.00	22.01
	2544	N	MET B 111	20.644	42.292	103.615	1.00	32.95
35	2545	CA	MET B 111	20.269	43.562	103.021	1.00	32.15
	2546	CB	MET B 111	20.020	43.395	101.510	1.00	34.96
	2547	CG	MET B 111	18.808	42.582	101.063	0.50	43.12
	2548	SD	MET B 111	18.803	42.277	99.228	0.50	49.17
	2549	CE	MET B 111	18.840	43.927	98.609	0.50	51.19
40	2550	C	MET B 111	19.050	44.150	103.738	1.00	36.15
	2551	O	MET B 111	18.278	43.421	104.373	1.00	38.18
	2552	N	ILE B 112	18.918	45.474	103.712	1.00	28.27
	2553	CA	ILE B 112	17.756	46.117	104.310	1.00	25.94



	2554	CB	ILE B 112	18.056	46.806	105.676	1.00	32.57
	2555	CG2	ILE B 112	18.298	45.767	106.759	1.00	32.50
	2556	CG1	ILE B 112	19.250	47.743	105.552	1.00	30.97
	2557	CD1	ILE B 112	19.462	48.564	106.780	1.00	29.61
5	2558	C	ILE B 112	17.313	47.176	103.326	1.00	25.29
	2559	O	ILE B 112	18.124	47.701	102.567	1.00	24.74
	2560	N	GLY B 113	16.030	47.497	103.341	1.00	25.33
	2561	CA	GLY B 113	15.515	48.492	102.425	1.00	30.23
	2562	C	GLY B 113	14.323	47.915	101.692	1.00	35.29
10	2563	O	GLY B 113	13.851	46.827	102.030	1.00	33.16
	2564	N	GLU B 114	13.822	48.647	100.704	1.00	37.27
	2565	CA	GLU B 114	12.682	48.185	99.921	1.00	38.51
	2566	CB	GLU B 114	11.825	49.379	99.511	1.00	40.21
	2567	CG	GLU B 114	10.960	49.894	100.634	1.00	46.45
15	2568	CD	GLU B 114	10.688	51.370	100.500	1.00	52.78
	2569	OE1	GLU B 114	11.617	52.167	100.762	1.00	60.29
	2570	OE2	GLU B 114	9.560	51.735	100.119	1.00	55.34
	2571	C	GLU B 114	13.259	47.456	98.712	1.00	39.80
	2572	O	GLU B 114	13.455	48.018	97.624	1.00	35.29
20	2573	N	THR B 115	13.540	46.185	98.940	1.00	42.25
	2574	CA	THR B 115	14.155	45.321	97.956	1.00	48.21
	2575	CB	THR B 115	14.681	44.066	98.677	1.00	48.20
	2576	OG1	THR B 115	13.624	43.472	99.444	1.00	45.45
	2577	CG2	THR B 115	15.820	44.453	99.618	1.00	48.69
25	2578	C	THR B 115	13.296	44.938	96.740	1.00	49.48
	2579	O	THR B 115	13.816	44.442	95.741	1.00	48.87
	2580	N	ASP B 116	11.994	45.200	96.821	1.00	49.31
	2581	CA	ASP B 116	11.070	44.889	95.733	1.00	50.98
	2582	CB	ASP B 116	9.621	44.970	96.234	1.00	59.20
30	2583	CG	ASP B 116	9.275	43.845	97.209	1.00	66.31
	2584	OD1	ASP B 116	10.202	43.096	97.616	1.00	68.99
	2585	OD2	ASP B 116	8.077	43.717	97.567	1.00	67.08
	2586	C	ASP B 116	11.235	45.790	94.513	1.00	47.58
	2587	O	ASP B 116	10.961	45.379	93.387	1.00	47.12
35	2588	N	ARG B 117	11.670	47.022	94.724	1.00	41.87
	2589	CA	ARG B 117	11.843	47.910	93.594	1.00	43.14
	2590	CB	ARG B 117	12.051	49.363	94.057	1.00	48.01
	2591	CG	ARG B 117	12.284	50.337	92.883	1.00	58.96
	2592	CD	ARG B 117	12.831	51.703	93.305	1.00	65.60
40	2593	NE	ARG B 117	13.493	52.390	92.188	1.00	76.02
	2594	CZ	ARG B 117	14.668	52.032	91.657	1.00	77.97
	2595	NH1	ARG B 117	15.336	50.988	92.137	1.00	77.31
	2596	NH2	ARG B 117	15.175	52.711	90.631	1.00	75.04

	2597	C	ARG B 117	13.029	47.466	92.734	1.00	38.08
	2598	O	ARG B 117	13.138	47.846	91.575	1.00	41.98
	2599	N	LEU B 118	13.904	46.636	93.284	1.00	34.54
	2600	CA	LEU B 118	15.086	46.207	92.541	1.00	35.55
5	2601	CB	LEU B 118	16.072	45.535	93.512	1.00	39.36
	2602	CG	LEU B 118	16.690	46.395	94.623	1.00	32.09
	2603	CD1	LEU B 118	17.269	45.487	95.670	1.00	30.29
	2604	CD2	LEU B 118	17.745	47.337	94.041	1.00	30.17
	2605	C	LEU B 118	14.841	45.286	91.325	1.00	31.41
10	2606	O	LEU B 118	13.938	44.457	91.319	1.00	31.36
	2607	N	PRO B 119	15.656	45.431	90.276	1.00	30.38
	2608	CD	PRO B 119	16.713	46.434	90.080	1.00	31.50
	2609	CA	PRO B 119	15.502	44.595	89.082	1.00	35.63
	2610	CB	PRO B 119	16.618	45.083	88.167	1.00	33.60
15	2611	CG	PRO B 119	16.783	46.514	88.585	1.00	32.98
	2612	C	PRO B 119	15.668	43.120	89.432	1.00	36.42
	2613	O	PRO B 119	16.320	42.759	90.415	1.00	34.89
	2614	N	LYS B 120	15.078	42.263	88.621	1.00	36.83
	2615	CA	LYS B 120	15.169	40.846	88.877	1.00	36.08
20	2616	CB	LYS B 120	14.562	40.090	87.710	1.00	35.56
	2617	CG	LYS B 120	14.383	38.610	87.966	1.00	38.99
	2618	CD	LYS B 120	14.017	37.915	86.665	1.00	40.22
	2619	CE	LYS B 120	14.047	36.418	86.838	1.00	34.37
	2620	NZ	LYS B 120	14.391	35.783	85.555	1.00	42.21
25	2621	C	LYS B 120	16.623	40.403	89.078	1.00	36.74
	2622	O	LYS B 120	16.956	39.727	90.051	1.00	36.28
	2623	N	GLN B 121	17.482	40.810	88.156	1.00	35.29
	2624	CA	GLN B 121	18.886	40.428	88.176	1.00	38.60
	2625	CB	GLN B 121	19.570	40.985	86.935	1.00	41.25
30	2626	CG	GLN B 121	20.845	40.290	86.553	1.00	51.81
	2627	CD	GLN B 121	21.324	40.707	85.173	0.50	51.96
	2628	OE1	GLN B 121	21.199	41.871	84.783	0.50	53.41
	2629	NE2	GLN B 121	21.884	39.760	84.433	0.50	50.04
	2630	C	GLN B 121	19.654	40.846	89.420	1.00	36.51
35	2631	O	GLN B 121	20.453	40.079	89.952	1.00	35.73
	2632	N	THR B 122	19.422	42.055	89.900	1.00	38.81
	2633	CA	THR B 122	20.154	42.487	91.076	1.00	34.30
	2634	CB	THR B 122	20.205	44.027	91.153	1.00	30.34
	2635	OG1	THR B 122	19.300	44.497	92.140	1.00	41.29
40	2636	CG2	THR B 122	19.830	44.622	89.830	1.00	24.97
	2637	C	THR B 122	19.571	41.854	92.341	1.00	30.92
	2638	O	THR B 122	20.315	41.487	93.238	1.00	38.46
	2639	N	PHE B 123	18.254	41.692	92.417	1.00	29.82

	2640	CA	PHE B 123	17.651	41.053	93.591	1.00	28.49
	2641	CB	PHE B 123	16.133	41.072	93.502	1.00	26.91
	2642	CG	PHE B 123	15.438	40.374	94.641	1.00	29.82
	2643	CD1	PHE B 123	15.034	41.084	95.767	1.00	38.16
5	2644	CD2	PHE B 123	15.135	39.013	94.565	1.00	35.67
	2645	CE1	PHE B 123	14.327	40.450	96.805	1.00	35.88
	2646	CE2	PHE B 123	14.432	38.360	95.592	1.00	34.78
	2647	CZ	PHE B 123	14.025	39.081	96.714	1.00	37.18
	2648	C	PHE B 123	18.093	39.597	93.650	1.00	29.77
10	2649	O	PHE B 123	18.194	39.017	94.720	1.00	32.37
	2650	N	GLU B 124	18.323	38.991	92.492	1.00	27.20
	2651	CA	GLU B 124	18.743	37.601	92.471	1.00	30.05
	2652	CB	GLU B 124	18.452	36.988	91.103	1.00	23.09
	2653	CG	GLU B 124	16.977	36.585	90.977	1.00	34.98
15	2654	CD	GLU B 124	16.628	35.990	89.627	1.00	38.90
	2655	OE1	GLU B 124	15.495	35.462	89.495	1.00	37.19
	2656	OE2	GLU B 124	17.487	36.052	88.707	1.00	40.98
	2657	C	GLU B 124	20.204	37.384	92.885	1.00	28.64
	2658	O	GLU B 124	20.528	36.370	93.504	1.00	29.87
20	2659	N	ALA B 125	21.066	38.341	92.553	1.00	27.14
	2660	CA	ALA B 125	22.474	38.284	92.911	1.00	26.83
	2661	CB	ALA B 125	23.229	39.432	92.238	1.00	23.38
	2662	C	ALA B 125	22.563	38.411	94.438	1.00	32.42
	2663	O	ALA B 125	23.241	37.627	95.113	1.00	35.19
25	2664	N	LEU B 126	21.862	39.395	94.988	1.00	30.70
	2665	CA	LEU B 126	21.873	39.581	96.429	1.00	32.67
	2666	CB	LEU B 126	21.207	40.921	96.793	1.00	28.66
	2667	CG	LEU B 126	21.954	42.117	96.153	1.00	38.06
	2668	CD1	LEU B 126	21.145	43.361	96.310	1.00	36.55
30	2669	CD2	LEU B 126	23.346	42.308	96.760	1.00	33.90
	2670	C	LEU B 126	21.219	38.404	97.166	1.00	26.75
	2671	O	LEU B 126	21.675	38.014	98.236	1.00	30.86
	2672	N	THR B 127	20.159	37.827	96.615	1.00	26.63
	2673	CA	THR B 127	19.530	36.691	97.282	1.00	26.35
35	2674	CB	THR B 127	18.273	36.225	96.549	1.00	30.96
	2675	OG1	THR B 127	17.325	37.295	96.541	1.00	36.62
	2676	CG2	THR B 127	17.646	35.012	97.255	1.00	29.20
	2677	C	THR B 127	20.538	35.540	97.364	1.00	26.73
	2678	O	THR B 127	20.700	34.921	98.418	1.00	23.88
40	2679	N	LYS B 128	21.235	35.262	96.266	1.00	27.34
	2680	CA	LYS B 128	22.261	34.201	96.298	1.00	32.49
	2681	CB	LYS B 128	22.887	33.989	94.908	1.00	31.84
	2682	CG	LYS B 128	21.920	33.495	93.842	1.00	41.04

	2683	CD	LYS B 128	22.612	33.466	92.494	1.00	43.34
	2684	CE	LYS B 128	21.630	33.215	91.385	1.00	49.73
	2685	NZ	LYS B 128	22.293	33.292	90.065	1.00	60.28
	2686	C	LYS B 128	23.396	34.501	97.313	1.00	25.67
5	2687	O	LYS B 128	23.862	33.582	97.984	1.00	23.77
	2688	N	ALA B 129	23.836	35.762	97.422	1.00	17.35
	2689	CA	ALA B 129	24.908	36.103	98.367	1.00	23.02
	2690	CB	ALA B 129	25.350	37.554	98.178	1.00	19.09
	2691	C	ALA B 129	24.420	35.873	99.808	1.00	23.63
10	2692	O	ALA B 129	25.176	35.515	100.722	1.00	24.77
	2693	N	GLU B 130	23.130	36.058	99.988	1.00	23.48
	2694	CA	GLU B 130	22.487	35.884	101.277	1.00	25.18
	2695	CB	GLU B 130	21.096	36.465	101.142	1.00	30.58
	2696	CG	GLU B 130	20.374	36.886	102.358	1.00	40.36
15	2697	CD	GLU B 130	19.130	37.668	101.948	1.00	50.17
	2698	OE1	GLU B 130	18.195	37.053	101.368	1.00	53.04
	2699	OE2	GLU B 130	19.103	38.899	102.171	1.00	46.62
	2700	C	GLU B 130	22.431	34.382	101.607	1.00	25.70
	2701	O	GLU B 130	22.785	33.954	102.717	1.00	22.61
20	2702	N	GLU B 131	21.991	33.590	100.631	1.00	23.28
	2703	CA	GLU B 131	21.867	32.155	100.801	1.00	27.87
	2704	CB	GLU B 131	21.144	31.533	99.605	1.00	30.60
	2705	CG	GLU B 131	19.715	32.042	99.454	1.00	45.10
	2706	CD	GLU B 131	18.983	31.435	98.269	1.00	51.15
25	2707	OE1	GLU B 131	19.633	31.154	97.232	1.00	56.43
	2708	OE2	GLU B 131	17.749	31.259	98.371	1.00	57.26
	2709	C	GLU B 131	23.221	31.502	100.979	1.00	29.58
	2710	O	GLU B 131	23.366	30.583	101.782	1.00	27.16
	2711	N	LEU B 132	24.204	31.985	100.227	1.00	23.40
30	2712	CA	LEU B 132	25.547	31.461	100.300	1.00	21.48
	2713	CB	LEU B 132	26.444	32.187	99.312	1.00	22.64
	2714	CG	LEU B 132	27.918	31.807	99.437	1.00	28.04
	2715	CD1	LEU B 132	28.085	30.436	98.834	1.00	31.43
	2716	CD2	LEU B 132	28.810	32.808	98.718	1.00	25.17
35	2717	C	LEU B 132	26.177	31.619	101.680	1.00	22.34
	2718	O	LEU B 132	26.814	30.706	102.194	1.00	19.64
	2719	N	THR B 133	25.982	32.789	102.267	1.00	20.35
	2720	CA	THR B 133	26.583	33.149	103.548	1.00	16.72
	2721	CB	THR B 133	27.127	34.597	103.465	1.00	24.60
40	2722	OG1	THR B 133	26.024	35.517	103.304	1.00	20.11
	2723	CG2	THR B 133	28.042	34.746	102.275	1.00	10.01
	2724	C	THR B 133	25.679	33.076	104.769	1.00	16.90
	2725	O	THR B 133	26.092	33.487	105.849	1.00	20.36

	2726	N	LYS B 134	24.473	32.537	104.618	1.00	17.94
	2727	CA	LYS B 134	23.526	32.494	105.729	1.00	24.44
	2728	CB	LYS B 134	22.174	31.928	105.262	1.00	29.56
	2729	CG	LYS B 134	22.109	30.423	105.187	1.00	34.27
5	2730	CD	LYS B 134	20.716	29.948	104.846	1.00	37.20
	2731	CE	LYS B 134	20.625	28.448	105.064	1.00	45.05
	2732	NZ	LYS B 134	19.242	27.934	104.866	1.00	56.01
	2733	C	LYS B 134	23.977	31.744	106.987	1.00	27.65
	2734	O	LYS B 134	23.516	32.054	108.098	1.00	26.24
10	2735	N	ASN B 135	24.872	30.771	106.841	1.00	22.66
	2736	CA	ASN B 135	25.324	30.031	108.020	1.00	22.43
	2737	CB	ASN B 135	25.638	28.582	107.649	1.00	21.85
	2738	CG	ASN B 135	24.461	27.870	107.035	1.00	25.43
	2739	OD1	ASN B 135	23.362	27.828	107.618	1.00	27.40
15	2740	ND2	ASN B 135	24.673	27.290	105.850	1.00	24.76
	2741	C	ASN B 135	26.558	30.665	108.668	1.00	22.00
	2742	O	ASN B 135	26.961	30.264	109.768	1.00	22.27
	2743	N	ASN B 136	27.142	31.668	108.009	1.00	19.49
	2744	CA	ASN B 136	28.356	32.291	108.543	1.00	19.27
20	2745	CB	ASN B 136	28.933	33.246	107.517	1.00	18.82
	2746	CG	ASN B 136	29.270	32.529	106.212	1.00	22.39
	2747	OD1	ASN B 136	29.070	31.307	106.091	1.00	18.22
	2748	ND2	ASN B 136	29.775	33.271	105.236	1.00	22.38
	2749	C	ASN B 136	28.197	32.946	109.900	1.00	25.31
25	2750	O	ASN B 136	27.154	33.525	110.231	1.00	21.59
	2751	N	THR B 137	29.250	32.842	110.700	1.00	25.22
	2752	CA	THR B 137	29.189	33.355	112.051	1.00	19.85
	2753	CB	THR B 137	29.548	32.241	113.061	1.00	20.99
	2754	OG1	THR B 137	30.888	31.797	112.807	1.00	15.64
30	2755	CG2	THR B 137	28.564	31.067	112.934	1.00	14.33
	2756	C	THR B 137	30.032	34.567	112.371	1.00	21.86
	2757	O	THR B 137	30.039	35.009	113.510	1.00	21.90
	2758	N	GLY B 138	30.748	35.106	111.389	1.00	25.84
	2759	CA	GLY B 138	31.560	36.279	111.660	1.00	21.49
35	2760	C	GLY B 138	30.734	37.550	111.454	1.00	25.55
	2761	O	GLY B 138	29.512	37.538	111.595	1.00	22.30
	2762	N	LEU B 139	31.417	38.642	111.124	1.00	17.36
	2763	CA	LEU B 139	30.802	39.937	110.887	1.00	22.33
	2764	CB	LEU B 139	31.874	40.900	110.352	1.00	15.14
40	2765	CG	ALEU B 139	31.496	42.372	110.095	0.50	15.42
	7712	CG	BLEU B 139	31.435	42.283	109.865	0.50	18.12
	2766	CD1	ALEU B 139	32.767	43.213	110.091	0.50	13.01
	7713	CD1	BLEU B 139	31.268	43.219	111.035	0.50	12.89

	2767	CD2ALEU B 139	30.760	42.530	108.768	0.50	3.11
	7714	CD2BLEU B 139	32.493	42.826	108.925	0.50	11.99
	2768	C LEU B 139	29.609	39.876	109.914	1.00	22.23
	2769	O LEU B 139	29.606	39.106	108.940	1.00	23.29
5	2770	N ILE B 140	28.582	40.670	110.197	1.00	22.63
	2771	CA ILE B 140	27.417	40.738	109.314	1.00	19.61
	2772	CB ILE B 140	26.104	40.852	110.099	1.00	20.05
	2773	CG2 ILE B 140	24.942	41.054	109.139	1.00	17.15
	2774	CG1 ILE B 140	25.871	39.575	110.900	1.00	17.59
10	2775	CD1 ILE B 140	24.620	39.603	111.742	1.00	22.94
	2776	C ILE B 140	27.571	41.986	108.462	1.00	20.58
	2777	O ILE B 140	27.719	43.068	109.001	1.00	22.60
	2778	N LEU B 141	27.604	41.829	107.140	1.00	23.29
	2779	CA LEU B 141	27.713	42.981	106.256	1.00	21.97
15	2780	CB LEU B 141	28.647	42.702	105.078	1.00	14.36
	2781	CG LEU B 141	28.671	43.774	103.989	1.00	16.38
	2782	CD1 LEU B 141	29.184	45.114	104.524	1.00	15.49
	2783	CD2 LEU B 141	29.561	43.296	102.871	1.00	16.28
	2784	C LEU B 141	26.281	43.247	105.784	1.00	26.03
20	2785	O LEU B 141	25.691	42.481	105.011	1.00	21.49
	2786	N ASN B 142	25.745	44.352	106.279	1.00	23.64
	2787	CA ASN B 142	24.377	44.755	106.021	1.00	23.57
	2788	CB ASN B 142	23.792	45.182	107.368	1.00	24.19
	2789	CG ASN B 142	22.302	45.192	107.392	1.00	31.71
25	2790	OD1 ASN B 142	21.657	44.358	106.765	1.00	40.59
	2791	ND2 ASN B 142	21.728	46.127	108.155	1.00	35.85
	2792	C ASN B 142	24.267	45.864	104.970	1.00	25.30
	2793	O ASN B 142	24.601	47.030	105.236	1.00	25.03
	2794	N PHE B 143	23.809	45.486	103.777	1.00	22.22
30	2795	CA PHE B 143	23.631	46.404	102.656	1.00	22.82
	2796	CB PHE B 143	23.622	45.647	101.328	1.00	23.81
	2797	CG PHE B 143	24.976	45.317	100.826	1.00	28.61
	2798	CD1 PHE B 143	25.479	44.029	100.948	1.00	27.59
	2799	CD2 PHE B 143	25.781	46.316	100.292	1.00	24.93
35	2800	CE1 PHE B 143	26.783	43.737	100.546	1.00	32.79
	2801	CE2 PHE B 143	27.080	46.043	99.890	1.00	33.32
	2802	CZ PHE B 143	27.588	44.741	100.019	1.00	31.39
	2803	C PHE B 143	22.321	47.155	102.719	1.00	25.32
	2804	O PHE B 143	21.268	46.533	102.670	1.00	30.65
40	2805	N ALA B 144	22.375	48.477	102.820	1.00	19.97
	2806	CA ALA B 144	21.158	49.283	102.832	1.00	24.36
	2807	CB ALA B 144	21.330	50.525	103.718	1.00	23.71
	2808	C ALA B 144	20.984	49.691	101.380	1.00	24.14

	2809	O	ALA B 144	21.728	50.532	100.886	1.00	27.10
	2810	N	LEU B 145	20.011	49.078	100.707	1.00	26.26
	2811	CA	LEU B 145	19.733	49.327	99.291	1.00	28.92
	2812	CB	LEU B 145	19.928	48.047	98.485	1.00	31.15
5	2813	CG	LEU B 145	21.351	47.546	98.471	1.00	40.89
	2814	CD1	LEU B 145	21.364	46.198	97.791	1.00	47.02
	2815	CD2	LEU B 145	22.257	48.544	97.755	1.00	39.70
	2816	C	LEU B 145	18.302	49.773	99.123	1.00	26.74
	2817	O	LEU B 145	17.397	49.182	99.698	1.00	30.12
10	2818	N	ASN B 146	18.092	50.775	98.285	1.00	26.59
	2819	CA	ASN B 146	16.758	51.322	98.097	1.00	27.70
	2820	CB	ASN B 146	15.878	50.364	97.309	1.00	32.44
	2821	CG	ASN B 146	14.761	51.081	96.625	1.00	43.00
	2822	OD1	ASN B 146	14.995	52.059	95.921	1.00	53.78
15	2823	ND2	ASN B 146	13.532	50.618	96.829	1.00	51.53
	2824	C	ASN B 146	16.210	51.529	99.499	1.00	21.98
	2825	O	ASN B 146	15.095	51.135	99.843	1.00	28.01
	2826	N	TYR B 147	17.033	52.161	100.314	1.00	25.91
	2827	CA	TYR B 147	16.716	52.403	101.711	1.00	24.07
20	2828	CB	TYR B 147	17.864	51.864	102.590	1.00	23.00
	2829	CG	TYR B 147	17.728	52.219	104.045	1.00	23.18
	2830	CD1	TYR B 147	17.057	51.370	104.930	1.00	15.53
	2831	CE1	TYR B 147	16.838	51.737	106.280	1.00	19.86
	2832	CD2	TYR B 147	18.191	53.446	104.528	1.00	23.25
25	2833	CE2	TYR B 147	17.973	53.826	105.877	1.00	24.34
	2834	CZ	TYR B 147	17.296	52.967	106.737	1.00	22.28
	2835	OH	TYR B 147	17.058	53.344	108.045	1.00	25.61
	2836	C	TYR B 147	16.514	53.870	102.009	1.00	18.19
	2837	O	TYR B 147	17.210	54.722	101.464	1.00	22.48
30	2838	N	GLY B 148	15.579	54.143	102.912	1.00	19.89
	2839	CA	GLY B 148	15.289	55.499	103.347	1.00	18.06
	2840	C	GLY B 148	14.813	55.418	104.796	1.00	20.57
	2841	O	GLY B 148	13.887	54.679	105.092	1.00	22.99
	2842	N	GLY B 149	15.431	56.172	105.702	1.00	23.59
35	2843	CA	GLY B 149	15.033	56.120	107.098	1.00	21.07
	2844	C	GLY B 149	13.553	56.359	107.337	1.00	24.39
	2845	O	GLY B 149	12.884	55.546	107.967	1.00	26.45
	2846	N	ARG B 150	13.032	57.471	106.832	1.00	22.81
	2847	CA	ARG B 150	11.639	57.777	107.042	1.00	22.16
40	2848	CB	ARG B 150	11.298	59.147	106.472	1.00	23.22
	2849	CG	ARG B 150	11.902	60.288	107.238	1.00	20.42
	2850	CD	ARG B 150	11.535	61.582	106.587	1.00	20.45
	2851	NE	ARG B 150	12.090	62.724	107.299	1.00	23.58

	2852	CZ	ARG B 150	12.082	63.960	106.821	1.00	26.72
	2853	NH1	ARG B 150	11.541	64.201	105.644	1.00	36.12
	2854	NH2	ARG B 150	12.647	64.944	107.496	1.00	31.06
	2855	C	ARG B 150	10.716	56.731	106.464	1.00	25.42
5	2856	O	ARG B 150	9.711	56.400	107.080	1.00	25.65
	2857	N	ALA B 151	11.047	56.205	105.289	1.00	23.69
	2858	CA	ALA B 151	10.209	55.185	104.669	1.00	21.06
	2859	CB	ALA B 151	10.690	54.884	103.246	1.00	17.00
	2860	C	ALA B 151	10.253	53.924	105.519	1.00	26.29
10	2861	O	ALA B 151	9.247	53.236	105.682	1.00	26.08
	2862	N	GLU B 152	11.429	53.609	106.051	1.00	26.21
	2863	CA	GLU B 152	11.560	52.444	106.908	1.00	28.33
	2864	CB	GLU B 152	12.995	52.297	107.394	1.00	28.33
	2865	CG	GLU B 152	13.131	51.210	108.428	1.00	26.75
15	2866	CD	GLU B 152	14.539	51.099	108.968	1.00	31.62
	2867	OE1	GLU B 152	15.174	52.140	109.231	1.00	27.86
	2868	OE2	GLU B 152	15.003	49.964	109.142	1.00	28.84
	2869	C	GLU B 152	10.629	52.579	108.127	1.00	31.42
	2870	O	GLU B 152	9.876	51.662	108.457	1.00	28.83
20	2871	N	ILE B 153	10.697	53.716	108.811	1.00	26.05
	2872	CA	ILE B 153	9.842	53.939	109.977	1.00	24.73
	2873	CB	ILE B 153	10.154	55.305	110.632	1.00	20.96
	2874	CG2	ILE B 153	9.162	55.596	111.738	1.00	25.69
	2875	CG1	ILE B 153	11.597	55.335	111.132	1.00	21.06
25	2876	CD1	ILE B 153	12.084	56.702	111.540	1.00	17.56
	2877	C	ILE B 153	8.362	53.938	109.534	1.00	33.77
	2878	O	ILE B 153	7.491	53.364	110.207	1.00	27.16
	2879	N	THR B 154	8.083	54.590	108.399	1.00	32.59
	2880	CA	THR B 154	6.717	54.675	107.886	1.00	31.80
30	2881	CB	THR B 154	6.635	55.352	106.510	1.00	30.80
	2882	OG1	THR B 154	7.136	56.687	106.593	1.00	32.03
	2883	CG2	THR B 154	5.180	55.397	106.038	1.00	32.24
	2884	C	THR B 154	6.115	53.297	107.729	1.00	31.38
	2885	O	THR B 154	5.004	53.044	108.189	1.00	35.76
35	2886	N	GLN B 155	6.845	52.419	107.061	1.00	26.39
	2887	CA	GLN B 155	6.392	51.062	106.831	1.00	29.59
	2888	CB	GLN B 155	7.404	50.344	105.928	1.00	32.82
	2889	CG	GLN B 155	7.537	48.850	106.156	1.00	47.28
	2890	CD	GLN B 155	8.589	48.517	107.202	1.00	55.24
40	2891	OE1	GLN B 155	8.885	47.348	107.456	1.00	61.93
	2892	NE2	GLN B 155	9.161	49.545	107.811	1.00	53.23
	2893	C	GLN B 155	6.187	50.300	108.147	1.00	36.36
	2894	O	GLN B 155	5.285	49.453	108.267	1.00	37.61



	2895	N	ALA B 156	7.019	50.595	109.138	1.00	33.13
	2896	CA	ALA B 156	6.899	49.912	110.411	1.00	35.24
	2897	CB	ALA B 156	8.108	50.198	111.284	1.00	31.07
	2898	C	ALA B 156	5.627	50.410	111.083	1.00	38.99
5	2899	O	ALA B 156	4.870	49.625	111.659	1.00	35.35
	2900	N	LEU B 157	5.393	51.718	111.011	1.00	37.53
	2901	CA	LEU B 157	4.204	52.279	111.612	1.00	40.76
	2902	CB	LEU B 157	4.303	53.810	111.729	1.00	36.56
	2903	CG	LEU B 157	5.384	54.475	112.612	1.00	39.52
10	2904	CD1	LEU B 157	4.794	55.669	113.354	1.00	31.99
	2905	CD2	LEU B 157	5.952	53.501	113.601	1.00	34.43
	2906	C	LEU B 157	2.948	51.884	110.826	1.00	45.84
	2907	O	LEU B 157	1.846	52.206	111.240	1.00	51.79
	2908	N	LYS B 158	3.112	51.188	109.701	1.00	48.01
15	2909	CA	LYS B 158	1.971	50.744	108.903	1.00	50.13
	2910	CB	LYS B 158	2.303	50.755	107.405	1.00	52.16
	2911	CG	LYS B 158	1.388	49.873	106.563	1.00	55.75
	2912	CD	LYS B 158	1.464	50.194	105.077	1.00	59.45
	2913	CE	LYS B 158	0.758	51.504	104.768	1.00	63.13
20	2914	NZ	LYS B 158	0.834	51.874	103.317	1.00	69.78
	2915	C	LYS B 158	1.590	49.332	109.336	1.00	50.95
	2916	O	LYS B 158	0.439	49.080	109.709	1.00	47.86
	2917	N	LEU B 159	2.554	48.416	109.270	1.00	49.09
	2918	CA	LEU B 159	2.325	47.035	109.695	1.00	51.98
25	2919	CB	LEU B 159	3.643	46.256	109.695	1.00	45.02
	2920	CG	LEU B 159	4.330	46.065	108.348	1.00	50.09
	2921	CD1	LEU B 159	5.652	45.339	108.555	1.00	45.54
	2922	CD2	LEU B 159	3.427	45.274	107.419	1.00	42.37
	2923	C	LEU B 159	1.738	47.003	111.122	1.00	53.19
30	2924	O	LEU B 159	0.740	46.336	111.381	1.00	52.23
	2925	N	ILE B 160	2.376	47.728	112.037	1.00	49.75
	2926	CA	ILE B 160	1.940	47.781	113.424	1.00	52.00
	2927	CB	ILE B 160	2.811	48.771	114.248	1.00	41.87
	2928	CG2	ILE B 160	2.145	49.086	115.566	1.00	41.35
35	2929	CG1	ILE B 160	4.200	48.169	114.486	1.00	39.81
	2930	CD1	ILE B 160	5.127	49.050	115.308	1.00	36.60
	2931	C	ILE B 160	0.467	48.162	113.570	1.00	57.66
	2932	O	ILE B 160	-0.317	47.413	114.163	1.00	55.02
	2933	N	SER B 161	0.084	49.318	113.032	1.00	62.54
40	2934	CA	SER B 161	-1.303	49.753	113.147	1.00	65.64
	2935	CB	SER B 161	-1.502	51.147	112.540	1.00	63.00
	2936	OG	SER B 161	-1.771	51.058	111.153	1.00	70.47
	2937	C	SER B 161	-2.223	48.744	112.462	1.00	65.11

	2938	O	SER B 161	-3.399	48.639	112.817	1.00	66.82
	2939	N	GLN B 162	-1.691	47.999	111.491	1.00	64.67
	2940	CA	GLN B 162	-2.489	46.985	110.795	1.00	61.52
	2941	CB	GLN B 162	-1.712	46.372	109.626	1.00	62.56
5	2942	CG	GLN B 162	-2.546	45.443	108.735	1.00	62.95
	2943	CD	GLN B 162	-3.816	46.112	108.216	1.00	64.55
	2944	OE1	GLN B 162	-4.919	45.833	108.699	1.00	65.77
	2945	NE2	GLN B 162	-3.664	47.010	107.239	1.00	59.74
	2946	C	GLN B 162	-2.835	45.887	111.785	1.00	60.02
10	2947	O	GLN B 162	-3.993	45.494	111.913	1.00	61.74
	2948	N	ASP B 163	-1.819	45.402	112.489	1.00	57.89
	2949	CA	ASP B 163	-1.997	44.351	113.473	1.00	56.71
	2950	CB	ASP B 163	-0.629	43.866	113.945	1.00	53.15
	2951	CG	ASP B 163	0.171	43.213	112.824	1.00	54.52
15	2952	OD1	ASP B 163	-0.255	43.294	111.649	1.00	54.00
	2953	OD2	ASP B 163	1.232	42.622	113.110	1.00	52.48
	2954	C	ASP B 163	-2.863	44.820	114.651	1.00	60.60
	2955	O	ASP B 163	-3.464	44.008	115.347	1.00	61.00
	2956	N	VAL B 164	-2.936	46.129	114.870	1.00	61.45
20	2957	CA	VAL B 164	-3.770	46.651	115.941	1.00	62.92
	2958	CB	VAL B 164	-3.478	48.145	116.212	1.00	59.61
	2959	CG1	VAL B 164	-4.519	48.725	117.148	1.00	59.53
	2960	CG2	VAL B 164	-2.106	48.290	116.849	1.00	60.81
	2961	C	VAL B 164	-5.234	46.456	115.535	1.00	66.02
25	2962	O	VAL B 164	-6.108	46.293	116.389	1.00	70.23
	2963	N	LEU B 165	-5.500	46.474	114.232	1.00	67.51
	2964	CA	LEU B 165	-6.855	46.249	113.743	1.00	70.12
	2965	CB	LEU B 165	-7.004	46.660	112.276	1.00	69.24
	2966	CG	LEU B 165	-7.248	48.133	111.955	1.00	71.78
30	2967	CD1	LEU B 165	-7.459	48.270	110.456	1.00	71.06
	2968	CD2	LEU B 165	-8.466	48.658	112.712	1.00	70.16
	2969	C	LEU B 165	-7.148	44.761	113.872	1.00	70.78
	2970	O	LEU B 165	-8.174	44.369	114.422	1.00	75.99
	2971	N	ASP B 166	-6.242	43.931	113.368	1.00	69.10
35	2972	CA	ASP B 166	-6.413	42.484	113.444	1.00	68.92
	2973	CB	ASP B 166	-5.349	41.793	112.598	1.00	70.91
	2974	CG	ASP B 166	-5.544	42.026	111.119	1.00	72.26
	2975	OD1	ASP B 166	-5.849	43.173	110.735	1.00	70.05
	2976	OD2	ASP B 166	-5.388	41.064	110.339	1.00	78.88
40	2977	C	ASP B 166	-6.328	41.990	114.885	1.00	67.02
	2978	O	ASP B 166	-6.261	40.787	115.134	1.00	67.41
	2979	N	ALA B 167	-6.322	42.933	115.823	1.00	66.51
	2980	CA	ALA B 167	-6.247	42.642	117.249	1.00	67.55

	2981	CB	ALA B 167	-7.598	42.133	117.749	1.00	68.20
	2982	C	ALA B 167	-5.139	41.659	117.636	1.00	67.29
	2983	O	ALA B 167	-5.202	41.030	118.696	1.00	66.48
	2984	N	LYS B 168	-4.128	41.524	116.780	1.00	68.10
5	2985	CA	LYS B 168	-3.002	40.639	117.067	1.00	67.35
	2986	CB	LYS B 168	-2.243	40.297	115.785	1.00	67.29
	2987	CG	LYS B 168	-3.094	39.699	114.685	1.00	67.40
	2988	CD	LYS B 168	-2.321	39.695	113.375	1.00	68.21
	2989	CE	LYS B 168	-3.230	39.441	112.177	1.00	70.84
10	2990	NZ	LYS B 168	-2.542	39.721	110.873	1.00	71.49
	2991	C	LYS B 168	-2.073	41.388	118.024	1.00	68.08
	2992	O	LYS B 168	-1.116	40.820	118.549	1.00	70.57
	2993	N	ILE B 169	-2.376	42.669	118.235	1.00	66.47
	2994	CA	ILE B 169	-1.621	43.558	119.119	1.00	65.99
15	2995	CB	ILE B 169	-0.449	44.254	118.381	1.00	66.94
	2996	CG2	ILE B 169	0.159	45.346	119.256	1.00	64.65
	2997	CG1	ILE B 169	0.615	43.237	117.997	1.00	66.17
	2998	CD1	ILE B 169	1.669	43.813	117.100	1.00	69.59
	2999	C	ILE B 169	-2.573	44.653	119.575	1.00	67.08
20	3000	O	ILE B 169	-3.541	44.968	118.886	1.00	67.10
	3001	N	ASN B 170	-2.296	45.243	120.731	1.00	69.58
	3002	CA	ASN B 170	-3.136	46.317	121.237	1.00	74.55
	3003	CB	ASN B 170	-3.553	46.041	122.684	1.00	78.76
	3004	CG	ASN B 170	-4.472	44.852	122.800	1.00	84.73
25	3005	OD1	ASN B 170	-5.528	44.810	122.162	1.00	87.68
	3006	ND2	ASN B 170	-4.082	43.872	123.614	1.00	86.89
	3007	C	ASN B 170	-2.397	47.642	121.177	1.00	74.23
	3008	O	ASN B 170	-1.174	47.689	121.283	1.00	73.78
	3009	N	PRO B 171	-3.133	48.743	120.994	1.00	74.60
30	3010	CD	PRO B 171	-4.592	48.871	120.841	1.00	74.97
	3011	CA	PRO B 171	-2.474	50.050	120.936	1.00	73.76
	3012	CB	PRO B 171	-3.623	50.998	120.573	1.00	75.11
	3013	CG	PRO B 171	-4.825	50.327	121.183	1.00	74.56
	3014	C	PRO B 171	-1.814	50.369	122.290	1.00	70.76
35	3015	O	PRO B 171	-1.180	51.416	122.471	1.00	70.02
	3016	N	GLY B 172	-1.971	49.445	123.236	1.00	66.76
	3017	CA	GLY B 172	-1.378	49.615	124.550	1.00	62.42
	3018	C	GLY B 172	-0.010	48.952	124.594	1.00	58.48
	3019	O	GLY B 172	0.795	49.230	125.483	1.00	56.36
40	3020	N	ASP B 173	0.247	48.073	123.626	1.00	55.58
	3021	CA	ASP B 173	1.515	47.358	123.531	1.00	54.78
	3022	CB	ASP B 173	1.297	45.930	123.016	1.00	61.84
	3023	CG	ASP B 173	0.356	45.115	123.894	1.00	69.38

	3024	OD1	ASP	B	173	0.352	45.326	125.130	1.00	71.85
	3025	OD2	ASP	B	173	-0.364	44.246	123.341	1.00	68.64
	3026	C	ASP	B	173	2.509	48.047	122.591	1.00	52.82
	3027	O	ASP	B	173	3.557	47.486	122.289	1.00	51.84
5	3028	N	ILE	B	174	2.175	49.245	122.120	1.00	47.54
	3029	CA	ILE	B	174	3.047	49.981	121.208	1.00	44.07
	3030	CB	ILE	B	174	2.236	50.996	120.368	1.00	46.52
	3031	CG2	ILE	B	174	3.175	51.872	119.556	1.00	38.68
	3032	CG1	ILE	B	174	1.267	50.244	119.450	1.00	45.33
10	3033	CD1	ILE	B	174	0.209	51.124	118.863	1.00	47.06
	3034	C	ILE	B	174	4.143	50.715	121.963	1.00	39.49
	3035	O	ILE	B	174	3.894	51.715	122.633	1.00	41.61
	3036	N	THR	B	175	5.368	50.220	121.832	1.00	38.50
	3037	CA	THR	B	175	6.505	50.809	122.527	1.00	36.69
15	3038	CB	THR	B	175	6.962	49.884	123.643	1.00	38.04
	3039	OG1	THR	B	175	7.449	48.672	123.057	1.00	34.13
	3040	CG2	THR	B	175	5.803	49.538	124.574	1.00	37.66
	3041	C	THR	B	175	7.689	50.974	121.591	1.00	34.23
	3042	O	THR	B	175	7.680	50.461	120.487	1.00	37.50
20	3043	N	GLU	B	176	8.725	51.660	122.051	1.00	35.67
	3044	CA	GLU	B	176	9.912	51.832	121.237	1.00	34.54
	3045	CB	GLU	B	176	10.956	52.644	121.996	1.00	32.39
	3046	CG	GLU	B	176	10.598	54.114	122.116	1.00	30.52
	3047	CD	GLU	B	176	11.571	54.901	122.996	1.00	33.75
25	3048	OE1	GLU	B	176	12.757	54.532	123.067	1.00	31.35
	3049	OE2	GLU	B	176	11.148	55.905	123.604	1.00	38.74
	3050	C	GLU	B	176	10.469	50.470	120.855	1.00	37.33
	3051	O	GLU	B	176	10.973	50.295	119.746	1.00	41.02
	3052	N	GLU	B	177	10.368	49.500	121.761	1.00	36.56
30	3053	CA	GLU	B	177	10.866	48.152	121.488	1.00	39.64
	3054	CB	GLU	B	177	10.801	47.271	122.740	1.00	39.81
	3055	CG	GLU	B	177	11.738	47.701	123.831	1.00	47.42
	3056	CD	GLU	B	177	13.175	47.659	123.378	0.50	47.30
	3057	OE1	GLU	B	177	13.692	46.546	123.141	0.50	49.07
35	3058	OE2	GLU	B	177	13.780	48.742	123.247	0.50	49.99
	3059	C	GLU	B	177	10.041	47.498	120.399	1.00	38.59
	3060	O	GLU	B	177	10.572	46.846	119.507	1.00	40.06
	3061	N	LEU	B	178	8.729	47.654	120.475	1.00	36.42
	3062	CA	LEU	B	178	7.889	47.048	119.460	1.00	34.35
40	3063	CB	LEU	B	178	6.422	47.386	119.699	1.00	35.56
	3064	CG	LEU	B	178	5.498	46.872	118.604	1.00	37.09
	3065	CD1	LEU	B	178	5.235	45.397	118.834	1.00	37.31
	3066	CD2	LEU	B	178	4.202	47.651	118.617	1.00	38.61

	3067	C	LEU B 178	8.329	47.593	118.109	1.00	30.31
	3068	O	LEU B 178	8.631	46.830	117.213	1.00	29.85
	3069	N	ILE B 179	8.380	48.919	117.979	1.00	29.17
	3070	CA	ILE B 179	8.774	49.559	116.722	1.00	27.53
5	3071	CB	ILE B 179	8.841	51.075	116.881	1.00	27.56
	3072	CG2	ILE B 179	9.490	51.693	115.650	1.00	25.40
	3073	CG1	ILE B 179	7.430	51.627	117.102	1.00	27.54
	3074	CD1	ILE B 179	7.381	53.085	117.567	1.00	26.80
	3075	C	ILE B 179	10.125	49.042	116.253	1.00	33.20
10	3076	O	ILE B 179	10.293	48.674	115.089	1.00	32.48
	3077	N	GLY B 180	11.090	48.992	117.165	1.00	34.27
	3078	CA	GLY B 180	12.402	48.494	116.791	1.00	36.90
	3079	C	GLY B 180	12.311	47.116	116.166	1.00	36.65
	3080	O	GLY B 180	13.151	46.739	115.344	1.00	35.80
15	3081	N	ASN B 181	11.279	46.368	116.547	1.00	35.83
	3082	CA	ASN B 181	11.078	45.016	116.036	1.00	38.97
	3083	CB	ASN B 181	10.179	44.204	116.974	1.00	41.40
	3084	CG	ASN B 181	10.931	43.599	118.150	1.00	43.49
	3085	OD1	ASN B 181	12.120	43.293	118.064	1.00	44.03
20	3086	ND2	ASN B 181	10.222	43.394	119.251	1.00	40.15
	3087	C	ASN B 181	10.472	44.970	114.635	1.00	39.06
	3088	O	ASN B 181	10.501	43.930	113.993	1.00	40.68
	3089	N	TYR B 182	9.924	46.085	114.163	1.00	35.54
	3090	CA	TYR B 182	9.322	46.130	112.836	1.00	31.61
25	3091	CB	TYR B 182	7.962	46.829	112.892	1.00	35.38
	3092	CG	TYR B 182	6.836	45.976	113.443	1.00	41.57
	3093	CD1	TYR B 182	6.841	45.543	114.769	1.00	43.98
	3094	CE1	TYR B 182	5.807	44.753	115.277	1.00	48.23
	3095	CD2	TYR B 182	5.765	45.597	112.633	1.00	47.00
30	3096	CE2	TYR B 182	4.728	44.809	113.130	1.00	51.63
	3097	CZ	TYR B 182	4.755	44.389	114.454	1.00	50.05
	3098	OH	TYR B 182	3.733	43.607	114.949	1.00	50.21
	3099	C	TYR B 182	10.201	46.839	111.804	1.00	34.91
	3100	O	TYR B 182	9.884	46.845	110.620	1.00	28.88
35	3101	N	LEU B 183	11.292	47.448	112.265	1.00	34.58
	3102	CA	LEU B 183	12.224	48.154	111.392	1.00	30.34
	3103	CB	LEU B 183	13.210	48.966	112.239	1.00	25.48
	3104	CG	LEU B 183	12.619	50.078	113.110	1.00	21.83
	3105	CD1	LEU B 183	13.704	50.710	113.990	1.00	17.47
40	3106	CD2	LEU B 183	11.980	51.119	112.184	1.00	22.76
	3107	C	LEU B 183	12.980	47.118	110.559	1.00	31.98
	3108	O	LEU B 183	12.973	45.940	110.902	1.00	35.39
	3109	N	PHE B 184	13.623	47.543	109.469	1.00	33.26

	3110	CA	PHE B 184	14.380	46.610	108.615	1.00	30.66
	3111	CB	PHE B 184	14.923	47.320	107.368	1.00	26.87
	3112	CG	PHE B 184	13.869	47.767	106.424	1.00	21.22
	3113	CD1	PHE B 184	14.075	48.879	105.616	1.00	28.77
5	3114	CD2	PHE B 184	12.637	47.120	106.382	1.00	28.11
	3115	CE1	PHE B 184	13.061	49.355	104.776	1.00	27.41
	3116	CE2	PHE B 184	11.616	47.580	105.546	1.00	30.97
	3117	CZ	PHE B 184	11.832	48.705	104.743	1.00	30.61
	3118	C	PHE B 184	15.554	45.959	109.340	1.00	30.78
10	3119	O	PHE B 184	16.050	44.926	108.894	1.00	35.61
	3120	N	THR B 185	15.999	46.556	110.446	1.00	27.49
	3121	CA	THR B 185	17.133	46.019	111.205	1.00	28.61
	3122	CB	THR B 185	17.836	47.137	111.963	1.00	28.32
	3123	OG1	THR B 185	16.862	48.117	112.340	1.00	31.84
15	3124	CG2	THR B 185	18.899	47.784	111.099	1.00	25.98
	3125	C	THR B 185	16.753	44.927	112.207	1.00	27.71
	3126	O	THR B 185	17.601	44.452	112.971	1.00	22.05
	3127	N	GLN B 186	15.481	44.531	112.193	1.00	27.90
	3128	CA	GLN B 186	14.956	43.501	113.106	1.00	32.32
20	3129	CB	GLN B 186	13.452	43.275	112.853	1.00	28.63
	3130	CG	GLN B 186	13.146	42.806	111.420	1.00	34.99
	3131	CD	GLN B 186	11.658	42.639	111.116	1.00	44.13
	3132	OE1	GLN B 186	11.039	41.629	111.466	1.00	47.36
	3133	NE2	GLN B 186	11.080	43.635	110.455	1.00	46.57
25	3134	C	GLN B 186	15.694	42.172	112.934	1.00	37.13
	3135	O	GLN B 186	15.886	41.422	113.893	1.00	34.51
	3136	N	HIS B 187	16.122	41.902	111.707	1.00	40.40
	3137	CA	HIS B 187	16.808	40.663	111.398	1.00	45.25
	3138	CB	HIS B 187	16.830	40.451	109.881	1.00	49.00
30	3139	CG	HIS B 187	15.463	40.470	109.257	1.00	55.14
	3140	CD2	HIS B 187	14.924	41.276	108.310	1.00	56.26
	3141	ND1	HIS B 187	14.461	39.594	109.626	1.00	56.79
	3142	CE1	HIS B 187	13.368	39.861	108.933	1.00	59.10
	3143	NE2	HIS B 187	13.621	40.878	108.128	1.00	56.59
35	3144	C	HIS B 187	18.205	40.545	111.981	1.00	45.55
	3145	O	HIS B 187	18.837	39.503	111.843	1.00	51.60
	3146	N	LEU B 188	18.686	41.599	112.636	1.00	42.37
	3147	CA	LEU B 188	20.005	41.558	113.263	1.00	40.97
	3148	CB	LEU B 188	20.652	42.947	113.293	1.00	35.87
40	3149	CG	LEU B 188	20.991	43.651	111.988	1.00	42.19
	3150	CD1	LEU B 188	21.334	45.130	112.275	1.00	29.86
	3151	CD2	LEU B 188	22.150	42.913	111.307	1.00	37.90
	3152	C	LEU B 188	19.799	41.112	114.703	1.00	43.92

	3153	O	LEU B 188	18.709	41.269	115.253	1.00	43.32
	3154	N	PRO B 189	20.840	40.543	115.340	1.00	48.66
	3155	CD	PRO B 189	22.170	40.110	114.876	1.00	47.98
	3156	CA	PRO B 189	20.610	40.138	116.727	1.00	47.81
5	3157	CB	PRO B 189	21.937	39.482	117.133	1.00	46.43
	3158	CG	PRO B 189	22.933	40.040	116.171	1.00	52.66
	3159	C	PRO B 189	20.262	41.371	117.547	1.00	47.90
	3160	O	PRO B 189	20.776	42.456	117.290	1.00	52.06
	3161	N	LYS B 190	19.378	41.189	118.523	1.00	50.76
10	3162	CA	LYS B 190	18.895	42.255	119.396	1.00	49.06
	3163	CB	LYS B 190	18.207	41.645	120.620	1.00	54.92
	3164	CG	LYS B 190	16.710	41.448	120.478	1.00	58.39
	3165	CD	LYS B 190	15.935	42.613	121.086	1.00	60.62
	3166	CE	LYS B 190	14.435	42.332	121.054	1.00	63.82
15	3167	NZ	LYS B 190	13.618	43.410	121.682	1.00	68.56
	3168	C	LYS B 190	19.863	43.327	119.876	1.00	46.84
	3169	O	LYS B 190	19.652	44.512	119.608	1.00	48.32
	3170	N	ASP B 191	20.910	42.924	120.590	1.00	42.66
	3171	CA	ASP B 191	21.866	43.883	121.146	1.00	40.83
20	3172	CB	ASP B 191	22.771	43.191	122.172	1.00	41.29
	3173	CG	ASP B 191	23.744	42.225	121.525	0.50	41.19
	3174	OD1	ASP B 191	23.289	41.246	120.894	0.50	40.87
	3175	OD2	ASP B 191	24.966	42.450	121.639	0.50	43.53
	3176	C	ASP B 191	22.744	44.562	120.099	1.00	38.36
25	3177	O	ASP B 191	23.549	45.437	120.431	1.00	37.06
	3178	N	LEU B 192	22.584	44.165	118.839	1.00	35.29
	3179	CA	LEU B 192	23.390	44.722	117.754	1.00	32.66
	3180	CB	LEU B 192	24.129	43.573	117.058	1.00	30.13
	3181	CG	LEU B 192	25.102	42.821	117.978	1.00	30.90
30	3182	CD1	LEU B 192	25.682	41.602	117.253	1.00	24.68
	3183	CD2	LEU B 192	26.208	43.778	118.423	1.00	22.06
	3184	C	LEU B 192	22.612	45.555	116.719	1.00	29.76
	3185	O	LEU B 192	23.164	46.001	115.716	1.00	28.64
	3186	N	ARG B 193	21.332	45.774	116.965	1.00	28.07
35	3187	CA	ARG B 193	20.516	46.534	116.036	1.00	24.84
	3188	CB	ARG B 193	19.075	46.454	116.493	1.00	29.60
	3189	CG	ARG B 193	18.483	45.102	116.199	1.00	35.47
	3190	CD	ARG B 193	17.229	44.893	116.958	1.00	34.10
	3191	NE	ARG B 193	16.590	43.658	116.545	1.00	35.72
40	3192	CZ	ARG B 193	15.365	43.321	116.918	1.00	40.63
	3193	NH1	ARG B 193	14.680	44.141	117.707	1.00	39.33
	3194	NH2	ARG B 193	14.828	42.179	116.499	1.00	38.62
	3195	C	ARG B 193	20.888	47.993	115.753	1.00	24.63

	3196	O	ARG B 193	20.708	48.458	114.633	1.00	29.02
	3197	N	ASP B 194	21.408	48.704	116.748	1.00	21.86
	3198	CA	ASP B 194	21.752	50.106	116.588	1.00	27.79
	3199	CB	ASP B 194	21.181	50.925	117.758	1.00	23.37
5	3200	CG	ASP B 194	19.681	50.698	117.959	1.00	31.92
	3201	OD1	ASP B 194	18.990	50.221	117.017	1.00	24.02
	3202	OD2	ASP B 194	19.190	51.008	119.065	1.00	29.28
	3203	C	ASP B 194	23.257	50.356	116.482	1.00	29.66
	3204	O	ASP B 194	24.039	49.857	117.283	1.00	27.44
10	3205	N	PRO B 195	23.671	51.160	115.492	1.00	27.35
	3206	CD	PRO B 195	22.843	51.936	114.548	1.00	24.09
	3207	CA	PRO B 195	25.095	51.455	115.318	1.00	25.11
	3208	CB	PRO B 195	25.130	52.351	114.074	1.00	16.73
	3209	CG	PRO B 195	23.785	52.120	113.395	1.00	30.34
15	3210	C	PRO B 195	25.663	52.186	116.527	1.00	22.97
	3211	O	PRO B 195	25.022	53.088	117.061	1.00	29.24
	3212	N	ASP B 196	26.862	51.807	116.953	1.00	20.37
	3213	CA	ASP B 196	27.520	52.489	118.065	1.00	21.30
	3214	CB	ASP B 196	28.571	51.578	118.733	1.00	25.77
20	3215	CG	ASP B 196	27.991	50.260	119.220	1.00	34.08
	3216	OD1	ASP B 196	27.919	49.290	118.432	1.00	31.05
	3217	OD2	ASP B 196	27.584	50.197	120.401	1.00	47.31
	3218	C	ASP B 196	28.251	53.682	117.442	1.00	24.25
	3219	O	ASP B 196	28.483	54.698	118.092	1.00	23.89
25	3220	N	LEU B 197	28.587	53.548	116.163	1.00	20.45
	3221	CA	LEU B 197	29.347	54.566	115.439	1.00	21.09
	3222	CB	LEU B 197	30.829	54.168	115.411	1.00	17.17
	3223	CG	LEU B 197	31.819	54.972	114.567	1.00	21.67
	3224	CD1	LEU B 197	31.807	56.443	115.001	1.00	17.51
30	3225	CD2	LEU B 197	33.220	54.377	114.745	1.00	20.31
	3226	C	LEU B 197	28.849	54.693	114.012	1.00	18.28
	3227	O	LEU B 197	28.488	53.703	113.394	1.00	27.66
	3228	N	ILE B 198	28.810	55.910	113.484	1.00	24.22
	3229	CA	ILE B 198	28.361	56.116	112.111	1.00	20.76
35	3230	CB	ILE B 198	26.979	56.832	112.035	1.00	24.65
	3231	CG2	ILE B 198	26.658	57.205	110.588	1.00	22.35
	3232	CG1	ILE B 198	25.868	55.911	112.573	1.00	24.33
	3233	CD1	ILE B 198	24.441	56.449	112.331	1.00	13.91
	3234	C	ILE B 198	29.436	56.982	111.508	1.00	22.92
40	3235	O	ILE B 198	29.793	58.028	112.067	1.00	21.02
	3236	N	ILE B 199	29.956	56.531	110.378	1.00	20.86
	3237	CA	ILE B 199	31.046	57.204	109.686	1.00	22.47
	3238	CB	ILE B 199	32.156	56.173	109.264	1.00	21.65



	3239	CG2	ILE	B	199	33.166	56.813	108.327	1.00	15.46
	3240	CG1	ILE	B	199	32.861	55.608	110.487	1.00	21.06
	3241	CD1	ILE	B	199	33.677	54.367	110.172	1.00	19.48
	3242	C	ILE	B	199	30.528	57.823	108.413	1.00	23.27
5	3243	O	ILE	B	199	29.819	57.161	107.667	1.00	22.12
	3244	N	ARG	B	200	30.860	59.083	108.150	1.00	24.06
	3245	CA	ARG	B	200	30.443	59.663	106.882	1.00	26.36
	3246	CB	ARG	B	200	29.435	60.794	107.040	1.00	28.57
	3247	CG	ARG	B	200	29.047	61.329	105.659	1.00	30.62
10	3248	CD	ARG	B	200	27.662	61.951	105.586	1.00	23.00
	3249	NE	ARG	B	200	27.261	62.017	104.181	1.00	33.99
	3250	CZ	ARG	B	200	26.017	62.212	103.754	1.00	37.38
	3251	NH1	ARG	B	200	25.026	62.368	104.624	1.00	38.80
	3252	NH2	ARG	B	200	25.758	62.251	102.452	1.00	33.16
15	3253	C	ARG	B	200	31.668	60.171	106.151	1.00	24.35
	3254	O	ARG	B	200	32.437	60.961	106.681	1.00	27.88
	3255	N	THR	B	201	31.856	59.700	104.931	1.00	25.54
	3256	CA	THR	B	201	33.009	60.095	104.149	1.00	24.26
	3257	CB	THR	B	201	33.505	58.905	103.311	1.00	21.31
20	3258	OG1	THR	B	201	32.465	58.454	102.438	1.00	24.56
	3259	CG2	THR	B	201	33.894	57.760	104.220	1.00	22.43
	3260	C	THR	B	201	32.769	61.320	103.254	1.00	32.99
	3261	O	THR	B	201	31.643	61.822	103.148	1.00	30.53
	3262	N	SER	B	202	33.860	61.794	102.644	1.00	34.88
25	3263	CA	SER	B	202	33.924	62.952	101.739	1.00	35.82
	3264	CB	SER	B	202	33.263	62.642	100.377	1.00	37.06
	3265	OG	SER	B	202	31.855	62.705	100.414	1.00	51.67
	3266	C	SER	B	202	33.439	64.307	102.269	1.00	32.43
	3267	O	SER	B	202	32.800	65.086	101.555	1.00	33.07
30	3268	N	GLY	B	203	33.766	64.584	103.526	1.00	34.34
	3269	CA	GLY	B	203	33.429	65.864	104.135	1.00	32.89
	3270	C	GLY	B	203	32.000	66.333	104.330	1.00	36.48
	3271	O	GLY	B	203	31.799	67.417	104.875	1.00	40.59
	3272	N	GLU	B	204	31.002	65.567	103.901	1.00	37.73
35	3273	CA	GLU	B	204	29.632	66.007	104.103	1.00	38.94
	3274	CB	GLU	B	204	28.646	65.157	103.278	1.00	46.86
	3275	CG	GLU	B	204	28.489	65.547	101.793	1.00	53.08
	3276	CD	GLU	B	204	28.643	67.048	101.529	1.00	61.66
	3277	OE1	GLU	B	204	27.909	67.872	102.128	1.00	62.64
40	3278	OE2	GLU	B	204	29.515	67.405	100.707	1.00	67.43
	3279	C	GLU	B	204	29.273	65.912	105.589	1.00	37.37
	3280	O	GLU	B	204	29.477	64.871	106.216	1.00	37.77
	3281	N	LEU	B	205	28.770	67.008	106.151	1.00	34.25

	3282	CA	LEU B 205	28.340	67.040	107.544	1.00	32.73
	3283	CB	LEU B 205	28.889	68.261	108.253	1.00	33.53
	3284	CG	LEU B 205	30.373	68.222	108.583	1.00	43.32
	3285	CD1	LEU B 205	30.774	69.503	109.298	1.00	45.04
5	3286	CD2	LEU B 205	30.654	67.039	109.460	1.00	47.01
	3287	C	LEU B 205	26.824	67.099	107.565	1.00	31.77
	3288	O	LEU B 205	26.240	68.171	107.698	1.00	30.71
	3289	N	ARG B 206	26.199	65.936	107.418	1.00	31.65
	3290	CA	ARG B 206	24.742	65.808	107.390	1.00	33.96
10	3291	CB	ARG B 206	24.218	66.447	106.106	1.00	27.85
	3292	CG	ARG B 206	24.737	65.766	104.852	1.00	35.96
	3293	CD	ARG B 206	24.019	66.259	103.616	1.00	38.42
	3294	NE	ARG B 206	24.470	67.594	103.281	1.00	52.98
	3295	CZ	ARG B 206	25.133	67.896	102.172	1.00	60.01
15	3296	NH1	ARG B 206	25.407	66.940	101.286	1.00	61.55
	3297	NH2	ARG B 206	25.548	69.144	101.965	1.00	61.47
	3298	C	ARG B 206	24.466	64.301	107.395	1.00	34.19
	3299	O	ARG B 206	25.350	63.539	107.012	1.00	33.63
	3300	N	LEU B 207	23.264	63.855	107.781	1.00	40.68
20	3301	CA	LEU B 207	22.983	62.393	107.832	1.00	40.85
	3302	CB	LEU B 207	22.361	62.014	109.176	1.00	50.50
	3303	CG	LEU B 207	23.194	62.241	110.438	1.00	54.44
	3304	CD1	LEU B 207	22.466	61.559	111.594	1.00	56.40
	3305	CD2	LEU B 207	24.617	61.664	110.275	1.00	56.45
25	3306	C	LEU B 207	22.174	61.675	106.729	1.00	41.87
	3307	O	LEU B 207	22.037	60.437	106.756	1.00	44.65
	3308	N	SER B 208	21.611	62.429	105.797	1.00	23.39
	3309	CA	SER B 208	20.886	61.851	104.674	1.00	23.62
	3310	CB	SER B 208	21.896	61.427	103.607	1.00	21.18
30	3311	OG	SER B 208	22.794	62.484	103.303	1.00	28.10
	3312	C	SER B 208	19.873	60.709	104.861	1.00	24.44
	3313	O	SER B 208	19.833	59.782	104.058	1.00	24.08
	3314	N	ASN B 209	19.060	60.770	105.906	1.00	23.07
	3315	CA	ASN B 209	18.014	59.770	106.115	1.00	20.17
35	3316	CB	ASN B 209	17.030	59.836	104.939	1.00	16.89
	3317	CG	ASN B 209	15.624	59.317	105.291	1.00	23.56
	3318	OD1	ASN B 209	15.266	59.152	106.460	1.00	20.45
	3319	ND2	ASN B 209	14.825	59.072	104.267	1.00	21.28
	3320	C	ASN B 209	18.523	58.339	106.308	1.00	22.19
40	3321	O	ASN B 209	17.815	57.372	106.003	1.00	19.12
	3322	N	PHE B 210	19.737	58.220	106.842	1.00	19.08
	3323	CA	PHE B 210	20.353	56.933	107.125	1.00	20.10
	3324	CB	PHE B 210	21.858	56.988	106.788	1.00	18.99

	3325	CG	PHE B 210	22.572	55.664	106.963	1.00	13.42
	3326	CD1	PHE B 210	22.236	54.575	106.189	1.00	15.68
	3327	CD2	PHE B 210	23.572	55.518	107.911	1.00	22.54
	3328	CE1	PHE B 210	22.886	53.331	106.345	1.00	16.33
5	3329	CE2	PHE B 210	24.235	54.286	108.084	1.00	20.30
	3330	CZ	PHE B 210	23.886	53.191	107.294	1.00	19.91
	3331	C	PHE B 210	20.167	56.515	108.609	1.00	21.99
	3332	O	PHE B 210	20.714	57.145	109.506	1.00	23.15
	3333	N	LEU B 211	19.407	55.449	108.853	1.00	17.41
10	3334	CA	LEU B 211	19.189	54.946	110.209	1.00	19.38
	3335	CB	LEU B 211	20.450	54.200	110.699	1.00	18.64
	3336	CG	LEU B 211	20.992	53.014	109.863	1.00	20.61
	3337	CD1	LEU B 211	22.236	52.388	110.539	1.00	14.24
	3338	CD2	LEU B 211	19.900	51.971	109.694	1.00	14.41
15	3339	C	LEU B 211	18.821	56.039	111.225	1.00	21.64
	3340	O	LEU B 211	19.417	56.121	112.294	1.00	24.17
	3341	N	PRO B 212	17.820	56.879	110.914	1.00	20.70
	3342	CD	PRO B 212	16.930	56.897	109.738	1.00	15.73
	3343	CA	PRO B 212	17.460	57.930	111.870	1.00	17.28
20	3344	CB	PRO B 212	16.356	58.715	111.131	1.00	18.15
	3345	CG	PRO B 212	15.737	57.701	110.241	1.00	18.34
	3346	C	PRO B 212	17.016	57.408	113.238	1.00	18.10
	3347	O	PRO B 212	17.323	58.015	114.272	1.00	17.48
	3348	N	TRP B 213	16.303	56.287	113.253	1.00	16.85
25	3349	CA	TRP B 213	15.845	55.716	114.516	1.00	15.52
	3350	CB	TRP B 213	14.672	54.763	114.280	1.00	18.31
	3351	CG	TRP B 213	14.197	53.998	115.507	1.00	19.78
	3352	CD2	TRP B 213	12.992	54.231	116.238	1.00	20.93
	3353	CE2	TRP B 213	12.949	53.284	117.299	1.00	23.61
30	3354	CE3	TRP B 213	11.940	55.144	116.103	1.00	20.45
	3355	CD1	TRP B 213	14.827	52.948	116.139	1.00	23.10
	3356	NE1	TRP B 213	14.080	52.514	117.217	1.00	20.80
	3357	CZ2	TRP B 213	11.900	53.233	118.205	1.00	20.64
	3358	CZ3	TRP B 213	10.891	55.089	117.014	1.00	25.73
35	3359	CH2	TRP B 213	10.878	54.140	118.049	1.00	21.59
	3360	C	TRP B 213	16.959	54.949	115.223	1.00	23.59
	3361	O	TRP B 213	17.204	55.184	116.411	1.00	24.89
	3362	N	GLN B 214	17.634	54.048	114.501	1.00	19.76
	3363	CA	GLN B 214	18.684	53.226	115.098	1.00	18.40
40	3364	CB	GLN B 214	19.108	52.108	114.136	1.00	20.97
	3365	CG	GLN B 214	17.961	51.178	113.643	1.00	17.98
	3366	CD	GLN B 214	17.292	51.673	112.355	1.00	19.05
	3367	OE1	GLN B 214	16.684	50.896	111.627	1.00	24.16

	3368	NE2	GLN	B	214	17.402	52.969	112.080	1.00	14.23
	3369	C	GLN	B	214	19.911	54.012	115.533	1.00	21.15
	3370	O	GLN	B	214	20.533	53.700	116.551	1.00	24.15
	3371	N	GLY	B	215	20.248	55.054	114.785	1.00	19.95
5	3372	CA	GLY	B	215	21.420	55.835	115.136	1.00	18.07
	3373	C	GLY	B	215	21.175	57.057	116.000	1.00	17.57
	3374	O	GLY	B	215	22.084	57.861	116.159	1.00	21.04
	3375	N	ALA	B	216	19.979	57.170	116.583	1.00	16.72
	3376	CA	ALA	B	216	19.603	58.303	117.429	1.00	18.74
10	3377	CB	ALA	B	216	18.262	58.024	118.109	1.00	15.47
	3378	C	ALA	B	216	20.628	58.703	118.484	1.00	24.10
	3379	O	ALA	B	216	20.732	59.890	118.829	1.00	24.63
	3380	N	TYR	B	217	21.372	57.727	119.003	1.00	19.17
	3381	CA	TYR	B	217	22.370	58.006	120.018	1.00	17.96
15	3382	CB	TYR	B	217	22.128	57.163	121.266	1.00	17.49
	3383	CG	TYR	B	217	20.811	57.389	121.969	1.00	22.00
	3384	CD1	TYR	B	217	19.732	56.564	121.720	1.00	21.84
	3385	CE1	TYR	B	217	18.541	56.714	122.392	1.00	22.15
	3386	CD2	TYR	B	217	20.659	58.404	122.921	1.00	25.70
20	3387	CE2	TYR	B	217	19.451	58.572	123.600	1.00	25.04
	3388	CZ	TYR	B	217	18.402	57.712	123.327	1.00	24.61
	3389	OH	TYR	B	217	17.202	57.812	123.988	1.00	32.77
	3390	C	TYR	B	217	23.779	57.704	119.561	1.00	19.52
	3391	O	TYR	B	217	24.706	57.774	120.343	1.00	20.65
25	3392	N	SER	B	218	23.951	57.348	118.305	1.00	24.16
	3393	CA	SER	B	218	25.277	56.991	117.824	1.00	21.90
	3394	CB	SER	B	218	25.169	56.464	116.388	1.00	20.83
	3395	OG	SER	B	218	24.270	55.388	116.334	1.00	25.16
	3396	C	SER	B	218	26.343	58.069	117.848	1.00	24.66
30	3397	O	SER	B	218	26.058	59.267	117.700	1.00	25.10
	3398	N	GLU	B	219	27.584	57.635	118.030	1.00	23.26
	3399	CA	GLU	B	219	28.715	58.555	117.959	1.00	23.06
	3400	CB	GLU	B	219	29.978	57.893	118.487	1.00	26.88
	3401	CG	GLU	B	219	30.027	57.777	119.998	1.00	29.20
35	3402	CD	GLU	B	219	29.938	59.133	120.657	1.00	35.05
	3403	OE1	GLU	B	219	30.523	60.092	120.099	1.00	31.68
	3404	OE2	GLU	B	219	29.285	59.232	121.723	1.00	39.48
	3405	C	GLU	B	219	28.872	58.803	116.457	1.00	22.44
	3406	O	GLU	B	219	28.765	57.871	115.671	1.00	26.36
40	3407	N	LEU	B	220	29.094	60.046	116.051	1.00	19.42
	3408	CA	LEU	B	220	29.247	60.352	114.642	1.00	22.83
	3409	CB	LEU	B	220	28.359	61.531	114.239	1.00	24.28
	3410	CG	LEU	B	220	26.864	61.417	114.562	1.00	28.95

	3411	CD1	LEU	B	220	26.181	62.762	114.313	1.00	26.28
	3412	CD2	LEU	B	220	26.231	60.310	113.725	1.00	21.77
	3413	C	LEU	B	220	30.695	60.682	114.331	1.00	28.66
	3414	O	LEU	B	220	31.373	61.364	115.106	1.00	29.42
5	3415	N	TYR	B	221	31.174	60.176	113.198	1.00	26.57
	3416	CA	TYR	B	221	32.531	60.445	112.785	1.00	25.77
	3417	CB	TYR	B	221	33.387	59.203	113.002	1.00	30.64
	3418	CG	TYR	B	221	34.798	59.352	112.501	1.00	28.47
	3419	CD1	TYR	B	221	35.776	60.016	113.247	1.00	27.97
10	3420	CE1	TYR	B	221	37.076	60.156	112.749	1.00	31.91
	3421	CD2	TYR	B	221	35.147	58.842	111.261	1.00	29.92
	3422	CE2	TYR	B	221	36.429	58.973	110.757	1.00	34.80
	3423	CZ	TYR	B	221	37.386	59.625	111.495	1.00	33.93
	3424	OH	TYR	B	221	38.631	59.717	110.932	1.00	36.72
15	3425	C	TYR	B	221	32.562	60.900	111.325	1.00	26.39
	3426	O	TYR	B	221	32.041	60.229	110.433	1.00	26.12
	3427	N	PHE	B	222	33.169	62.060	111.096	1.00	28.99
	3428	CA	PHE	B	222	33.259	62.636	109.761	1.00	30.66
	3429	CB	PHE	B	222	32.581	64.006	109.739	1.00	27.90
20	3430	CG	PHE	B	222	31.150	63.990	110.223	1.00	30.94
	3431	CD1	PHE	B	222	30.854	64.199	111.562	1.00	26.72
	3432	CD2	PHE	B	222	30.100	63.799	109.329	1.00	25.45
	3433	CE1	PHE	B	222	29.528	64.221	112.008	1.00	29.30
	3434	CE2	PHE	B	222	28.770	63.818	109.765	1.00	28.44
25	3435	CZ	PHE	B	222	28.485	64.031	111.109	1.00	26.71
	3436	C	PHE	B	222	34.693	62.778	109.237	1.00	33.34
	3437	O	PHE	B	222	35.596	63.275	109.936	1.00	33.20
	3438	N	THR	B	223	34.903	62.330	108.004	1.00	30.45
	3439	CA	THR	B	223	36.211	62.438	107.396	1.00	29.68
30	3440	CB	THR	B	223	36.969	61.086	107.372	1.00	30.28
	3441	OG1	THR	B	223	38.226	61.268	106.700	1.00	31.52
	3442	CG2	THR	B	223	36.166	60.000	106.636	1.00	27.87
	3443	C	THR	B	223	36.103	63.001	105.986	1.00	32.33
	3444	O	THR	B	223	35.110	62.789	105.281	1.00	33.29
35	3445	N	ASP	B	224	37.131	63.742	105.593	1.00	35.64
	3446	CA	ASP	B	224	37.181	64.352	104.274	1.00	37.82
	3447	CB	ASP	B	224	38.186	65.514	104.269	1.00	42.98
	3448	CG	ASP	B	224	37.678	66.737	105.041	1.00	49.87
	3449	OD1	ASP	B	224	38.506	67.578	105.466	1.00	53.04
40	3450	OD2	ASP	B	224	36.446	66.864	105.213	1.00	47.11
	3451	C	ASP	B	224	37.574	63.333	103.226	1.00	37.09
	3452	O	ASP	B	224	37.227	63.496	102.064	1.00	41.40
	3453	N	THR	B	225	38.266	62.270	103.635	1.00	32.76

	3454	CA	THR B 225	38.721	61.262	102.684	1.00	33.53
	3455	CB	THR B 225	39.566	60.161	103.397	1.00	35.17
	3456	OG1	THR B 225	38.726	59.128	103.900	1.00	42.49
	3457	CG2	THR B 225	40.339	60.770	104.571	1.00	34.60
5	3458	C	THR B 225	37.544	60.668	101.916	1.00	32.31
	3459	O	THR B 225	36.458	60.515	102.462	1.00	34.88
	3460	N	LEU B 226	37.756	60.382	100.637	1.00	29.05
	3461	CA	LEU B 226	36.714	59.843	99.773	1.00	27.20
	3462	CB	LEU B 226	37.040	60.168	98.295	1.00	28.79
10	3463	CG	LEU B 226	37.418	61.639	97.949	1.00	37.28
	3464	CD1	LEU B 226	37.716	61.789	96.447	1.00	33.45
	3465	CD2	LEU B 226	36.299	62.594	98.326	1.00	27.20
	3466	C	LEU B 226	36.622	58.332	100.006	1.00	25.56
	3467	O	LEU B 226	37.622	57.691	100.287	1.00	28.35
15	3468	N	TRP B 227	35.424	57.771	99.875	1.00	22.24
	3469	CA	TRP B 227	35.201	56.344	100.124	1.00	24.88
	3470	CB	TRP B 227	33.769	55.909	99.750	1.00	18.45
	3471	CG	TRP B 227	33.547	54.405	100.010	1.00	17.38
	3472	CD2	TRP B 227	33.648	53.731	101.274	1.00	13.07
20	3473	CE2	TRP B 227	33.484	52.348	101.033	1.00	21.01
	3474	CE3	TRP B 227	33.866	54.166	102.586	1.00	17.99
	3475	CD1	TRP B 227	33.323	53.432	99.080	1.00	18.00
	3476	NE1	TRP B 227	33.289	52.185	99.688	1.00	23.23
	3477	CZ2	TRP B 227	33.533	51.400	102.052	1.00	20.26
25	3478	CZ3	TRP B 227	33.915	53.223	103.604	1.00	13.54
	3479	CH2	TRP B 227	33.749	51.857	103.329	1.00	20.07
	3480	C	TRP B 227	36.200	55.392	99.461	1.00	22.11
	3481	O	TRP B 227	36.690	54.491	100.120	1.00	20.54
	3482	N	PRO B 228	36.498	55.567	98.152	1.00	23.83
30	3483	CD	PRO B 228	35.906	56.471	97.148	1.00	23.00
	3484	CA	PRO B 228	37.461	54.657	97.522	1.00	24.37
	3485	CB	PRO B 228	37.564	55.189	96.106	1.00	26.63
	3486	CG	PRO B 228	36.181	55.716	95.858	1.00	22.18
	3487	C	PRO B 228	38.814	54.646	98.248	1.00	30.07
35	3488	O	PRO B 228	39.518	53.638	98.206	1.00	28.97
	3489	N	ASP B 229	39.162	55.752	98.918	1.00	27.59
	3490	CA	ASP B 229	40.417	55.835	99.680	1.00	27.10
	3491	CB	ASP B 229	40.993	57.253	99.621	1.00	22.79
	3492	CG	ASP B 229	41.361	57.656	98.216	1.00	28.55
40	3493	OD1	ASP B 229	41.893	56.790	97.495	1.00	28.11
	3494	OD2	ASP B 229	41.122	58.820	97.824	1.00	32.16
	3495	C	ASP B 229	40.270	55.416	101.151	1.00	30.44
	3496	O	ASP B 229	41.243	55.416	101.911	1.00	32.48

	3497	N	PHE B 230	39.057	55.072	101.565	1.00	28.78
	3498	CA	PHE B 230	38.858	54.657	102.941	1.00	32.14
	3499	CB	PHE B 230	37.368	54.717	103.321	1.00	29.15
	3500	CG	PHE B 230	37.132	54.863	104.796	1.00	25.20
5	3501	CD1	PHE B 230	37.106	56.121	105.387	1.00	20.53
	3502	CD2	PHE B 230	37.019	53.733	105.612	1.00	27.26
	3503	CE1	PHE B 230	36.977	56.266	106.788	1.00	23.77
	3504	CE2	PHE B 230	36.889	53.859	107.004	1.00	25.29
	3505	CZ	PHE B 230	36.872	55.133	107.595	1.00	21.17
10	3506	C	PHE B 230	39.372	53.211	102.991	1.00	35.95
	3507	O	PHE B 230	38.812	52.313	102.347	1.00	34.94
	3508	N	ASP B 231	40.457	52.998	103.729	1.00	35.76
	3509	CA	ASP B 231	41.058	51.675	103.839	1.00	36.15
	3510	CB	ASP B 231	42.464	51.677	103.222	1.00	38.44
15	3511	CG	ASP B 231	43.348	52.817	103.757	1.00	40.16
	3512	OD1	ASP B 231	43.095	53.339	104.872	1.00	36.00
	3513	OD2	ASP B 231	44.311	53.177	103.053	1.00	39.05
	3514	C	ASP B 231	41.133	51.226	105.296	1.00	37.65
	3515	O	ASP B 231	40.482	51.807	106.162	1.00	38.69
20	3516	N	GLU B 232	41.923	50.193	105.574	1.00	36.68
	3517	CA	GLU B 232	42.023	49.721	106.947	1.00	40.29
	3518	CB	GLU B 232	42.905	48.477	107.057	1.00	39.41
	3519	CG	GLU B 232	42.906	47.950	108.481	1.00	45.48
	3520	CD	GLU B 232	43.689	46.676	108.650	1.00	48.29
25	3521	OE1	GLU B 232	43.688	45.848	107.714	1.00	47.88
	3522	OE2	GLU B 232	44.289	46.497	109.733	1.00	57.88
	3523	C	GLU B 232	42.557	50.784	107.905	1.00	37.12
	3524	O	GLU B 232	42.112	50.873	109.045	1.00	34.10
	3525	N	ALA B 233	43.514	51.581	107.442	1.00	32.75
30	3526	CA	ALA B 233	44.087	52.621	108.279	1.00	33.35
	3527	CB	ALA B 233	45.269	53.312	107.541	1.00	33.16
	3528	C	ALA B 233	42.989	53.622	108.611	1.00	31.39
	3529	O	ALA B 233	42.838	54.041	109.756	1.00	34.43
	3530	N	ALA B 234	42.215	54.000	107.597	1.00	34.34
35	3531	CA	ALA B 234	41.106	54.942	107.780	1.00	35.18
	3532	CB	ALA B 234	40.392	55.185	106.447	1.00	32.87
	3533	C	ALA B 234	40.106	54.405	108.805	1.00	33.76
	3534	O	ALA B 234	39.577	55.147	109.630	1.00	34.19
	3535	N	LEU B 235	39.845	53.108	108.730	1.00	32.88
40	3536	CA	LEU B 235	38.921	52.469	109.645	1.00	32.86
	3537	CB	LEU B 235	38.592	51.051	109.156	1.00	30.34
	3538	CG	LEU B 235	37.909	50.106	110.155	0.50	29.55
	7715	CG	BLEU B 235	37.491	50.268	109.878	0.50	33.85

	3539	CD1ALEU B 235	36.634	50.750	110.689	0.50	23.08
	7716	CD1BLEU B 235	38.059	49.635	111.117	0.50	34.91
	3540	CD2ALEU B 235	37.605	48.760	109.481	0.50	24.26
	7717	CD2BLEU B 235	36.319	51.180	110.214	0.50	26.51
5	3541	C LEU B 235	39.485	52.428	111.059	1.00	33.84
	3542	O LEU B 235	38.730	52.614	112.013	1.00	35.68
	3543	N GLN B 236	40.799	52.204	111.191	1.00	34.72
	3544	CA GLN B 236	41.458	52.142	112.509	1.00	37.61
	3545	CB GLN B 236	42.897	51.614	112.409	1.00	40.01
10	3546	CG GLN B 236	43.002	50.164	111.963	1.00	46.44
	3547	CD GLN B 236	44.438	49.668	111.833	0.50	48.60
	3548	OE1 GLN B 236	45.282	50.313	111.206	0.50	50.28
	3549	NE2 GLN B 236	44.713	48.504	112.413	0.50	50.23
	3550	C GLN B 236	41.485	53.518	113.131	1.00	34.38
15	3551	O GLN B 236	41.377	53.660	114.337	1.00	37.00
	3552	N GLU B 237	41.626	54.526	112.287	1.00	34.02
	3553	CA GLU B 237	41.655	55.916	112.723	1.00	36.74
	3554	CB GLU B 237	42.054	56.778	111.512	1.00	40.61
	3555	CG GLU B 237	42.505	58.201	111.811	1.00	50.00
20	3556	CD GLU B 237	43.837	58.551	111.124	0.50	49.21
	3557	OE1 GLU B 237	43.923	58.449	109.877	0.50	45.09
	3558	OE2 GLU B 237	44.797	58.927	111.837	0.50	45.97
	3559	C GLU B 237	40.261	56.314	113.274	1.00	39.51
	3560	O GLU B 237	40.148	57.025	114.286	1.00	34.30
25	3561	N ALA B 238	39.197	55.847	112.611	1.00	36.92
	3562	CA ALA B 238	37.838	56.153	113.066	1.00	36.36
	3563	CB ALA B 238	36.815	55.773	111.993	1.00	31.11
	3564	C ALA B 238	37.531	55.399	114.368	1.00	34.47
	3565	O ALA B 238	36.923	55.950	115.290	1.00	32.45
30	3566	N ILE B 239	37.937	54.134	114.432	1.00	31.64
	3567	CA ILE B 239	37.704	53.333	115.629	1.00	34.91
	3568	CB ILE B 239	38.139	51.859	115.412	1.00	32.78
	3569	CG2 ILE B 239	38.145	51.099	116.734	1.00	30.29
	3570	CG1 ILE B 239	37.191	51.191	114.424	1.00	28.70
35	3571	CD1 ILE B 239	37.478	49.758	114.206	1.00	28.85
	3572	C ILE B 239	38.484	53.938	116.797	1.00	38.35
	3573	O ILE B 239	38.119	53.765	117.953	1.00	38.23
	3574	N LEU B 240	39.538	54.680	116.474	1.00	41.75
	3575	CA LEU B 240	40.381	55.308	117.478	1.00	44.59
40	3576	CB LEU B 240	41.745	55.626	116.879	1.00	53.14
	3577	CG LEU B 240	42.915	55.772	117.848	1.00	59.52
	3578	CD1 LEU B 240	42.931	54.590	118.814	1.00	60.12
	3579	CD2 LEU B 240	44.219	55.849	117.046	1.00	60.96



	3580	C	LEU B 240	39.718	56.577	117.974	1.00	43.68
	3581	O	LEU B 240	39.840	56.938	119.138	1.00	42.27
	3582	N	ALA B 241	39.025	57.264	117.077	1.00	43.61
	3583	CA	ALA B 241	38.309	58.474	117.454	1.00	42.13
5	3584	CB	ALA B 241	37.793	59.177	116.218	1.00	39.52
	3585	C	ALA B 241	37.140	58.054	118.356	1.00	45.61
	3586	O	ALA B 241	36.839	58.714	119.347	1.00	46.87
	3587	N	TYR B 242	36.489	56.946	118.013	1.00	41.35
	3588	CA	TYR B 242	35.375	56.452	118.804	1.00	40.90
10	3589	CB	TYR B 242	34.882	55.132	118.232	1.00	33.63
	3590	CG	TYR B 242	33.810	54.455	119.050	1.00	34.18
	3591	CD1	TYR B 242	32.503	54.925	119.046	1.00	33.89
	3592	CE1	TYR B 242	31.496	54.263	119.744	1.00	34.52
	3593	CD2	TYR B 242	34.091	53.306	119.785	1.00	32.47
15	3594	CE2	TYR B 242	33.091	52.633	120.491	1.00	34.77
	3595	CZ	TYR B 242	31.796	53.114	120.464	1.00	34.76
	3596	OH	TYR B 242	30.803	52.441	121.137	1.00	37.17
	3597	C	TYR B 242	35.787	56.244	120.249	1.00	44.94
	3598	O	TYR B 242	35.017	56.518	121.165	1.00	43.16
20	3599	N	ASN B 243	37.002	55.750	120.459	1.00	52.36
	3600	CA	ASN B 243	37.476	55.503	121.823	1.00	59.53
	3601	CB	ASN B 243	38.645	54.516	121.820	1.00	60.33
	3602	CG	ASN B 243	38.177	53.081	121.814	1.00	64.06
	3603	OD1	ASN B 243	37.824	52.528	120.774	1.00	63.68
25	3604	ND2	ASN B 243	38.147	52.473	122.995	1.00	71.78
	3605	C	ASN B 243	37.842	56.737	122.642	1.00	57.77
	3606	O	ASN B 243	37.750	56.709	123.861	1.00	55.33
	3607	N	ARG B 244	38.255	57.811	121.982	1.00	61.44
	3608	CA	ARG B 244	38.596	59.037	122.692	1.00	65.29
30	3609	CB	ARG B 244	39.355	60.007	121.786	1.00	67.27
	3610	CG	ARG B 244	40.861	59.826	121.751	1.00	69.08
	3611	CD	ARG B 244	41.277	58.542	121.067	1.00	78.11
	3612	NE	ARG B 244	42.631	58.644	120.520	1.00	87.12
	3613	CZ	ARG B 244	42.959	59.386	119.461	1.00	90.41
35	3614	NH1	ARG B 244	42.027	60.090	118.827	1.00	90.95
	3615	NH2	ARG B 244	44.219	59.432	119.040	1.00	90.42
	3616	C	ARG B 244	37.316	59.706	123.180	1.00	65.73
	3617	O	ARG B 244	37.351	60.637	123.987	1.00	69.31
	3618	N	ARG B 245	36.179	59.236	122.685	1.00	67.17
40	3619	CA	ARG B 245	34.905	59.806	123.100	1.00	70.63
	3620	CB	ARG B 245	33.773	59.289	122.204	1.00	68.46
	3621	CG	ARG B 245	33.981	59.535	120.705	1.00	63.35
	3622	CD	ARG B 245	34.201	61.000	120.385	1.00	58.68

	3623	NE	ARG B 245	34.354	61.238	118.950	1.00	55.72
	3624	CZ	ARG B 245	33.375	61.136	118.049	1.00	55.80
	3625	NH1	ARG B 245	32.140	60.792	118.422	1.00	49.88
	3626	NH2	ARG B 245	33.626	61.397	116.766	1.00	48.05
5	3627	C	ARG B 245	34.663	59.400	124.555	1.00	73.72
	3628	O	ARG B 245	33.530	59.373	125.033	1.00	73.30
	3629	N	HIS B 246	35.758	59.092	125.246	1.00	78.53
	3630	CA	HIS B 246	35.739	58.667	126.640	1.00	79.67
	3631	CB	HIS B 246	35.285	59.821	127.536	0.50	77.47
10	3632	CG	HIS B 246	36.235	60.975	127.551	0.50	76.13
	3633	CD2	HIS B 246	36.073	62.269	127.187	0.50	75.47
	3634	ND1	HIS B 246	37.542	60.856	127.974	0.50	75.21
	3635	CE1	HIS B 246	38.144	62.027	127.869	0.50	75.76
	3636	NE2	HIS B 246	37.275	62.901	127.393	0.50	75.39
15	3637	C	HIS B 246	34.810	57.475	126.814	1.00	81.08
	3638	O	HIS B 246	35.298	56.328	126.722	1.00	79.86
	3639	OT	HIS B 246	33.602	57.712	127.018	1.00	85.74
	3640	CB	THR C 17	17.766	31.634	166.129	1.00	89.46
	3641	OG1	THR C 17	18.926	30.998	166.678	0.00	88.43
20	3642	CG2	THR C 17	16.516	30.947	166.660	0.00	88.43
	3643	C	THR C 17	19.041	32.312	164.062	1.00	87.60
	3644	O	THR C 17	19.850	31.754	163.308	1.00	88.65
	3645	N	THR C 17	17.827	30.127	164.127	1.00	90.55
	3646	CA	THR C 17	17.810	31.551	164.582	1.00	89.32
25	3647	N	GLN C 18	19.175	33.578	164.466	1.00	82.84
	3648	CA	GLN C 18	20.291	34.430	164.040	1.00	76.79
	3649	CB	GLN C 18	21.618	33.817	164.456	1.00	76.72
	3650	CG	GLN C 18	21.870	33.867	165.930	1.00	79.93
	3651	CD	GLN C 18	22.864	32.820	166.340	1.00	83.36
30	3652	OE1	GLN C 18	23.849	32.580	165.635	1.00	84.01
	3653	NE2	GLN C 18	22.621	32.183	167.481	1.00	84.67
	3654	C	GLN C 18	20.302	34.675	162.533	1.00	71.77
	3655	O	GLN C 18	21.260	34.336	161.828	1.00	72.61
	3656	N	VAL C 19	19.221	35.272	162.050	1.00	62.21
35	3657	CA	VAL C 19	19.077	35.582	160.644	1.00	55.05
	3658	CB	VAL C 19	18.346	34.437	159.912	1.00	54.61
	3659	CG1	VAL C 19	17.987	34.857	158.513	1.00	54.84
	3660	CG2	VAL C 19	19.235	33.214	159.864	1.00	54.69
	3661	C	VAL C 19	18.280	36.875	160.518	1.00	48.33
40	3662	O	VAL C 19	17.224	37.021	161.128	1.00	49.49
	3663	N	PRO C 20	18.785	37.841	159.742	1.00	41.15
	3664	CD	PRO C 20	19.995	37.871	158.903	1.00	41.03
	3665	CA	PRO C 20	18.024	39.078	159.614	1.00	37.57

	3666	CB	PRO	C	20	18.941	39.941	158.754	1.00	37.93
	3667	CG	PRO	C	20	19.662	38.947	157.918	1.00	37.00
	3668	C	PRO	C	20	16.673	38.764	158.959	1.00	39.10
	3669	O	PRO	C	20	16.612	38.047	157.969	1.00	44.71
5	3670	N	ALA	C	21	15.589	39.285	159.518	1.00	34.69
	3671	CA	ALA	C	21	14.269	39.014	158.982	1.00	34.36
	3672	CB	ALA	C	21	13.226	39.378	160.001	1.00	27.90
	3673	C	ALA	C	21	13.949	39.698	157.659	1.00	37.80
	3674	O	ALA	C	21	13.119	39.201	156.891	1.00	35.81
10	3675	N	HIS	C	22	14.581	40.845	157.412	1.00	36.62
	3676	CA	HIS	C	22	14.375	41.613	156.179	1.00	29.22
	3677	CB	HIS	C	22	13.423	42.787	156.461	1.00	24.47
	3678	CG	HIS	C	22	13.078	43.622	155.260	1.00	24.90
	3679	CD2	HIS	C	22	13.565	43.626	153.994	1.00	22.52
15	3680	ND1	HIS	C	22	12.075	44.570	155.285	1.00	17.38
	3681	CE1	HIS	C	22	11.954	45.113	154.086	1.00	24.47
	3682	NE2	HIS	C	22	12.845	44.557	153.283	1.00	18.24
	3683	C	HIS	C	22	15.730	42.109	155.661	1.00	28.44
	3684	O	HIS	C	22	16.443	42.835	156.352	1.00	30.22
20	3685	N	ILE	C	23	16.088	41.678	154.456	1.00	25.79
	3686	CA	ILE	C	23	17.338	42.074	153.829	1.00	23.19
	3687	CB	ILE	C	23	18.169	40.852	153.410	1.00	20.32
	3688	CG2	ILE	C	23	19.549	41.298	152.959	1.00	17.32
	3689	CG1	ILE	C	23	18.326	39.890	154.585	1.00	27.89
25	3690	CD1	ILE	C	23	19.156	38.647	154.242	1.00	24.27
	3691	C	ILE	C	23	17.059	42.882	152.565	1.00	28.34
	3692	O	ILE	C	23	16.256	42.467	151.715	1.00	27.98
	3693	N	GLY	C	24	17.700	44.046	152.440	1.00	26.92
	3694	CA	GLY	C	24	17.523	44.845	151.241	1.00	16.98
30	3695	C	GLY	C	24	18.759	44.564	150.415	1.00	21.39
	3696	O	GLY	C	24	19.835	44.453	150.981	1.00	24.27
	3697	N	ILE	C	25	18.629	44.400	149.098	1.00	24.88
	3698	CA	ILE	C	25	19.806	44.138	148.266	1.00	22.68
	3699	CB	ILE	C	25	19.855	42.695	147.721	1.00	22.91
35	3700	CG2	ILE	C	25	21.196	42.461	147.019	1.00	19.00
	3701	CG1	ILE	C	25	19.658	41.688	148.846	1.00	24.24
	3702	CD1	ILE	C	25	19.737	40.235	148.396	1.00	26.48
	3703	C	ILE	C	25	19.804	45.038	147.036	1.00	26.88
	3704	O	ILE	C	25	18.799	45.150	146.341	1.00	28.50
40	3705	N	ILE	C	26	20.935	45.672	146.776	1.00	25.93
	3706	CA	ILE	C	26	21.085	46.529	145.621	1.00	26.95
	3707	CB	ILE	C	26	21.830	47.816	146.026	1.00	26.32
	3708	CG2	ILE	C	26	22.146	48.663	144.800	1.00	23.96

	3709	CG1	ILE	C	26	20.972	48.583	147.036	1.00	25.81
	3710	CD1	ILE	C	26	21.613	49.854	147.556	1.00	33.20
	3711	C	ILE	C	26	21.904	45.680	144.651	1.00	30.45
	3712	O	ILE	C	26	23.114	45.511	144.817	1.00	28.02
5	3713	N	MET	C	27	21.223	45.113	143.660	1.00	33.77
	3714	CA	MET	C	27	21.860	44.238	142.675	1.00	36.80
	3715	CB	MET	C	27	20.800	43.365	142.004	1.00	35.31
	3716	CG	MET	C	27	19.954	42.600	143.002	1.00	34.88
	3717	SD	MET	C	27	18.597	41.632	142.282	1.00	47.55
10	3718	CE	MET	C	27	17.711	42.896	141.280	1.00	28.38
	3719	C	MET	C	27	22.625	45.023	141.627	1.00	37.91
	3720	O	MET	C	27	22.081	45.387	140.588	1.00	47.12
	3721	N	ASP	C	28	23.894	45.279	141.900	1.00	35.00
	3722	CA	ASP	C	28	24.713	46.041	140.980	1.00	32.21
15	3723	CB	ASP	C	28	25.281	47.253	141.710	1.00	31.66
	3724	CG	ASP	C	28	25.898	48.267	140.769	1.00	44.52
	3725	OD1	ASP	C	28	25.950	47.999	139.542	1.00	48.22
	3726	OD2	ASP	C	28	26.335	49.335	141.261	1.00	44.37
	3727	C	ASP	C	28	25.850	45.164	140.468	1.00	35.86
20	3728	O	ASP	C	28	26.305	44.258	141.173	1.00	31.11
	3729	N	GLY	C	29	26.297	45.433	139.242	1.00	35.45
	3730	CA	GLY	C	29	27.395	44.671	138.672	1.00	41.03
	3731	C	GLY	C	29	27.125	43.832	137.430	1.00	41.19
	3732	O	GLY	C	29	28.075	43.362	136.809	1.00	43.39
25	3733	N	ASN	C	30	25.860	43.634	137.061	1.00	40.34
	3734	CA	ASN	C	30	25.535	42.833	135.879	1.00	40.95
	3735	CB	ASN	C	30	24.038	42.903	135.581	1.00	38.03
	3736	CG	ASN	C	30	23.219	42.196	136.624	1.00	39.00
	3737	OD1	ASN	C	30	21.998	42.178	136.567	1.00	47.36
30	3738	ND2	ASN	C	30	23.895	41.601	137.594	1.00	46.14
	3739	C	ASN	C	30	26.324	43.236	134.642	1.00	45.52
	3740	O	ASN	C	30	26.990	42.402	134.031	1.00	44.94
	3741	N	GLY	C	31	26.254	44.513	134.276	1.00	49.28
	3742	CA	GLY	C	31	26.979	44.988	133.105	1.00	52.06
35	3743	C	GLY	C	31	28.488	44.821	133.206	1.00	53.62
	3744	O	GLY	C	31	29.154	44.444	132.242	1.00	53.00
	3745	N	ARG	C	32	29.022	45.107	134.387	1.00	57.14
	3746	CA	ARG	C	32	30.450	45.004	134.653	1.00	58.08
	3747	CB	ARG	C	32	30.723	45.474	136.081	1.00	61.04
40	3748	CG	ARG	C	32	32.135	45.928	136.362	1.00	65.01
	3749	CD	ARG	C	32	32.225	46.389	137.808	1.00	70.42
	3750	NE	ARG	C	32	33.548	46.886	138.185	1.00	75.28
	3751	CZ	ARG	C	32	33.885	47.245	139.422	1.00	75.06

	3752	NH1	ARG	C	32	32.997	47.159	140.404	1.00	77.24
	3753	NH2	ARG	C	32	35.107	47.695	139.680	1.00	74.52
	3754	C	ARG	C	32	30.854	43.547	134.495	1.00	58.36
	3755	O	ARG	C	32	31.968	43.236	134.055	1.00	57.54
5	3756	N	TRP	C	33	29.921	42.668	134.851	1.00	57.35
	3757	CA	TRP	C	33	30.108	41.221	134.780	1.00	58.89
	3758	CB	TRP	C	33	28.922	40.517	135.434	1.00	56.96
	3759	CG	TRP	C	33	29.147	39.068	135.736	1.00	57.31
	3760	CD2	TRP	C	33	28.623	37.949	135.012	1.00	56.57
10	3761	CE2	TRP	C	33	29.080	36.782	135.662	1.00	59.52
	3762	CE3	TRP	C	33	27.810	37.819	133.876	1.00	53.88
	3763	CD1	TRP	C	33	29.884	38.549	136.761	1.00	56.67
	3764	NE1	TRP	C	33	29.847	37.180	136.726	1.00	58.01
	3765	CZ2	TRP	C	33	28.753	35.496	135.214	1.00	57.55
15	3766	CZ3	TRP	C	33	27.486	36.548	133.430	1.00	53.85
	3767	CH2	TRP	C	33	27.957	35.399	134.100	1.00	57.94
	3768	C	TRP	C	33	30.226	40.756	133.333	1.00	62.21
	3769	O	TRP	C	33	30.986	39.839	133.025	1.00	62.52
	3770	N	ALA	C	34	29.460	41.390	132.449	1.00	66.86
20	3771	CA	ALA	C	34	29.476	41.058	131.027	1.00	64.42
	3772	CB	ALA	C	34	28.338	41.765	130.318	1.00	63.41
	3773	C	ALA	C	34	30.816	41.463	130.412	1.00	64.55
	3774	O	ALA	C	34	31.551	40.616	129.900	1.00	61.59
	3775	N	LYS	C	35	31.141	42.753	130.473	1.00	64.45
25	3776	CA	LYS	C	35	32.403	43.241	129.917	1.00	65.11
	3777	CB	LYS	C	35	32.760	44.613	130.512	1.00	67.23
	3778	CG	LYS	C	35	34.051	45.221	129.959	1.00	68.76
	3779	CD	LYS	C	35	34.376	46.562	130.610	1.00	69.91
	3780	CE	LYS	C	35	35.637	47.170	130.018	0.00	69.34
30	3781	NZ	LYS	C	35	35.954	48.491	130.627	0.00	69.34
	3782	C	LYS	C	35	33.545	42.251	130.170	1.00	63.79
	3783	O	LYS	C	35	34.271	41.894	129.246	1.00	64.62
	3784	N	LYS	C	36	33.690	41.802	131.414	1.00	65.10
	3785	CA	LYS	C	36	34.742	40.856	131.774	1.00	67.07
35	3786	CB	LYS	C	36	34.750	40.617	133.286	1.00	68.92
	3787	CG	LYS	C	36	35.039	41.876	134.099	1.00	73.70
	3788	CD	LYS	C	36	35.042	41.610	135.602	1.00	75.38
	3789	CE	LYS	C	36	35.206	42.913	136.385	1.00	76.29
	3790	NZ	LYS	C	36	35.151	42.711	137.864	1.00	77.65
40	3791	C	LYS	C	36	34.590	39.530	131.037	1.00	68.16
	3792	O	LYS	C	36	35.580	38.937	130.622	1.00	66.22
	3793	N	ARG	C	37	33.357	39.059	130.883	1.00	70.84
	3794	CA	ARG	C	37	33.112	37.807	130.166	1.00	74.96

	3795	CB	ARG	C	37	31.777	37.165	130.582	1.00	74.86
	3796	CG	ARG	C	37	31.584	36.876	132.067	1.00	77.72
	3797	CD	ARG	C	37	32.344	35.649	132.557	1.00	79.98
	3798	NE	ARG	C	37	32.115	35.410	133.983	1.00	79.14
5	3799	CZ	ARG	C	37	32.357	36.307	134.935	1.00	81.76
	3800	NH1	ARG	C	37	32.833	37.504	134.618	1.00	81.30
	3801	NH2	ARG	C	37	32.126	36.015	136.208	1.00	82.86
	3802	C	ARG	C	37	33.040	38.136	128.672	1.00	78.06
	3803	O	ARG	C	37	32.396	37.412	127.907	1.00	79.60
10	3804	N	MET	C	38	33.692	39.231	128.271	1.00	79.62
	3805	CA	MET	C	38	33.693	39.685	126.878	1.00	79.53
	3806	CB	MET	C	38	34.867	39.065	126.104	1.00	81.03
	3807	CG	MET	C	38	36.251	39.538	126.552	0.50	84.63
	3808	SD	MET	C	38	36.542	41.317	126.320	0.50	91.56
15	3809	CE	MET	C	38	37.402	41.334	124.744	0.50	89.98
	3810	C	MET	C	38	32.372	39.303	126.213	1.00	80.27
	3811	O	MET	C	38	32.353	38.812	125.086	1.00	82.15
	3812	N	GLN	C	39	31.271	39.529	126.924	1.00	77.24
	3813	CA	GLN	C	39	29.943	39.196	126.431	1.00	75.73
20	3814	CB	GLN	C	39	29.323	38.130	127.333	1.00	75.41
	3815	CG	GLN	C	39	29.708	36.722	126.972	1.00	79.54
	3816	CD	GLN	C	39	29.008	36.259	125.713	1.00	84.07
	3817	OE1	GLN	C	39	27.788	36.076	125.702	1.00	86.89
	3818	NE2	GLN	C	39	29.772	36.077	124.638	1.00	84.73
25	3819	C	GLN	C	39	29.016	40.404	126.369	1.00	76.86
	3820	O	GLN	C	39	29.317	41.463	126.918	1.00	72.76
	3821	N	PRO	C	40	27.870	40.261	125.685	1.00	79.61
	3822	CD	PRO	C	40	27.353	39.073	124.982	1.00	79.53
	3823	CA	PRO	C	40	26.922	41.376	125.586	1.00	82.15
30	3824	CB	PRO	C	40	25.863	40.839	124.625	1.00	81.95
	3825	CG	PRO	C	40	25.870	39.359	124.916	1.00	80.73
	3826	C	PRO	C	40	26.349	41.691	126.970	1.00	83.70
	3827	O	PRO	C	40	26.137	40.779	127.773	1.00	84.90
	3828	N	ARG	C	41	26.097	42.967	127.253	1.00	82.09
35	3829	CA	ARG	C	41	25.560	43.347	128.553	1.00	81.22
	3830	CB	ARG	C	41	25.462	44.862	128.671	1.00	84.25
	3831	CG	ARG	C	41	26.806	45.553	128.592	1.00	90.77
	3832	CD	ARG	C	41	26.829	46.842	129.402	1.00	96.30
	3833	NE	ARG	C	41	25.642	47.674	129.206	1.00	97.94
40	3834	CZ	ARG	C	41	24.495	47.525	129.867	1.00	100.00
	3835	NH1	ARG	C	41	24.358	46.572	130.782	1.00	99.09
	3836	NH2	ARG	C	41	23.479	48.340	129.615	1.00	100.00
	3837	C	ARG	C	41	24.202	42.721	128.836	1.00	79.36

	3838	O	ARG	C	41	23.687	42.801	129.951	1.00	78.20
	3839	N	VAL	C	42	23.627	42.096	127.818	1.00	78.38
	3840	CA	VAL	C	42	22.342	41.430	127.960	1.00	77.59
	3841	CB	VAL	C	42	21.754	41.070	126.574	1.00	80.47
5	3842	CG1	VAL	C	42	20.314	40.567	126.723	1.00	78.74
	3843	CG2	VAL	C	42	21.830	42.286	125.649	1.00	81.57
	3844	C	VAL	C	42	22.597	40.145	128.739	1.00	74.75
	3845	O	VAL	C	42	21.778	39.716	129.553	1.00	73.19
	3846	N	PHE	C	43	23.755	39.549	128.470	1.00	72.61
10	3847	CA	PHE	C	43	24.199	38.309	129.103	1.00	72.09
	3848	CB	PHE	C	43	25.603	37.964	128.578	1.00	76.00
	3849	CG	PHE	C	43	26.122	36.621	129.019	1.00	80.02
	3850	CD1	PHE	C	43	25.381	35.462	128.802	1.00	80.50
	3851	CD2	PHE	C	43	27.380	36.513	129.617	1.00	81.80
15	3852	CE1	PHE	C	43	25.887	34.212	129.172	1.00	83.11
	3853	CE2	PHE	C	43	27.896	35.269	129.991	1.00	81.49
	3854	CZ	PHE	C	43	27.148	34.116	129.768	1.00	82.33
	3855	C	PHE	C	43	24.221	38.486	130.623	1.00	69.70
	3856	O	PHE	C	43	23.858	37.580	131.381	1.00	67.55
20	3857	N	GLY	C	44	24.636	39.670	131.053	1.00	67.24
	3858	CA	GLY	C	44	24.705	39.963	132.470	1.00	67.74
	3859	C	GLY	C	44	23.371	39.910	133.183	1.00	65.78
	3860	O	GLY	C	44	23.268	39.317	134.250	1.00	63.85
	3861	N	HIS	C	45	22.341	40.514	132.600	1.00	68.86
25	3862	CA	HIS	C	45	21.031	40.531	133.243	1.00	70.24
	3863	CB	HIS	C	45	20.066	41.439	132.480	1.00	72.54
	3864	CG	HIS	C	45	20.232	42.881	132.827	1.00	74.88
	3865	CD2	HIS	C	45	19.485	43.701	133.607	1.00	76.22
	3866	ND1	HIS	C	45	21.344	43.609	132.462	1.00	76.88
30	3867	CE1	HIS	C	45	21.281	44.812	133.006	1.00	77.83
	3868	NE2	HIS	C	45	20.162	44.890	133.706	1.00	79.93
	3869	C	HIS	C	45	20.404	39.175	133.469	1.00	70.19
	3870	O	HIS	C	45	19.630	38.996	134.410	1.00	71.45
	3871	N	LYS	C	46	20.732	38.220	132.609	1.00	69.28
35	3872	CA	LYS	C	46	20.204	36.874	132.752	1.00	67.06
	3873	CB	LYS	C	46	20.374	36.114	131.439	1.00	69.71
	3874	CG	LYS	C	46	19.576	36.745	130.311	1.00	73.94
	3875	CD	LYS	C	46	20.016	36.243	128.953	1.00	78.13
	3876	CE	LYS	C	46	19.266	36.946	127.834	1.00	73.85
40	3877	NZ	LYS	C	46	19.924	36.652	126.537	1.00	76.00
	3878	C	LYS	C	46	20.960	36.196	133.894	1.00	61.62
	3879	O	LYS	C	46	20.371	35.477	134.701	1.00	62.46
	3880	N	ALA	C	47	22.265	36.443	133.963	1.00	56.09

	3881	CA	ALA	C	47	23.089	35.886	135.027	1.00	52.02
	3882	CB	ALA	C	47	24.545	36.231	134.792	1.00	47.51
	3883	C	ALA	C	47	22.594	36.521	136.325	1.00	52.61
	3884	O	ALA	C	47	22.721	35.947	137.405	1.00	54.08
5	3885	N	GLY	C	48	22.018	37.711	136.196	1.00	47.82
	3886	CA	GLY	C	48	21.482	38.411	137.346	1.00	48.41
	3887	C	GLY	C	48	20.168	37.814	137.823	1.00	46.39
	3888	O	GLY	C	48	19.974	37.630	139.025	1.00	46.40
	3889	N	MET	C	49	19.259	37.521	136.895	1.00	48.45
10	3890	CA	MET	C	49	17.971	36.927	137.260	1.00	51.02
	3891	CB	MET	C	49	17.078	36.740	136.017	1.00	50.30
	3892	CG	MET	C	49	16.791	38.019	135.226	0.50	50.78
	3893	SD	MET	C	49	15.509	37.839	133.932	0.50	52.84
	3894	CE	MET	C	49	16.470	37.197	132.580	0.50	52.92
15	3895	C	MET	C	49	18.260	35.569	137.915	1.00	50.78
	3896	O	MET	C	49	17.587	35.158	138.872	1.00	47.19
	3897	N	GLU	C	50	19.273	34.884	137.388	1.00	50.30
	3898	CA	GLU	C	50	19.676	33.591	137.920	1.00	51.93
	3899	CB	GLU	C	50	20.857	33.011	137.121	1.00	56.53
20	3900	CG	GLU	C	50	20.486	32.172	135.899	1.00	58.85
	3901	CD	GLU	C	50	19.909	30.813	136.271	0.50	59.97
	3902	OE1	GLU	C	50	20.613	30.025	136.939	0.50	59.17
	3903	OE2	GLU	C	50	18.752	30.532	135.893	0.50	59.42
	3904	C	GLU	C	50	20.108	33.797	139.360	1.00	51.27
25	3905	O	GLU	C	50	19.551	33.194	140.285	1.00	52.02
	3906	N	ALA	C	51	21.110	34.654	139.541	1.00	46.84
	3907	CA	ALA	C	51	21.631	34.930	140.873	1.00	46.05
	3908	CB	ALA	C	51	22.655	36.060	140.820	1.00	43.49
	3909	C	ALA	C	51	20.483	35.290	141.810	1.00	44.87
30	3910	O	ALA	C	51	20.467	34.886	142.978	1.00	46.67
	3911	N	LEU	C	52	19.501	36.023	141.303	1.00	39.99
	3912	CA	LEU	C	52	18.401	36.387	142.172	1.00	40.63
	3913	CB	LEU	C	52	17.487	37.421	141.525	1.00	34.74
	3914	CG	LEU	C	52	16.286	37.752	142.406	1.00	38.38
35	3915	CD1	LEU	C	52	16.759	38.180	143.781	1.00	35.72
	3916	CD2	LEU	C	52	15.456	38.844	141.744	1.00	34.81
	3917	C	LEU	C	52	17.621	35.144	142.524	1.00	42.82
	3918	O	LEU	C	52	17.266	34.940	143.681	1.00	44.64
	3919	N	GLN	C	53	17.369	34.302	141.524	1.00	45.67
40	3920	CA	GLN	C	53	16.637	33.065	141.749	1.00	39.98
	3921	CB	GLN	C	53	16.615	32.216	140.481	1.00	45.02
	3922	CG	GLN	C	53	15.819	30.933	140.641	1.00	48.64
	3923	CD	GLN	C	53	14.339	31.151	140.453	1.00	54.22



	3924	OE1	GLN	C	53	13.805	32.209	140.786	1.00	50.81
	3925	NE2	GLN	C	53	13.659	30.143	139.918	1.00	59.26
	3926	C	GLN	C	53	17.263	32.252	142.877	1.00	35.99
	3927	O	GLN	C	53	16.570	31.832	143.806	1.00	37.06
5	3928	N	THR	C	54	18.573	32.029	142.801	1.00	33.35
	3929	CA	THR	C	54	19.249	31.252	143.831	1.00	35.53
	3930	CB	THR	C	54	20.666	30.820	143.391	1.00	41.53
	3931	OG1	THR	C	54	21.614	31.178	144.410	1.00	49.70
	3932	CG2	THR	C	54	21.049	31.459	142.057	1.00	45.08
10	3933	C	THR	C	54	19.333	31.950	145.192	1.00	41.61
	3934	O	THR	C	54	19.184	31.289	146.234	1.00	45.87
	3935	N	VAL	C	55	19.560	33.270	145.210	1.00	41.10
	3936	CA	VAL	C	55	19.625	33.977	146.493	1.00	34.43
	3937	CB	VAL	C	55	20.059	35.453	146.332	1.00	37.63
15	3938	CG1	VAL	C	55	19.629	36.262	147.555	1.00	30.28
	3939	CG2	VAL	C	55	21.572	35.530	146.164	1.00	32.21
	3940	C	VAL	C	55	18.284	33.933	147.214	1.00	34.84
	3941	O	VAL	C	55	18.242	33.681	148.418	1.00	37.05
	3942	N	THR	C	56	17.184	34.148	146.500	1.00	34.08
20	3943	CA	THR	C	56	15.900	34.122	147.189	1.00	39.09
	3944	CB	THR	C	56	14.747	34.804	146.345	1.00	37.55
	3945	OG1	THR	C	56	13.747	33.854	145.993	1.00	33.79
	3946	CG2	THR	C	56	15.281	35.449	145.112	1.00	32.22
	3947	C	THR	C	56	15.507	32.716	147.660	1.00	43.96
25	3948	O	THR	C	56	14.929	32.564	148.737	1.00	46.05
	3949	N	LYS	C	57	15.830	31.685	146.879	1.00	48.79
	3950	CA	LYS	C	57	15.521	30.308	147.293	1.00	48.90
	3951	CB	LYS	C	57	15.898	29.296	146.188	1.00	52.74
	3952	CG	LYS	C	57	14.857	29.134	145.059	1.00	52.40
30	3953	CD	LYS	C	57	15.501	28.636	143.761	1.00	51.18
	3954	CE	LYS	C	57	16.247	27.315	143.964	1.00	55.45
	3955	NZ	LYS	C	57	16.972	26.840	142.742	1.00	56.95
	3956	C	LYS	C	57	16.308	29.994	148.570	1.00	44.46
	3957	O	LYS	C	57	15.754	29.463	149.528	1.00	41.87
35	3958	N	ALA	C	58	17.593	30.342	148.578	1.00	42.62
	3959	CA	ALA	C	58	18.459	30.106	149.736	1.00	44.85
	3960	CB	ALA	C	58	19.888	30.477	149.387	1.00	41.91
	3961	C	ALA	C	58	18.009	30.872	150.987	1.00	47.20
	3962	O	ALA	C	58	17.939	30.313	152.082	1.00	49.88
40	3963	N	ALA	C	59	17.705	32.155	150.824	1.00	48.26
	3964	CA	ALA	C	59	17.247	32.969	151.945	1.00	48.92
	3965	CB	ALA	C	59	17.132	34.437	151.516	1.00	48.10
	3966	C	ALA	C	59	15.890	32.463	152.448	1.00	48.20

	3967	O	ALA	C	59	15.592	32.525	153.641	1.00	47.27
	3968	N	ASN	C	60	15.049	31.986	151.535	1.00	50.05
	3969	CA	ASN	C	60	13.742	31.481	151.940	1.00	50.08
	3970	CB	ASN	C	60	12.910	31.088	150.720	1.00	50.21
5	3971	CG	ASN	C	60	11.544	30.549	151.096	1.00	47.17
	3972	OD1	ASN	C	60	10.804	31.170	151.859	1.00	48.10
	3973	ND2	ASN	C	60	11.199	29.390	150.553	1.00	52.47
	3974	C	ASN	C	60	13.953	30.271	152.832	1.00	48.58
	3975	O	ASN	C	60	13.235	30.075	153.812	1.00	43.95
10	3976	N	LYS	C	61	14.962	29.473	152.498	1.00	49.56
	3977	CA	LYS	C	61	15.263	28.287	153.283	1.00	52.82
	3978	CB	LYS	C	61	16.133	27.310	152.486	1.00	55.50
	3979	CG	LYS	C	61	15.344	26.497	151.464	0.50	56.50
	3980	CD	LYS	C	61	16.244	25.671	150.557	0.50	57.55
15	3981	CE	LYS	C	61	15.434	25.044	149.425	0.50	59.27
	3982	NZ	LYS	C	61	16.286	24.453	148.356	0.50	58.56
	3983	C	LYS	C	61	15.950	28.635	154.584	1.00	53.05
	3984	O	LYS	C	61	15.680	28.008	155.603	1.00	53.98
	3985	N	LEU	C	62	16.828	29.637	154.554	1.00	53.09
20	3986	CA	LEU	C	62	17.558	30.040	155.757	1.00	49.37
	3987	CB	LEU	C	62	18.758	30.907	155.372	1.00	51.65
	3988	CG	LEU	C	62	19.851	30.131	154.625	1.00	53.47
	3989	CD1	LEU	C	62	20.858	31.079	153.984	1.00	54.37
	3990	CD2	LEU	C	62	20.543	29.203	155.605	1.00	58.84
25	3991	C	LEU	C	62	16.711	30.745	156.821	1.00	44.05
	3992	O	LEU	C	62	17.205	31.049	157.905	1.00	43.02
	3993	N	GLY	C	63	15.437	30.989	156.515	1.00	42.77
	3994	CA	GLY	C	63	14.543	31.631	157.471	1.00	42.56
	3995	C	GLY	C	63	14.281	33.124	157.285	1.00	46.38
30	3996	O	GLY	C	63	13.477	33.707	158.021	1.00	47.95
	3997	N	VAL	C	64	14.951	33.751	156.319	1.00	41.15
	3998	CA	VAL	C	64	14.755	35.174	156.075	1.00	37.24
	3999	CB	VAL	C	64	15.690	35.674	154.958	1.00	32.18
	4000	CG1	VAL	C	64	15.420	37.137	154.663	1.00	26.01
35	4001	CG2	VAL	C	64	17.129	35.493	155.375	1.00	29.77
	4002	C	VAL	C	64	13.307	35.405	155.666	1.00	38.48
	4003	O	VAL	C	64	12.812	34.757	154.755	1.00	42.78
	4004	N	LYS	C	65	12.624	36.326	156.337	1.00	37.18
	4005	CA	LYS	C	65	11.225	36.614	156.020	1.00	36.84
40	4006	CB	LYS	C	65	10.543	37.237	157.237	1.00	37.16
	4007	CG	LYS	C	65	10.540	36.368	158.475	1.00	48.04
	4008	CD	LYS	C	65	9.496	35.282	158.366	1.00	55.63
	4009	CE	LYS	C	65	9.552	34.341	159.553	1.00	62.33

	4010	NZ	LYS	C	65	8.499	33.277	159.454	1.00	68.48
	4011	C	LYS	C	65	10.970	37.532	154.810	1.00	36.85
	4012	O	LYS	C	65	9.912	37.460	154.189	1.00	34.32
	4013	N	VAL	C	66	11.922	38.404	154.485	1.00	33.57
5	4014	CA	VAL	C	66	11.725	39.344	153.393	1.00	30.33
	4015	CB	VAL	C	66	11.070	40.662	153.887	1.00	33.74
	4016	CG1	VAL	C	66	10.829	41.609	152.704	1.00	30.96
	4017	CG2	VAL	C	66	9.785	40.386	154.637	1.00	28.24
	4018	C	VAL	C	66	13.028	39.777	152.767	1.00	32.21
10	4019	O	VAL	C	66	14.014	39.951	153.465	1.00	34.40
	4020	N	ILE	C	67	13.047	39.908	151.447	1.00	32.30
	4021	CA	ILE	C	67	14.211	40.458	150.776	1.00	35.16
	4022	CB	ILE	C	67	15.105	39.437	150.004	1.00	34.65
	4023	CG2	ILE	C	67	15.548	38.331	150.921	1.00	42.46
15	4024	CG1	ILE	C	67	14.377	38.839	148.821	1.00	43.52
	4025	CD1	ILE	C	67	15.249	37.832	148.078	1.00	43.70
	4026	C	ILE	C	67	13.648	41.485	149.805	1.00	34.60
	4027	O	ILE	C	67	12.730	41.193	149.020	1.00	33.34
	4028	N	THR	C	68	14.147	42.715	149.925	1.00	32.22
20	4029	CA	THR	C	68	13.737	43.796	149.041	1.00	26.44
	4030	CB	THR	C	68	13.342	45.052	149.806	1.00	27.24
	4031	OG1	THR	C	68	12.171	44.757	150.582	1.00	34.45
	4032	CG2	THR	C	68	13.020	46.200	148.837	1.00	19.90
	4033	C	THR	C	68	14.913	44.018	148.111	1.00	25.73
25	4034	O	THR	C	68	16.045	44.310	148.516	1.00	27.54
	4035	N	VAL	C	69	14.597	43.832	146.842	1.00	22.43
	4036	CA	VAL	C	69	15.546	43.875	145.764	1.00	27.12
	4037	CB	VAL	C	69	15.388	42.523	144.999	1.00	31.23
	4038	CG1	VAL	C	69	15.536	42.707	143.526	1.00	36.65
30	4039	CG2	VAL	C	69	16.372	41.507	145.563	1.00	22.44
	4040	C	VAL	C	69	15.412	45.103	144.849	1.00	26.70
	4041	O	VAL	C	69	14.315	45.486	144.440	1.00	25.35
	4042	N	TYR	C	70	16.550	45.715	144.532	1.00	29.49
	4043	CA	TYR	C	70	16.585	46.904	143.693	1.00	30.67
35	4044	CB	TYR	C	70	16.969	48.100	144.569	1.00	32.06
	4045	CG	TYR	C	70	16.959	49.462	143.909	1.00	32.88
	4046	CD1	TYR	C	70	15.926	49.850	143.048	1.00	32.61
	4047	CE1	TYR	C	70	15.881	51.150	142.524	1.00	38.51
	4048	CD2	TYR	C	70	17.944	50.403	144.224	1.00	32.63
40	4049	CE2	TYR	C	70	17.909	51.695	143.717	1.00	35.72
	4050	CZ	TYR	C	70	16.878	52.067	142.868	1.00	44.78
	4051	OH	TYR	C	70	16.854	53.358	142.381	1.00	51.16
	4052	C	TYR	C	70	17.592	46.709	142.571	1.00	33.45

	4053	O	TYR	C	70	18.781	46.559	142.817	1.00	33.76
	4054	N	ALA	C	71	17.105	46.690	141.339	1.00	43.29
	4055	CA	ALA	C	71	17.965	46.522	140.173	1.00	51.74
	4056	CB	ALA	C	71	17.134	46.080	138.982	1.00	57.23
5	4057	C	ALA	C	71	18.575	47.885	139.915	1.00	56.26
	4058	O	ALA	C	71	17.860	48.816	139.563	1.00	59.24
	4059	N	PHE	C	72	19.890	48.008	140.080	1.00	63.67
	4060	CA	PHE	C	72	20.531	49.310	139.913	1.00	68.57
	4061	CB	PHE	C	72	20.423	50.066	141.226	1.00	66.99
10	4062	CG	PHE	C	72	20.906	51.467	141.150	1.00	69.20
	4063	CD1	PHE	C	72	20.046	52.488	140.765	1.00	70.92
	4064	CD2	PHE	C	72	22.221	51.774	141.459	1.00	70.72
	4065	CE1	PHE	C	72	20.491	53.803	140.692	1.00	75.26
	4066	CE2	PHE	C	72	22.682	53.087	141.389	1.00	76.22
15	4067	CZ	PHE	C	72	21.815	54.106	141.006	1.00	75.23
	4068	C	PHE	C	72	21.998	49.327	139.471	1.00	74.50
	4069	O	PHE	C	72	22.721	48.337	139.618	1.00	75.94
	4070	N	SER	C	73	22.419	50.479	138.936	1.00	77.97
	4071	CA	SER	C	73	23.794	50.718	138.474	1.00	78.87
20	4072	CB	SER	C	73	24.100	49.921	137.199	1.00	79.15
	4073	OG	SER	C	73	25.443	50.134	136.779	1.00	75.19
	4074	C	SER	C	73	24.049	52.210	138.212	1.00	78.23
	4075	O	SER	C	73	23.531	52.795	137.253	1.00	76.98
	4076	N	TRP	C	77	29.239	54.105	129.323	1.00	100.00
25	4077	CA	TRP	C	77	28.028	54.688	128.747	1.00	100.00
	4078	CB	TRP	C	77	27.252	53.622	127.964	1.00	100.00
	4079	CG	TRP	C	77	26.491	52.688	128.865	1.00	100.00
	4080	CD2	TRP	C	77	27.022	51.558	129.574	1.00	100.00
	4081	CE2	TRP	C	77	25.981	51.047	130.386	1.00	100.00
30	4082	CE3	TRP	C	77	28.280	50.931	129.607	1.00	100.00
	4083	CD1	TRP	C	77	25.183	52.806	129.258	1.00	100.00
	4084	NE1	TRP	C	77	24.872	51.825	130.173	1.00	100.00
	4085	CZ2	TRP	C	77	26.159	49.934	131.223	1.00	100.00
	4086	CZ3	TRP	C	77	28.457	49.824	130.441	1.00	100.00
35	4087	CH2	TRP	C	77	27.399	49.340	131.238	1.00	100.00
	4088	C	TRP	C	77	27.128	55.251	129.855	1.00	100.00
	4089	O	TRP	C	77	27.150	54.777	131.001	1.00	100.00
	4090	N	THR	C	78	26.332	56.255	129.508	1.00	100.00
	4091	CA	THR	C	78	25.427	56.856	130.477	1.00	100.00
40	4092	CB	THR	C	78	25.763	58.354	130.709	1.00	100.00
	4093	OG1	THR	C	78	24.836	58.909	131.652	1.00	100.00
	4094	CG2	THR	C	78	25.695	59.138	129.399	1.00	100.00
	4095	C	THR	C	78	23.969	56.718	130.033	1.00	100.00

	4096	O	THR	C	78	23.063	56.679	130.875	1.00100.00
	4097	N	ARG	C	79	23.750	56.630	128.718	1.00100.00
	4098	CA	ARG	C	79	22.401	56.498	128.165	1.00 99.68
	4099	CB	ARG	C	79	22.449	55.947	126.733	1.00 97.66
5	4100	CG	ARG	C	79	21.109	55.425	126.250	0.50 92.39
	4101	CD	ARG	C	79	21.117	55.091	124.778	0.50 87.35
	4102	NE	ARG	C	79	22.388	54.519	124.366	1.00 82.65
	4103	CZ	ARG	C	79	22.565	53.834	123.241	1.00 85.75
	4104	NH1	ARG	C	79	21.544	53.631	122.421	1.00 83.74
10	4105	NH2	ARG	C	79	23.766	53.365	122.927	1.00 87.05
	4106	C	ARG	C	79	21.543	55.592	129.042	1.00 99.27
	4107	O	ARG	C	79	21.673	54.369	129.012	1.00 99.16
	4108	N	PRO	C	80	20.651	56.193	129.842	1.00 99.66
	4109	CD	PRO	C	80	20.484	57.646	130.018	1.00100.00
15	4110	CA	PRO	C	80	19.760	55.460	130.744	1.00100.00
	4111	CB	PRO	C	80	18.977	56.579	131.434	1.00100.00
	4112	CG	PRO	C	80	19.946	57.727	131.424	1.00100.00
	4113	C	PRO	C	80	18.843	54.455	130.055	1.00 99.32
	4114	O	PRO	C	80	18.769	53.299	130.465	1.00100.00
20	4115	N	ASP	C	81	18.145	54.899	129.012	1.00100.00
	4116	CA	ASP	C	81	17.219	54.031	128.288	1.00100.00
	4117	CB	ASP	C	81	16.718	54.732	127.014	1.00 99.89
	4118	CG	ASP	C	81	17.819	54.957	125.992	1.00 98.62
	4119	OD1	ASP	C	81	18.053	54.070	125.141	1.00 96.94
25	4120	OD2	ASP	C	81	18.458	56.026	126.048	1.00 98.46
	4121	C	ASP	C	81	17.831	52.675	127.939	1.00 99.98
	4122	O	ASP	C	81	17.185	51.641	128.103	1.00100.00
	4123	N	GLN	C	82	19.078	52.677	127.474	1.00 99.65
	4124	CA	GLN	C	82	19.752	51.436	127.108	1.00 99.13
30	4125	CB	GLN	C	82	21.161	51.725	126.584	1.00 99.61
	4126	CG	GLN	C	82	21.945	50.483	126.189	1.00 98.06
	4127	CD	GLN	C	82	23.340	50.813	125.710	1.00 99.40
	4128	OE1	GLN	C	82	24.089	51.521	126.387	1.00100.00
	4129	NE2	GLN	C	82	23.703	50.299	124.539	1.00100.00
35	4130	C	GLN	C	82	19.830	50.476	128.290	1.00 99.80
	4131	O	GLN	C	82	20.038	49.276	128.108	1.00100.00
	4132	N	GLU	C	83	19.670	51.005	129.501	1.00 99.41
	4133	CA	GLU	C	83	19.712	50.179	130.705	1.00100.00
	4134	CB	GLU	C	83	20.513	50.867	131.818	1.00 99.04
40	4135	CG	GLU	C	83	22.019	50.701	131.689	1.00100.00
	4136	CD	GLU	C	83	22.760	51.071	132.958	1.00100.00
	4137	OE1	GLU	C	83	22.455	50.480	134.019	1.00100.00
	4138	OE2	GLU	C	83	23.651	51.946	132.892	1.00100.00

	4139	C	GLU	C	83	18.311	49.869	131.210	1.00	100.00
	4140	O	GLU	C	83	17.878	48.711	131.205	1.00	100.00
	4141	N	VAL	C	84	17.606	50.911	131.643	1.00	99.20
	4142	CA	VAL	C	84	16.254	50.762	132.153	1.00	98.23
5	4143	CB	VAL	C	84	15.572	52.137	132.324	1.00	96.19
	4144	CG1	VAL	C	84	15.392	52.804	130.981	1.00	96.01
	4145	CG2	VAL	C	84	14.241	51.969	133.019	1.00	97.72
	4146	C	VAL	C	84	15.421	49.882	131.220	1.00	98.71
	4147	O	VAL	C	84	14.484	49.219	131.660	1.00	98.61
10	4148	N	LYS	C	85	15.774	49.869	129.936	1.00	99.20
	4149	CA	LYS	C	85	15.061	49.054	128.952	1.00	100.00
	4150	CB	LYS	C	85	15.771	49.092	127.590	1.00	100.00
	4151	CG	LYS	C	85	15.166	48.156	126.539	1.00	100.00
	4152	CD	LYS	C	85	15.963	48.146	125.229	1.00	100.00
15	4153	CE	LYS	C	85	15.997	49.524	124.559	1.00	100.00
	4154	NZ	LYS	C	85	16.541	49.472	123.163	1.00	97.62
	4155	C	LYS	C	85	14.991	47.612	129.430	1.00	99.90
	4156	O	LYS	C	85	13.949	46.960	129.328	1.00	100.00
	4157	N	PHE	C	86	16.111	47.118	129.952	1.00	99.82
20	4158	CA	PHE	C	86	16.169	45.747	130.435	1.00	99.57
	4159	CB	PHE	C	86	17.554	45.141	130.158	1.00	99.80
	4160	CG	PHE	C	86	17.764	44.773	128.706	1.00	100.00
	4161	CD1	PHE	C	86	18.118	45.742	127.766	1.00	100.00
	4162	CD2	PHE	C	86	17.520	43.470	128.264	1.00	100.00
25	4163	CE1	PHE	C	86	18.220	45.419	126.406	1.00	100.00
	4164	CE2	PHE	C	86	17.618	43.136	126.907	1.00	100.00
	4165	CZ	PHE	C	86	17.967	44.114	125.980	1.00	100.00
	4166	C	PHE	C	86	15.783	45.605	131.900	1.00	96.75
	4167	O	PHE	C	86	15.489	44.504	132.363	1.00	95.12
30	4168	N	ILE	C	87	15.777	46.714	132.631	1.00	94.49
	4169	CA	ILE	C	87	15.366	46.661	134.024	1.00	93.97
	4170	CB	ILE	C	87	15.910	47.860	134.838	1.00	95.12
	4171	CG2	ILE	C	87	15.311	47.856	136.241	1.00	94.67
	4172	CG1	ILE	C	87	17.438	47.766	134.932	1.00	96.30
35	4173	CD1	ILE	C	87	18.083	48.818	135.827	1.00	96.41
	4174	C	ILE	C	87	13.839	46.677	133.986	1.00	93.00
	4175	O	ILE	C	87	13.174	46.232	134.917	1.00	93.40
	4176	N	MET	C	88	13.294	47.184	132.885	1.00	91.72
	4177	CA	MET	C	88	11.850	47.227	132.684	1.00	91.20
40	4178	CB	MET	C	88	11.434	48.504	131.955	1.00	93.65
	4179	CG	MET	C	88	11.452	49.742	132.827	1.00	97.31
	4180	SD	MET	C	88	10.094	49.755	134.003	1.00	98.60
	4181	CE	MET	C	88	9.173	51.163	133.425	1.00	100.00

	4182	C	MET	C	88	11.503	46.023	131.830	1.00	90.25
	4183	O	MET	C	88	10.514	46.018	131.102	1.00	91.33
	4184	N	ASN	C	89	12.350	45.008	131.914	1.00	88.07
	4185	CA	ASN	C	89	12.149	43.780	131.169	1.00	86.29
5	4186	CB	ASN	C	89	13.200	43.657	130.063	1.00	85.94
	4187	CG	ASN	C	89	12.974	42.447	129.176	1.00	86.20
	4188	OD1	ASN	C	89	11.934	42.326	128.523	1.00	86.40
	4189	ND2	ASN	C	89	13.948	41.542	129.149	1.00	84.07
	4190	C	ASN	C	89	12.257	42.603	132.137	1.00	85.10
10	4191	O	ASN	C	89	11.776	41.504	131.849	1.00	83.55
	4192	N	LEU	C	90	12.882	42.849	133.290	1.00	83.52
	4193	CA	LEU	C	90	13.062	41.817	134.309	1.00	82.04
	4194	CB	LEU	C	90	13.641	42.403	135.606	1.00	83.23
	4195	CG	LEU	C	90	14.955	43.186	135.626	1.00	86.11
15	4196	CD1	LEU	C	90	15.255	43.538	137.073	1.00	86.97
	4197	CD2	LEU	C	90	16.103	42.383	135.024	1.00	88.64
	4198	C	LEU	C	90	11.742	41.127	134.634	1.00	78.38
	4199	O	LEU	C	90	11.632	39.906	134.526	1.00	77.33
	4200	N	PRO	C	91	10.724	41.902	135.044	1.00	74.61
20	4201	CD	PRO	C	91	10.730	43.367	135.210	1.00	74.00
	4202	CA	PRO	C	91	9.409	41.351	135.388	1.00	73.87
	4203	CB	PRO	C	91	8.533	42.596	135.466	1.00	73.87
	4204	CG	PRO	C	91	9.478	43.607	136.019	1.00	73.72
	4205	C	PRO	C	91	8.880	40.323	134.381	1.00	72.14
25	4206	O	PRO	C	91	8.462	39.222	134.760	1.00	70.25
	4207	N	VAL	C	92	8.907	40.696	133.102	1.00	69.70
	4208	CA	VAL	C	92	8.437	39.834	132.024	1.00	64.32
	4209	CB	VAL	C	92	8.491	40.562	130.667	1.00	60.80
	4210	CG1	VAL	C	92	7.749	39.760	129.624	1.00	58.91
30	4211	CG2	VAL	C	92	7.880	41.940	130.794	1.00	58.62
	4212	C	VAL	C	92	9.276	38.557	131.941	1.00	65.71
	4213	O	VAL	C	92	8.736	37.452	132.034	1.00	65.75
	4214	N	GLU	C	93	10.590	38.698	131.770	1.00	64.50
	4215	CA	GLU	C	93	11.454	37.523	131.695	1.00	65.61
35	4216	CB	GLU	C	93	12.895	37.915	131.349	1.00	67.89
	4217	CG	GLU	C	93	13.132	38.130	129.859	1.00	79.14
	4218	CD	GLU	C	93	14.568	37.826	129.438	1.00	84.92
	4219	OE1	GLU	C	93	15.019	36.665	129.608	1.00	85.68
	4220	OE2	GLU	C	93	15.244	38.748	128.932	1.00	87.81
40	4221	C	GLU	C	93	11.452	36.697	132.980	1.00	63.49
	4222	O	GLU	C	93	11.355	35.470	132.931	1.00	60.46
	4223	N	PHE	C	94	11.546	37.364	134.128	1.00	64.06
	4224	CA	PHE	C	94	11.572	36.648	135.393	1.00	63.69

	4225	CB	PHE	C	94	11.644	37.603	136.585	1.00	58.50
	4226	CG	PHE	C	94	12.357	37.015	137.779	1.00	55.40
	4227	CD1	PHE	C	94	13.725	36.718	137.711	1.00	53.81
	4228	CD2	PHE	C	94	11.672	36.730	138.953	1.00	52.29
5	4229	CE1	PHE	C	94	14.399	36.146	138.791	1.00	46.35
	4230	CE2	PHE	C	94	12.341	36.155	140.040	1.00	49.21
	4231	CZ	PHE	C	94	13.708	35.863	139.952	1.00	45.78
	4232	C	PHE	C	94	10.355	35.767	135.545	1.00	64.59
	4233	O	PHE	C	94	10.475	34.616	135.955	1.00	66.62
10	4234	N	TYR	C	95	9.186	36.306	135.207	1.00	66.68
	4235	CA	TYR	C	95	7.941	35.552	135.325	1.00	68.13
	4236	CB	TYR	C	95	6.743	36.397	134.880	1.00	67.03
	4237	CG	TYR	C	95	5.413	35.698	135.118	1.00	70.73
	4238	CD1	TYR	C	95	4.801	35.719	136.375	1.00	70.36
15	4239	CE1	TYR	C	95	3.612	35.036	136.603	1.00	69.50
	4240	CD2	TYR	C	95	4.795	34.973	134.100	1.00	70.92
	4241	CE2	TYR	C	95	3.612	34.286	134.321	1.00	68.14
	4242	CZ	TYR	C	95	3.027	34.320	135.568	1.00	68.35
	4243	OH	TYR	C	95	1.856	33.632	135.772	1.00	69.53
20	4244	C	TYR	C	95	7.942	34.249	134.531	1.00	68.26
	4245	O	TYR	C	95	7.589	33.186	135.050	1.00	69.49
	4246	N	ASP	C	96	8.350	34.334	133.274	1.00	67.04
	4247	CA	ASP	C	96	8.365	33.170	132.412	1.00	67.38
	4248	CB	ASP	C	96	8.550	33.610	130.957	1.00	73.55
25	4249	CG	ASP	C	96	7.487	34.609	130.509	1.00	81.81
	4250	OD1	ASP	C	96	6.280	34.333	130.701	1.00	81.35
	4251	OD2	ASP	C	96	7.860	35.671	129.956	1.00	87.43
	4252	C	ASP	C	96	9.419	32.127	132.768	1.00	64.31
	4253	O	ASP	C	96	9.147	30.925	132.714	1.00	63.30
30	4254	N	ASN	C	97	10.610	32.572	133.155	1.00	57.19
	4255	CA	ASN	C	97	11.673	31.618	133.452	1.00	55.33
	4256	CB	ASN	C	97	12.964	32.030	132.736	1.00	56.64
	4257	CG	ASN	C	97	12.707	32.648	131.374	1.00	63.54
	4258	OD1	ASN	C	97	11.734	32.310	130.692	1.00	63.51
35	4259	ND2	ASN	C	97	13.589	33.555	130.963	1.00	64.53
	4260	C	ASN	C	97	12.007	31.366	134.911	1.00	51.15
	4261	O	ASN	C	97	12.890	30.554	135.195	1.00	50.70
	4262	N	TYR	C	98	11.332	32.048	135.834	1.00	45.78
	4263	CA	TYR	C	98	11.643	31.861	137.249	1.00	43.99
40	4264	CB	TYR	C	98	12.712	32.878	137.697	1.00	43.12
	4265	CG	TYR	C	98	13.990	32.846	136.892	1.00	39.28
	4266	CD1	TYR	C	98	14.164	33.675	135.775	1.00	39.52
	4267	CE1	TYR	C	98	15.338	33.632	135.018	1.00	38.23



	4268	CD2	TYR	C	98	15.019	31.977	137.232	1.00	41.27
	4269	CE2	TYR	C	98	16.192	31.925	136.485	1.00	41.90
	4270	CZ	TYR	C	98	16.348	32.747	135.383	1.00	43.66
	4271	OH	TYR	C	98	17.515	32.668	134.657	1.00	46.42
5	4272	C	TYR	C	98	10.480	31.918	138.236	1.00	37.98
	4273	O	TYR	C	98	10.505	31.224	139.241	1.00	44.08
	4274	N	VAL	C	99	9.470	32.737	137.968	1.00	38.63
	4275	CA	VAL	C	99	8.357	32.862	138.899	1.00	40.62
	4276	CB	VAL	C	99	7.298	33.857	138.389	1.00	38.63
10	4277	CG1	VAL	C	99	6.039	33.784	139.243	1.00	37.12
	4278	CG2	VAL	C	99	7.859	35.257	138.473	1.00	41.48
	4279	C	VAL	C	99	7.699	31.541	139.263	1.00	44.39
	4280	O	VAL	C	99	7.294	31.347	140.408	1.00	44.45
	4281	N	PRO	C	100	7.566	30.621	138.293	1.00	45.22
15	4282	CD	PRO	C	100	7.681	30.773	136.835	1.00	43.74
	4283	CA	PRO	C	100	6.943	29.337	138.631	1.00	43.32
	4284	CB	PRO	C	100	6.787	28.647	137.267	1.00	46.01
	4285	CG	PRO	C	100	7.802	29.340	136.394	1.00	48.55
	4286	C	PRO	C	100	7.786	28.541	139.621	1.00	40.37
20	4287	O	PRO	C	100	7.245	27.936	140.548	1.00	34.50
	4288	N	GLU	C	101	9.107	28.544	139.447	1.00	38.25
	4289	CA	GLU	C	101	9.933	27.813	140.395	1.00	36.91
	4290	CB	GLU	C	101	11.390	27.738	139.941	1.00	37.85
	4291	CG	GLU	C	101	12.275	27.099	141.026	1.00	45.61
25	4292	CD	GLU	C	101	13.669	26.691	140.562	1.00	47.55
	4293	OE1	GLU	C	101	14.181	27.234	139.557	1.00	55.15
	4294	OE2	GLU	C	101	14.273	25.824	141.234	1.00	53.96
	4295	C	GLU	C	101	9.841	28.469	141.783	1.00	41.17
	4296	O	GLU	C	101	9.750	27.778	142.794	1.00	41.49
30	4297	N	LEU	C	102	9.840	29.799	141.844	1.00	38.40
	4298	CA	LEU	C	102	9.736	30.463	143.148	1.00	39.37
	4299	CB	LEU	C	102	9.887	31.981	143.027	1.00	32.70
	4300	CG	LEU	C	102	11.231	32.515	142.560	1.00	34.31
	4301	CD1	LEU	C	102	11.205	34.042	142.723	1.00	30.71
35	4302	CD2	LEU	C	102	12.370	31.864	143.372	1.00	26.85
	4303	C	LEU	C	102	8.388	30.166	143.779	1.00	34.03
	4304	O	LEU	C	102	8.269	30.080	145.001	1.00	37.09
	4305	N	HIS	C	103	7.364	30.034	142.945	1.00	35.67
	4306	CA	HIS	C	103	6.036	29.723	143.453	1.00	37.76
40	4307	CB	HIS	C	103	5.016	29.781	142.324	1.00	37.42
	4308	CG	HIS	C	103	3.631	29.410	142.752	1.00	45.02
	4309	CD2	HIS	C	103	2.835	28.375	142.395	1.00	41.99
	4310	ND1	HIS	C	103	2.912	30.146	143.670	1.00	43.96

	4311	CE1	HIS	C	103	1.733	29.583	143.857	1.00	39.46
	4312	NE2	HIS	C	103	1.661	28.507	143.096	1.00	39.31
	4313	C	HIS	C	103	6.047	28.325	144.109	1.00	36.64
	4314	O	HIS	C	103	5.445	28.106	145.167	1.00	39.74
5	4315	N	ALA	C	104	6.762	27.388	143.501	1.00	33.64
	4316	CA	ALA	C	104	6.843	26.039	144.048	1.00	38.23
	4317	CB	ALA	C	104	7.452	25.099	143.017	1.00	36.93
	4318	C	ALA	C	104	7.664	26.002	145.347	1.00	39.96
	4319	O	ALA	C	104	7.698	24.984	146.041	1.00	38.94
10	4320	N	ASN	C	105	8.326	27.111	145.666	1.00	42.67
	4321	CA	ASN	C	105	9.139	27.212	146.875	1.00	40.83
	4322	CB	ASN	C	105	10.471	27.880	146.565	1.00	44.24
	4323	CG	ASN	C	105	11.546	26.877	146.214	1.00	54.34
	4324	OD1	ASN	C	105	12.159	26.275	147.098	1.00	58.51
15	4325	ND2	ASN	C	105	11.772	26.674	144.918	1.00	57.57
	4326	C	ASN	C	105	8.408	27.978	147.961	1.00	36.65
	4327	O	ASN	C	105	8.956	28.231	149.029	1.00	38.30
	4328	N	ASN	C	106	7.165	28.341	147.669	1.00	31.47
	4329	CA	ASN	C	106	6.310	29.047	148.614	1.00	32.59
20	4330	CB	ASN	C	106	6.237	28.270	149.940	1.00	25.95
	4331	CG	ASN	C	106	5.085	28.706	150.806	1.00	28.79
	4332	OD1	ASN	C	106	5.131	28.583	152.044	1.00	39.11
	4333	ND2	ASN	C	106	4.035	29.216	150.177	1.00	18.29
	4334	C	ASN	C	106	6.791	30.478	148.868	1.00	37.27
25	4335	O	ASN	C	106	6.723	30.984	149.998	1.00	37.11
	4336	N	VAL	C	107	7.269	31.122	147.802	1.00	38.25
	4337	CA	VAL	C	107	7.752	32.493	147.866	1.00	32.93
	4338	CB	VAL	C	107	9.001	32.668	146.988	1.00	34.91
	4339	CG1	VAL	C	107	9.350	34.141	146.856	1.00	36.48
30	4340	CG2	VAL	C	107	10.163	31.898	147.593	1.00	34.17
	4341	C	VAL	C	107	6.660	33.436	147.386	1.00	30.10
	4342	O	VAL	C	107	6.129	33.267	146.308	1.00	35.79
	4343	N	LYS	C	108	6.306	34.418	148.201	1.00	29.93
	4344	CA	LYS	C	108	5.290	35.377	147.813	1.00	29.99
35	4345	CB	LYS	C	108	4.573	35.887	149.043	1.00	23.81
	4346	CG	LYS	C	108	3.422	36.795	148.728	1.00	23.43
	4347	CD	LYS	C	108	2.704	37.138	149.988	1.00	23.35
	4348	CE	LYS	C	108	1.477	37.938	149.693	1.00	28.12
	4349	NZ	LYS	C	108	0.797	38.237	150.987	1.00	41.42
40	4350	C	LYS	C	108	5.984	36.537	147.085	1.00	37.15
	4351	O	LYS	C	108	7.026	37.032	147.533	1.00	36.43
	4352	N	ILE	C	109	5.426	36.963	145.955	1.00	37.43
	4353	CA	ILE	C	109	6.041	38.042	145.197	1.00	32.52

	4354	CB	ILE C 109	6.253	37.639	143.736	1.00	32.74
	4355	CG2	ILE C 109	6.689	38.862	142.901	1.00	30.74
	4356	CG1	ILE C 109	7.333	36.566	143.665	1.00	25.71
	4357	CD1	ILE C 109	7.343	35.820	142.359	1.00	28.25
5	4358	C	ILE C 109	5.237	39.313	145.234	1.00	35.25
	4359	O	ILE C 109	4.017	39.289	145.050	1.00	31.66
	4360	N	GLN C 110	5.934	40.424	145.481	1.00	33.38
	4361	CA	GLN C 110	5.309	41.745	145.528	1.00	34.12
	4362	CB	GLN C 110	4.945	42.122	146.966	1.00	35.50
10	4363	CG	GLN C 110	3.690	41.395	147.452	1.00	47.92
	4364	CD	GLN C 110	3.193	41.853	148.815	1.00	50.30
	4365	OE1	GLN C 110	3.860	41.673	149.830	1.00	52.40
	4366	NE2	GLN C 110	2.007	42.450	148.838	1.00	55.24
	4367	C	GLN C 110	6.208	42.806	144.904	1.00	31.60
15	4368	O	GLN C 110	7.418	42.647	144.837	1.00	28.72
	4369	N	MET C 111	5.609	43.879	144.414	1.00	36.14
	4370	CA	MET C 111	6.392	44.927	143.783	1.00	38.74
	4371	CB	MET C 111	5.969	45.112	142.312	1.00	42.32
	4372	CG	MET C 111	4.740	45.997	142.062	0.50	51.32
20	4373	SD	MET C 111	5.074	47.793	142.027	0.50	60.68
	4374	CE	MET C 111	5.368	48.092	140.277	0.50	54.09
	4375	C	MET C 111	6.217	46.212	144.574	1.00	40.03
	4376	O	MET C 111	5.150	46.483	145.117	1.00	40.74
	4377	N	ILE C 112	7.289	46.989	144.641	1.00	36.48
25	4378	CA	ILE C 112	7.330	48.254	145.366	1.00	35.98
	4379	CB	ILE C 112	8.340	48.107	146.560	1.00	37.87
	4380	CG2	ILE C 112	9.552	47.291	146.115	1.00	44.88
	4381	CG1	ILE C 112	8.880	49.437	147.043	1.00	39.86
	4382	CD1	ILE C 112	10.083	49.250	148.011	1.00	29.10
30	4383	C	ILE C 112	7.794	49.274	144.316	1.00	34.11
	4384	O	ILE C 112	8.714	49.005	143.549	1.00	34.63
	4385	N	GLY C 113	7.149	50.429	144.252	1.00	31.51
	4386	CA	GLY C 113	7.560	51.404	143.266	1.00	37.27
	4387	C	GLY C 113	6.391	52.034	142.551	1.00	41.21
35	4388	O	GLY C 113	5.244	51.791	142.920	1.00	39.65
	4389	N	GLU C 114	6.680	52.846	141.534	1.00	44.32
	4390	CA	GLU C 114	5.621	53.514	140.786	1.00	48.01
	4391	CB	GLU C 114	6.071	54.918	140.341	1.00	46.64
	4392	CG	GLU C 114	6.266	55.875	141.528	1.00	50.66
40	4393	CD	GLU C 114	6.525	57.323	141.132	0.50	54.50
	4394	OE1	GLU C 114	7.474	57.593	140.363	0.50	54.59
	4395	OE2	GLU C 114	5.775	58.200	141.607	0.50	56.50
	4396	C	GLU C 114	5.159	52.656	139.610	1.00	49.43

	4397	O	GLU C 114	5.914	52.357	138.684	1.00	42.71
	4398	N	THR C 115	3.891	52.269	139.691	1.00	57.23
	4399	CA	THR C 115	3.231	51.406	138.723	1.00	66.32
	4400	CB	THR C 115	2.086	50.642	139.422	1.00	66.98
5	4401	OG1	THR C 115	2.640	49.561	140.182	1.00	68.82
	4402	CG2	THR C 115	1.092	50.109	138.422	1.00	69.47
	4403	C	THR C 115	2.691	52.056	137.458	1.00	70.12
	4404	O	THR C 115	3.243	51.868	136.379	1.00	71.21
	4405	N	ASP C 116	1.606	52.806	137.599	1.00	76.70
10	4406	CA	ASP C 116	0.961	53.461	136.467	1.00	85.00
	4407	CB	ASP C 116	0.193	54.708	136.946	1.00	89.21
	4408	CG	ASP C 116	1.106	55.789	137.503	1.00	92.57
	4409	OD1	ASP C 116	1.827	55.516	138.486	1.00	96.54
	4410	OD2	ASP C 116	1.096	56.915	136.958	1.00	93.68
15	4411	C	ASP C 116	1.893	53.824	135.299	1.00	86.90
	4412	O	ASP C 116	1.493	53.735	134.132	1.00	89.82
	4413	N	ARG C 117	3.128	54.221	135.600	1.00	85.40
	4414	CA	ARG C 117	4.069	54.584	134.542	1.00	82.93
	4415	CB	ARG C 117	5.007	55.693	135.031	1.00	88.04
20	4416	CG	ARG C 117	4.339	57.050	135.235	1.00	91.42
	4417	CD	ARG C 117	5.383	58.098	135.603	1.00	97.30
	4418	NE	ARG C 117	4.811	59.416	135.880	1.00	100.00
	4419	CZ	ARG C 117	5.528	60.489	136.212	1.00	100.00
	4420	NH1	ARG C 117	6.851	60.404	136.307	1.00	100.00
25	4421	NH2	ARG C 117	4.925	61.647	136.457	1.00	99.91
	4422	C	ARG C 117	4.890	53.396	134.023	1.00	78.37
	4423	O	ARG C 117	6.039	53.552	133.612	1.00	79.69
	4424	N	LEU C 118	4.290	52.212	134.035	1.00	71.60
	4425	CA	LEU C 118	4.957	51.004	133.564	1.00	63.84
30	4426	CB	LEU C 118	4.723	49.861	134.547	1.00	63.29
	4427	CG	LEU C 118	5.351	49.923	135.932	1.00	63.95
	4428	CD1	LEU C 118	4.533	49.085	136.902	1.00	62.50
	4429	CD2	LEU C 118	6.791	49.438	135.852	1.00	63.07
	4430	C	LEU C 118	4.371	50.600	132.225	1.00	60.28
35	4431	O	LEU C 118	3.220	50.904	131.935	1.00	62.17
	4432	N	PRO C 119	5.159	49.917	131.383	1.00	59.08
	4433	CD	PRO C 119	6.600	49.645	131.529	1.00	54.66
	4434	CA	PRO C 119	4.663	49.476	130.070	1.00	59.07
	4435	CB	PRO C 119	5.895	48.843	129.423	1.00	54.86
40	4436	CG	PRO C 119	7.045	49.537	130.096	1.00	53.90
	4437	C	PRO C 119	3.567	48.432	130.314	1.00	60.63
	4438	O	PRO C 119	3.703	47.604	131.210	1.00	63.38
	4439	N	LYS C 120	2.494	48.456	129.532	1.00	61.40

	4440	CA	LYS	C	120	1.415	47.489	129.720	1.00	63.20
	4441	CB	LYS	C	120	0.403	47.591	128.577	1.00	64.08
	4442	CG	LYS	C	120	-0.695	46.529	128.649	1.00	70.62
	4443	CD	LYS	C	120	-1.299	46.209	127.285	1.00	74.30
5	4444	CE	LYS	C	120	-2.265	45.032	127.382	1.00	75.36
	4445	NZ	LYS	C	120	-2.812	44.609	126.065	1.00	79.11
	4446	C	LYS	C	120	1.912	46.038	129.800	1.00	65.83
	4447	O	LYS	C	120	1.241	45.161	130.350	1.00	68.00
	4448	N	GLN	C	121	3.092	45.790	129.252	1.00	64.42
10	4449	CA	GLN	C	121	3.661	44.447	129.213	1.00	61.55
	4450	CB	GLN	C	121	4.749	44.407	128.138	1.00	67.96
	4451	CG	GLN	C	121	5.430	43.073	127.924	1.00	73.00
	4452	CD	GLN	C	121	6.555	43.188	126.910	1.00	77.34
	4453	OE1	GLN	C	121	7.380	44.101	126.997	1.00	81.52
15	4454	NE2	GLN	C	121	6.595	42.267	125.947	1.00	75.88
	4455	C	GLN	C	121	4.227	43.986	130.547	1.00	57.43
	4456	O	GLN	C	121	3.992	42.855	130.976	1.00	51.69
	4457	N	THR	C	122	4.990	44.859	131.193	1.00	54.95
	4458	CA	THR	C	122	5.588	44.517	132.471	1.00	53.09
20	4459	CB	THR	C	122	6.786	45.437	132.786	1.00	54.04
	4460	OG1	THR	C	122	6.370	46.807	132.738	1.00	61.46
	4461	CG2	THR	C	122	7.888	45.223	131.773	1.00	53.49
	4462	C	THR	C	122	4.568	44.580	133.609	1.00	49.16
	4463	O	THR	C	122	4.612	43.765	134.529	1.00	43.66
25	4464	N	PHE	C	123	3.656	45.546	133.542	1.00	44.60
	4465	CA	PHE	C	123	2.630	45.700	134.562	1.00	46.54
	4466	CB	PHE	C	123	1.749	46.907	134.251	1.00	48.52
	4467	CG	PHE	C	123	0.557	47.027	135.142	1.00	47.64
	4468	CD1	PHE	C	123	0.661	47.629	136.387	1.00	48.19
30	4469	CD2	PHE	C	123	-0.674	46.514	134.745	1.00	49.10
	4470	CE1	PHE	C	123	-0.452	47.717	137.231	1.00	49.08
	4471	CE2	PHE	C	123	-1.784	46.596	135.576	1.00	48.70
	4472	CZ	PHE	C	123	-1.671	47.200	136.826	1.00	47.27
	4473	C	PHE	C	123	1.774	44.440	134.603	1.00	48.23
35	4474	O	PHE	C	123	1.224	44.083	135.641	1.00	48.30
	4475	N	GLU	C	124	1.656	43.768	133.465	1.00	50.07
	4476	CA	GLU	C	124	0.878	42.541	133.410	1.00	50.89
	4477	CB	GLU	C	124	0.401	42.259	131.989	1.00	56.25
	4478	CG	GLU	C	124	-0.891	42.961	131.631	1.00	63.86
40	4479	CD	GLU	C	124	-1.241	42.795	130.167	1.00	72.04
	4480	OE1	GLU	C	124	-2.367	43.176	129.776	1.00	74.31
	4481	OE2	GLU	C	124	-0.384	42.285	129.405	1.00	74.57
	4482	C	GLU	C	124	1.696	41.366	133.921	1.00	47.43

	4483	O	GLU C 124	1.144	40.435	134.492	1.00	45.94
	4484	N	ALA C 125	3.008	41.406	133.708	1.00	45.60
	4485	CA	ALA C 125	3.873	40.337	134.185	1.00	45.26
	4486	CB	ALA C 125	5.247	40.458	133.572	1.00	43.59
5	4487	C	ALA C 125	3.965	40.436	135.706	1.00	46.19
	4488	O	ALA C 125	4.113	39.434	136.392	1.00	49.50
	4489	N	LEU C 126	3.868	41.652	136.228	1.00	44.37
	4490	CA	LEU C 126	3.938	41.851	137.659	1.00	43.90
	4491	CB	LEU C 126	4.142	43.324	137.995	1.00	47.09
10	4492	CG	LEU C 126	5.534	43.910	137.772	1.00	56.05
	4493	CD1	LEU C 126	5.486	45.396	138.094	1.00	55.29
	4494	CD2	LEU C 126	6.565	43.189	138.642	1.00	51.74
	4495	C	LEU C 126	2.669	41.355	138.336	1.00	44.20
	4496	O	LEU C 126	2.745	40.538	139.247	1.00	43.01
15	4497	N	THR C 127	1.510	41.849	137.905	1.00	38.69
	4498	CA	THR C 127	0.258	41.429	138.511	1.00	43.89
	4499	CB	THR C 127	-0.975	42.078	137.806	1.00	44.40
	4500	OG1	THR C 127	-1.186	41.483	136.523	1.00	52.01
	4501	CG2	THR C 127	-0.760	43.560	137.627	1.00	35.77
20	4502	C	THR C 127	0.138	39.888	138.502	1.00	45.75
	4503	O	THR C 127	-0.196	39.281	139.521	1.00	46.43
	4504	N	LYS C 128	0.443	39.260	137.369	1.00	43.51
	4505	CA	LYS C 128	0.374	37.809	137.268	1.00	43.22
	4506	CB	LYS C 128	0.810	37.328	135.879	1.00	46.50
25	4507	CG	LYS C 128	-0.320	37.255	134.846	1.00	53.06
	4508	CD	LYS C 128	0.206	37.317	133.395	1.00	54.08
	4509	CE	LYS C 128	1.217	36.210	133.079	1.00	55.38
	4510	NZ	LYS C 128	1.772	36.307	131.690	1.00	54.80
	4511	C	LYS C 128	1.243	37.151	138.318	1.00	41.13
30	4512	O	LYS C 128	0.823	36.168	138.921	1.00	42.15
	4513	N	ALA C 129	2.448	37.676	138.544	1.00	37.07
	4514	CA	ALA C 129	3.332	37.080	139.550	1.00	32.17
	4515	CB	ALA C 129	4.695	37.696	139.486	1.00	32.08
	4516	C	ALA C 129	2.734	37.262	140.949	1.00	33.20
35	4517	O	ALA C 129	2.764	36.357	141.772	1.00	33.88
	4518	N	GLU C 130	2.173	38.430	141.209	1.00	30.81
	4519	CA	GLU C 130	1.572	38.681	142.499	1.00	37.35
	4520	CB	GLU C 130	1.188	40.154	142.629	1.00	34.26
	4521	CG	GLU C 130	2.331	41.052	143.030	1.00	46.91
40	4522	CD	GLU C 130	1.986	42.533	142.904	1.00	52.02
	4523	OE1	GLU C 130	0.820	42.901	143.175	1.00	55.37
	4524	OE2	GLU C 130	2.883	43.330	142.541	1.00	55.68
	4525	C	GLU C 130	0.338	37.800	142.733	1.00	40.32

	4526	O	GLU C 130	0.185	37.232	143.812	1.00	38.84
	4527	N	GLU C 131	-0.542	37.696	141.735	1.00	42.99
	4528	CA	GLU C 131	-1.754	36.870	141.863	1.00	41.94
	4529	CB	GLU C 131	-2.699	37.113	140.689	1.00	42.52
5	4530	CG	GLU C 131	-3.172	38.545	140.567	1.00	49.00
	4531	CD	GLU C 131	-3.993	38.770	139.316	1.00	56.19
	4532	OE1	GLU C 131	-3.615	38.233	138.243	1.00	54.60
	4533	OE2	GLU C 131	-5.007	39.495	139.406	1.00	57.39
	4534	C	GLU C 131	-1.403	35.385	141.941	1.00	36.97
10	4535	O	GLU C 131	-2.041	34.619	142.647	1.00	37.41
	4536	N	LEU C 132	-0.373	34.978	141.222	1.00	36.31
	4537	CA	LEU C 132	0.039	33.593	141.269	1.00	34.02
	4538	CB	LEU C 132	1.217	33.344	140.336	1.00	31.89
	4539	CG	LEU C 132	1.899	32.008	140.646	1.00	32.55
15	4540	CD1	LEU C 132	0.931	30.865	140.348	1.00	36.20
	4541	CD2	LEU C 132	3.152	31.867	139.838	1.00	29.32
	4542	C	LEU C 132	0.476	33.194	142.665	1.00	39.07
	4543	O	LEU C 132	0.145	32.109	143.140	1.00	41.88
	4544	N	THR C 133	1.223	34.085	143.316	1.00	38.62
20	4545	CA	THR C 133	1.809	33.822	144.629	1.00	29.37
	4546	CB	THR C 133	3.287	34.243	144.610	1.00	33.30
	4547	OG1	THR C 133	3.374	35.643	144.313	1.00	37.89
	4548	CG2	THR C 133	4.046	33.494	143.542	1.00	23.91
	4549	C	THR C 133	1.164	34.446	145.861	1.00	23.23
25	4550	O	THR C 133	1.678	34.287	146.972	1.00	25.92
	4551	N	LYS C 134	0.026	35.103	145.696	1.00	20.63
	4552	CA	LYS C 134	-0.596	35.797	146.816	1.00	26.69
	4553	CB	LYS C 134	-1.834	36.560	146.340	1.00	29.11
	4554	CG	LYS C 134	-3.075	35.710	146.032	1.00	38.30
30	4555	CD	LYS C 134	-4.295	36.618	145.798	1.00	37.37
	4556	CE	LYS C 134	-5.595	35.825	145.708	1.00	47.49
	4557	NZ	LYS C 134	-6.770	36.698	145.378	1.00	53.34
	4558	C	LYS C 134	-0.952	35.020	148.088	1.00	35.20
	4559	O	LYS C 134	-1.166	35.642	149.137	1.00	33.49
35	4560	N	ASN C 135	-1.032	33.689	148.008	1.00	31.97
	4561	CA	ASN C 135	-1.376	32.880	149.175	1.00	30.03
	4562	CB	ASN C 135	-2.286	31.702	148.799	1.00	27.20
	4563	CG	ASN C 135	-3.501	32.112	148.044	1.00	32.30
	4564	OD1	ASN C 135	-4.279	32.953	148.500	1.00	33.62
40	4565	ND2	ASN C 135	-3.700	31.500	146.875	1.00	29.74
	4566	C	ASN C 135	-0.116	32.281	149.793	1.00	27.47
	4567	O	ASN C 135	-0.164	31.714	150.899	1.00	27.25
	4568	N	ASN C 136	0.998	32.364	149.078	1.00	21.13

	4569	CA	ASN C 136	2.220	31.772	149.587	1.00	23.82
	4570	CB	ASN C 136	3.324	31.886	148.550	1.00	31.72
	4571	CG	ASN C 136	2.972	31.145	147.252	1.00	36.09
	4572	OD1	ASN C 136	1.806	30.782	147.020	1.00	33.17
5	4573	ND2	ASN C 136	3.972	30.939	146.393	1.00	32.31
	4574	C	ASN C 136	2.613	32.365	150.937	1.00	33.45
	4575	O	ASN C 136	2.464	33.573	151.189	1.00	27.62
	4576	N	THR C 137	3.109	31.491	151.812	1.00	35.22
	4577	CA	THR C 137	3.434	31.882	153.170	1.00	31.42
10	4578	CB	THR C 137	2.616	31.010	154.151	1.00	35.30
	4579	OG1	THR C 137	3.011	29.645	153.985	1.00	26.96
	4580	CG2	THR C 137	1.126	31.120	153.867	1.00	26.14
	4581	C	THR C 137	4.907	31.812	153.561	1.00	30.15
	4582	O	THR C 137	5.235	31.879	154.744	1.00	37.21
15	4583	N	GLY C 138	5.789	31.624	152.596	1.00	27.48
	4584	CA	GLY C 138	7.207	31.614	152.911	1.00	25.54
	4585	C	GLY C 138	7.764	33.027	152.659	1.00	29.42
	4586	O	GLY C 138	7.020	34.014	152.670	1.00	24.97
	4587	N	LEU C 139	9.069	33.124	152.437	1.00	27.16
20	4588	CA	LEU C 139	9.745	34.397	152.155	1.00	31.50
	4589	CB	LEU C 139	11.121	34.112	151.573	1.00	32.48
	4590	CG	LEU C 139	11.777	35.330	150.944	1.00	38.95
	4591	CD1	LEU C 139	12.211	36.244	152.058	1.00	41.22
	4592	CD2	LEU C 139	12.971	34.923	150.100	1.00	39.90
25	4593	C	LEU C 139	9.011	35.328	151.178	1.00	32.73
	4594	O	LEU C 139	8.460	34.876	150.186	1.00	36.70
	4595	N	ILE C 140	9.008	36.629	151.456	1.00	36.14
	4596	CA	ILE C 140	8.367	37.591	150.557	1.00	33.30
	4597	CB	ILE C 140	7.641	38.688	151.340	1.00	30.43
30	4598	CG2	ILE C 140	7.125	39.773	150.393	1.00	24.34
	4599	CG1	ILE C 140	6.507	38.068	152.151	1.00	32.72
	4600	CD1	ILE C 140	5.577	39.089	152.793	1.00	34.82
	4601	C	ILE C 140	9.448	38.246	149.678	1.00	39.29
	4602	O	ILE C 140	10.381	38.862	150.194	1.00	40.35
35	4603	N	LEU C 141	9.344	38.072	148.359	1.00	40.55
	4604	CA	LEU C 141	10.290	38.678	147.420	1.00	37.32
	4605	CB	LEU C 141	10.559	37.751	146.250	1.00	32.87
	4606	CG	LEU C 141	11.472	38.352	145.194	1.00	38.60
	4607	CD1	LEU C 141	12.836	38.702	145.829	1.00	40.60
40	4608	CD2	LEU C 141	11.638	37.368	144.063	1.00	27.24
	4609	C	LEU C 141	9.674	39.993	146.924	1.00	42.04
	4610	O	LEU C 141	8.684	40.007	146.179	1.00	38.17
	4611	N	ASN C 142	10.284	41.091	147.373	1.00	43.59



	4612	CA	ASN C 142	9.858	42.457	147.080	1.00	37.85
	4613	CB	ASN C 142	9.954	43.276	148.376	1.00	41.42
	4614	CG	ASN C 142	8.780	44.183	148.583	1.00	45.02
	4615	OD1	ASN C 142	7.646	43.734	148.676	1.00	55.26
5	4616	ND2	ASN C 142	9.042	45.473	148.670	1.00	49.53
	4617	C	ASN C 142	10.748	43.076	145.998	1.00	33.00
	4618	O	ASN C 142	11.934	43.334	146.234	1.00	33.45
	4619	N	PHE C 143	10.172	43.305	144.821	1.00	27.20
	4620	CA	PHE C 143	10.882	43.897	143.674	1.00	30.23
10	4621	CB	PHE C 143	10.313	43.408	142.339	1.00	33.74
	4622	CG	PHE C 143	10.967	42.184	141.804	1.00	32.51
	4623	CD1	PHE C 143	10.394	40.933	142.004	1.00	36.50
	4624	CD2	PHE C 143	12.145	42.283	141.073	1.00	33.66
	4625	CE1	PHE C 143	10.990	39.777	141.473	1.00	42.69
15	4626	CE2	PHE C 143	12.751	41.154	140.542	1.00	41.29
	4627	CZ	PHE C 143	12.168	39.887	140.742	1.00	42.01
	4628	C	PHE C 143	10.692	45.388	143.669	1.00	31.95
	4629	O	PHE C 143	9.553	45.857	143.599	1.00	33.79
	4630	N	ALA C 144	11.786	46.139	143.729	1.00	28.74
20	4631	CA	ALA C 144	11.677	47.591	143.697	1.00	27.17
	4632	CB	ALA C 144	12.732	48.221	144.601	1.00	22.07
	4633	C	ALA C 144	11.887	48.004	142.255	1.00	27.40
	4634	O	ALA C 144	13.002	47.966	141.760	1.00	35.67
	4635	N	LEU C 145	10.812	48.377	141.573	1.00	33.08
25	4636	CA	LEU C 145	10.889	48.783	140.167	1.00	36.13
	4637	CB	LEU C 145	10.008	47.899	139.295	1.00	36.45
	4638	CG	LEU C 145	10.417	46.445	139.279	1.00	41.19
	4639	CD1	LEU C 145	9.258	45.607	138.760	1.00	44.01
	4640	CD2	LEU C 145	11.659	46.290	138.431	1.00	41.90
30	4641	C	LEU C 145	10.385	50.184	140.008	1.00	34.95
	4642	O	LEU C 145	9.369	50.539	140.610	1.00	38.00
	4643	N	ASN C 146	11.066	50.985	139.196	1.00	32.66
	4644	CA	ASN C 146	10.585	52.342	138.994	1.00	35.64
	4645	CB	ASN C 146	9.185	52.272	138.397	1.00	42.83
35	4646	CG	ASN C 146	8.934	53.336	137.389	1.00	50.07
	4647	OD1	ASN C 146	9.695	53.483	136.444	1.00	60.09
	4648	ND2	ASN C 146	7.848	54.083	137.566	1.00	54.53
	4649	C	ASN C 146	10.494	52.927	140.388	1.00	28.83
	4650	O	ASN C 146	9.539	53.623	140.728	1.00	29.80
40	4651	N	TYR C 147	11.494	52.621	141.196	1.00	29.02
	4652	CA	TYR C 147	11.505	53.056	142.584	1.00	26.77
	4653	CB	TYR C 147	11.650	51.823	143.492	1.00	23.80
	4654	CG	TYR C 147	11.870	52.153	144.948	1.00	24.51

	4655	CD1	TYR	C	147	10.788	52.267	145.827	1.00	21.05
	4656	CE1	TYR	C	147	10.974	52.649	147.157	1.00	23.22
	4657	CD2	TYR	C	147	13.157	52.420	145.438	1.00	23.78
	4658	CE2	TYR	C	147	13.358	52.802	146.773	1.00	25.77
5	4659	CZ	TYR	C	147	12.256	52.916	147.622	1.00	25.77
	4660	OH	TYR	C	147	12.429	53.326	148.923	1.00	26.96
	4661	C	TYR	C	147	12.598	54.063	142.936	1.00	24.26
	4662	O	TYR	C	147	13.752	53.921	142.525	1.00	19.48
	4663	N	GLY	C	148	12.199	55.051	143.732	1.00	23.20
10	4664	CA	GLY	C	148	13.093	56.082	144.224	1.00	19.99
	4665	C	GLY	C	148	12.659	56.398	145.646	1.00	20.64
	4666	O	GLY	C	148	11.467	56.610	145.888	1.00	27.37
	4667	N	GLY	C	149	13.609	56.433	146.578	1.00	17.54
	4668	CA	GLY	C	149	13.300	56.706	147.972	1.00	18.72
15	4669	C	GLY	C	149	12.677	58.058	148.237	1.00	21.09
	4670	O	GLY	C	149	11.663	58.176	148.943	1.00	25.28
	4671	N	ARG	C	150	13.277	59.102	147.692	1.00	18.97
	4672	CA	ARG	C	150	12.700	60.415	147.894	1.00	16.95
	4673	CB	ARG	C	150	13.616	61.488	147.335	1.00	18.89
20	4674	CG	ARG	C	150	14.899	61.649	148.103	1.00	18.72
	4675	CD	ARG	C	150	15.754	62.690	147.419	1.00	18.25
	4676	NE	ARG	C	150	16.956	62.991	148.182	1.00	29.35
	4677	CZ	ARG	C	150	17.896	63.851	147.797	1.00	33.24
	4678	NH1	ARG	C	150	17.781	64.500	146.649	1.00	30.92
25	4679	NH2	ARG	C	150	18.946	64.075	148.574	1.00	34.03
	4680	C	ARG	C	150	11.348	60.501	147.193	1.00	19.08
	4681	O	ARG	C	150	10.442	61.177	147.668	1.00	19.23
	4682	N	ALA	C	151	11.215	59.822	146.057	1.00	17.96
	4683	CA	ALA	C	151	9.966	59.876	145.306	1.00	21.55
30	4684	CB	ALA	C	151	10.118	59.149	143.948	1.00	14.32
	4685	C	ALA	C	151	8.911	59.197	146.158	1.00	27.16
	4686	O	ALA	C	151	7.789	59.675	146.274	1.00	22.60
	4687	N	GLU	C	152	9.306	58.080	146.766	1.00	26.55
	4688	CA	GLU	C	152	8.415	57.325	147.620	1.00	25.92
35	4689	CB	GLU	C	152	9.110	56.075	148.128	1.00	23.08
	4690	CG	GLU	C	152	8.296	55.376	149.182	1.00	21.99
	4691	CD	GLU	C	152	9.038	54.238	149.804	1.00	27.72
	4692	OE1	GLU	C	152	10.282	54.327	149.939	1.00	26.76
	4693	OE2	GLU	C	152	8.368	53.261	150.173	1.00	26.93
40	4694	C	GLU	C	152	7.930	58.149	148.802	1.00	25.46
	4695	O	GLU	C	152	6.751	58.135	149.147	1.00	30.63
	4696	N	ILE	C	153	8.845	58.872	149.422	1.00	24.51
	4697	CA	ILE	C	153	8.492	59.710	150.557	1.00	22.15

	4698	CB	ILE C 153	9.771	60.219	151.255	1.00	18.76
	4699	CG2	ILE C 153	9.445	61.218	152.343	1.00	15.00
	4700	CG1	ILE C 153	10.547	59.015	151.807	1.00	19.70
	4701	CD1	ILE C 153	11.845	59.401	152.453	1.00	12.57
5	4702	C	ILE C 153	7.642	60.887	150.098	1.00	24.42
	4703	O	ILE C 153	6.764	61.343	150.826	1.00	23.60
	4704	N	THR C 154	7.901	61.375	148.887	1.00	27.67
	4705	CA	THR C 154	7.147	62.510	148.344	1.00	33.05
	4706	CB	THR C 154	7.771	63.025	147.038	1.00	29.89
10	4707	OG1	THR C 154	9.087	63.514	147.315	1.00	32.23
	4708	CG2	THR C 154	6.929	64.153	146.431	1.00	29.53
	4709	C	THR C 154	5.716	62.076	148.066	1.00	34.66
	4710	O	THR C 154	4.762	62.810	148.330	1.00	32.24
	4711	N	GLN C 155	5.586	60.874	147.525	1.00	31.09
15	4712	CA	GLN C 155	4.295	60.307	147.225	1.00	34.01
	4713	CB	GLN C 155	4.477	58.948	146.550	1.00	32.86
	4714	CG	GLN C 155	3.260	58.036	146.645	1.00	41.82
	4715	CD	GLN C 155	3.250	57.121	147.866	0.50	42.27
	4716	OE1	GLN C 155	2.251	56.448	148.139	0.50	45.72
20	4717	NE2	GLN C 155	4.362	57.079	148.594	0.50	40.46
	4718	C	GLN C 155	3.504	60.141	148.521	1.00	40.92
	4719	O	GLN C 155	2.301	60.397	148.557	1.00	43.33
	4720	N	ALA C 156	4.171	59.708	149.587	1.00	40.28
	4721	CA	ALA C 156	3.466	59.518	150.855	1.00	41.50
25	4722	CB	ALA C 156	4.338	58.776	151.851	1.00	31.31
	4723	C	ALA C 156	3.060	60.877	151.414	1.00	42.38
	4724	O	ALA C 156	2.041	61.000	152.103	1.00	41.62
	4725	N	LEU C 157	3.863	61.896	151.127	1.00	43.35
	4726	CA	LEU C 157	3.549	63.240	151.583	1.00	50.05
30	4727	CB	LEU C 157	4.707	64.200	151.296	1.00	56.43
	4728	CG	LEU C 157	4.371	65.704	151.284	1.00	63.86
	4729	CD1	LEU C 157	3.442	66.091	152.435	1.00	63.15
	4730	CD2	LEU C 157	5.660	66.498	151.353	1.00	66.44
	4731	C	LEU C 157	2.279	63.742	150.888	1.00	52.61
35	4732	O	LEU C 157	1.456	64.414	151.508	1.00	51.25
	4733	N	LYS C 158	2.118	63.430	149.605	1.00	49.91
	4734	CA	LYS C 158	0.918	63.871	148.923	1.00	52.32
	4735	CB	LYS C 158	1.001	63.599	147.415	1.00	54.37
	4736	CG	LYS C 158	1.824	64.645	146.684	1.00	57.56
40	4737	CD	LYS C 158	1.586	64.638	145.180	1.00	66.46
	4738	CE	LYS C 158	2.177	63.411	144.502	1.00	70.25
	4739	NZ	LYS C 158	2.087	63.521	143.013	1.00	72.75
	4740	C	LYS C 158	-0.268	63.152	149.549	1.00	51.48

	4741	O	LYS	C	158	-1.141	63.785	150.134	1.00	53.12
	4742	N	LEU	C	159	-0.289	61.829	149.448	1.00	47.95
	4743	CA	LEU	C	159	-1.375	61.059	150.023	1.00	46.67
	4744	CB	LEU	C	159	-1.000	59.591	150.125	1.00	42.10
5	4745	CG	LEU	C	159	-1.123	58.748	148.866	1.00	47.90
	4746	CD1	LEU	C	159	-0.514	57.353	149.130	1.00	42.88
	4747	CD2	LEU	C	159	-2.593	58.655	148.474	1.00	47.11
	4748	C	LEU	C	159	-1.731	61.565	151.412	1.00	48.84
	4749	O	LEU	C	159	-2.901	61.758	151.717	1.00	50.30
10	4750	N	ILE	C	160	-0.725	61.779	152.256	1.00	48.10
	4751	CA	ILE	C	160	-0.979	62.251	153.612	1.00	42.12
	4752	CB	ILE	C	160	0.317	62.279	154.464	1.00	33.80
	4753	CG2	ILE	C	160	0.124	63.107	155.730	1.00	27.08
	4754	CG1	ILE	C	160	0.711	60.853	154.854	1.00	35.90
15	4755	CD1	ILE	C	160	1.964	60.778	155.721	1.00	30.71
	4756	C	ILE	C	160	-1.624	63.623	153.652	1.00	47.63
	4757	O	ILE	C	160	-2.587	63.828	154.383	1.00	53.80
	4758	N	SER	C	161	-1.101	64.565	152.872	1.00	54.79
	4759	CA	SER	C	161	-1.634	65.925	152.865	1.00	56.36
20	4760	CB	SER	C	161	-0.685	66.870	152.129	1.00	55.27
	4761	OG	SER	C	161	-0.789	66.674	150.734	1.00	55.86
	4762	C	SER	C	161	-3.024	66.014	152.240	1.00	58.24
	4763	O	SER	C	161	-3.780	66.928	152.543	1.00	61.75
	4764	N	GLN	C	162	-3.368	65.079	151.367	1.00	60.91
25	4765	CA	GLN	C	162	-4.693	65.120	150.765	1.00	63.44
	4766	CB	GLN	C	162	-4.782	64.192	149.558	1.00	66.58
	4767	CG	GLN	C	162	-5.915	64.562	148.618	1.00	73.11
	4768	CD	GLN	C	162	-5.897	66.043	148.264	1.00	75.38
	4769	OE1	GLN	C	162	-6.273	66.891	149.077	1.00	77.43
30	4770	NE2	GLN	C	162	-5.443	66.361	147.053	1.00	75.93
	4771	C	GLN	C	162	-5.688	64.674	151.818	1.00	64.83
	4772	O	GLN	C	162	-6.830	65.143	151.857	1.00	67.20
	4773	N	ASP	C	163	-5.245	63.761	152.674	1.00	61.05
	4774	CA	ASP	C	163	-6.090	63.259	153.732	1.00	58.73
35	4775	CB	ASP	C	163	-5.533	61.953	154.284	1.00	56.56
	4776	CG	ASP	C	163	-5.765	60.787	153.343	1.00	58.58
	4777	OD1	ASP	C	163	-6.291	61.021	152.235	1.00	57.64
	4778	OD2	ASP	C	163	-5.421	59.637	153.704	1.00	61.09
	4779	C	ASP	C	163	-6.221	64.292	154.833	1.00	59.79
40	4780	O	ASP	C	163	-7.123	64.206	155.658	1.00	61.10
	4781	N	VAL	C	164	-5.331	65.278	154.850	1.00	57.44
	4782	CA	VAL	C	164	-5.423	66.311	155.868	1.00	57.23
	4783	CB	VAL	C	164	-4.072	67.039	156.075	1.00	57.70

	4784	CG1 VAL C 164	-4.273	68.315	156.890	1.00	56.93
	4785	CG2 VAL C 164	-3.100	66.114	156.809	1.00	57.90
	4786	C VAL C 164	-6.503	67.295	155.434	1.00	57.90
	4787	O VAL C 164	-7.146	67.936	156.267	1.00	56.47
5	4788	N LEU C 165	-6.710	67.400	154.125	1.00	58.68
	4789	CA LEU C 165	-7.740	68.290	153.599	1.00	59.82
	4790	CB LEU C 165	-7.456	68.672	152.141	1.00	57.26
	4791	CG LEU C 165	-6.389	69.735	151.865	1.00	52.27
	4792	CD1 LEU C 165	-6.502	70.161	150.411	1.00	48.22
10	4793	CD2 LEU C 165	-6.572	70.943	152.775	1.00	52.39
	4794	C LEU C 165	-9.103	67.612	153.699	1.00	58.62
	4795	O LEU C 165	-10.119	68.278	153.856	1.00	63.56
	4796	N ASP C 166	-9.118	66.288	153.596	1.00	57.10
	4797	CA ASP C 166	-10.354	65.529	153.707	1.00	56.13
15	4798	CB ASP C 166	-10.224	64.164	153.026	1.00	57.52
	4799	CG ASP C 166	-9.941	64.278	151.539	1.00	60.82
	4800	OD1 ASP C 166	-9.851	65.427	151.042	1.00	59.72
	4801	OD2 ASP C 166	-9.807	63.217	150.875	1.00	59.48
	4802	C ASP C 166	-10.653	65.325	155.185	1.00	55.65
20	4803	O ASP C 166	-11.531	64.540	155.545	1.00	59.75
	4804	N ALA C 167	-9.899	66.026	156.028	1.00	50.15
	4805	CA ALA C 167	-10.049	65.970	157.482	1.00	49.11
	4806	CB ALA C 167	-11.336	66.663	157.898	1.00	50.28
	4807	C ALA C 167	-10.003	64.576	158.092	1.00	48.61
25	4808	O ALA C 167	-10.379	64.394	159.255	1.00	47.68
	4809	N LYS C 168	-9.547	63.595	157.317	1.00	48.78
	4810	CA LYS C 168	-9.457	62.231	157.819	1.00	47.85
	4811	CB LYS C 168	-9.092	61.265	156.695	1.00	48.37
	4812	CG LYS C 168	-10.169	61.117	155.639	1.00	53.23
30	4813	CD LYS C 168	-9.908	59.903	154.762	1.00	54.65
	4814	CE LYS C 168	-11.174	59.440	154.064	1.00	54.00
	4815	NZ LYS C 168	-10.919	58.298	153.125	1.00	56.00
	4816	C LYS C 168	-8.413	62.166	158.918	1.00	48.79
	4817	O LYS C 168	-8.389	61.234	159.721	1.00	50.06
35	4818	N ILE C 169	-7.559	63.182	158.967	1.00	49.58
	4819	CA ILE C 169	-6.514	63.238	159.970	1.00	49.53
	4820	CB ILE C 169	-5.350	62.298	159.573	1.00	51.16
	4821	CG2 ILE C 169	-4.291	63.047	158.784	1.00	50.39
	4822	CG1 ILE C 169	-4.787	61.632	160.826	1.00	56.35
40	4823	CD1 ILE C 169	-4.632	60.104	160.692	1.00	61.39
	4824	C ILE C 169	-6.049	64.680	160.116	1.00	51.38
	4825	O ILE C 169	-6.247	65.503	159.224	1.00	50.06
	4826	N ASN C 170	-5.463	65.000	161.259	1.00	55.38

	4827	CA	ASN C 170	-4.999	66.355	161.485	1.00	59.71
	4828	CB	ASN C 170	-5.379	66.828	162.893	1.00	65.84
	4829	CG	ASN C 170	-6.879	66.735	163.164	1.00	73.16
	4830	OD1	ASN C 170	-7.700	67.258	162.400	1.00	78.58
5	4831	ND2	ASN C 170	-7.242	66.073	164.259	1.00	74.53
	4832	C	ASN C 170	-3.491	66.397	161.330	1.00	60.85
	4833	O	ASN C 170	-2.811	65.375	161.462	1.00	55.85
	4834	N	PRO C 171	-2.947	67.578	161.014	1.00	61.61
	4835	CD	PRO C 171	-3.637	68.807	160.589	1.00	62.89
10	4836	CA	PRO C 171	-1.497	67.706	160.858	1.00	60.64
	4837	CB	PRO C 171	-1.316	69.175	160.432	1.00	62.63
	4838	CG	PRO C 171	-2.596	69.855	160.880	1.00	64.88
	4839	C	PRO C 171	-0.750	67.342	162.153	1.00	58.26
	4840	O	PRO C 171	0.467	67.144	162.149	1.00	57.03
15	4841	N	GLY C 172	-1.488	67.238	163.254	1.00	55.17
	4842	CA	GLY C 172	-0.876	66.875	164.522	1.00	56.02
	4843	C	GLY C 172	-0.844	65.367	164.760	1.00	53.93
	4844	O	GLY C 172	-0.234	64.883	165.715	1.00	52.47
	4845	N	ASP C 173	-1.519	64.627	163.888	1.00	52.98
20	4846	CA	ASP C 173	-1.575	63.172	163.971	1.00	51.33
	4847	CB	ASP C 173	-2.868	62.641	163.331	1.00	58.17
	4848	CG	ASP C 173	-4.132	63.224	163.942	1.00	64.93
	4849	OD1	ASP C 173	-5.174	63.209	163.243	1.00	61.87
	4850	OD2	ASP C 173	-4.092	63.678	165.111	1.00	69.74
25	4851	C	ASP C 173	-0.396	62.600	163.184	1.00	46.90
	4852	O	ASP C 173	-0.106	61.404	163.275	1.00	40.33
	4853	N	ILE C 174	0.247	63.453	162.384	1.00	41.02
	4854	CA	ILE C 174	1.378	63.035	161.555	1.00	39.01
	4855	CB	ILE C 174	1.759	64.121	160.534	1.00	37.57
30	4856	CG2	ILE C 174	2.968	63.657	159.721	1.00	29.58
	4857	CG1	ILE C 174	0.554	64.411	159.625	1.00	33.69
	4858	CD1	ILE C 174	0.768	65.493	158.588	1.00	36.81
	4859	C	ILE C 174	2.580	62.711	162.423	1.00	37.84
	4860	O	ILE C 174	3.152	63.590	163.064	1.00	39.87
35	4861	N	THR C 175	2.942	61.434	162.439	1.00	31.23
	4862	CA	THR C 175	4.046	60.942	163.246	1.00	31.96
	4863	CB	THR C 175	3.526	60.156	164.454	1.00	28.78
	4864	OG1	THR C 175	2.798	59.020	163.975	1.00	30.53
	4865	CG2	THR C 175	2.598	61.002	165.295	1.00	28.80
40	4866	C	THR C 175	4.860	59.968	162.396	1.00	31.08
	4867	O	THR C 175	4.449	59.601	161.309	1.00	30.44
	4868	N	GLU C 176	6.001	59.535	162.915	1.00	30.24
	4869	CA	GLU C 176	6.846	58.601	162.204	1.00	28.02

	4870	CB	GLU C 176	8.067	58.250	163.053	1.00	28.45
	4871	CG	GLU C 176	9.067	59.386	163.078	1.00	29.81
	4872	CD	GLU C 176	10.236	59.097	163.938	1.00	33.40
	4873	OE1	GLU C 176	10.707	57.941	163.938	1.00	38.39
5	4874	OE2	GLU C 176	10.695	60.033	164.610	1.00	44.42
	4875	C	GLU C 176	6.085	57.357	161.835	1.00	27.65
	4876	O	GLU C 176	6.092	56.941	160.680	1.00	28.70
	4877	N	GLU C 177	5.414	56.763	162.808	1.00	30.92
	4878	CA	GLU C 177	4.645	55.556	162.551	1.00	33.32
10	4879	CB	GLU C 177	3.963	55.057	163.837	1.00	44.97
	4880	CG	GLU C 177	3.847	56.083	164.977	1.00	56.94
	4881	CD	GLU C 177	5.193	56.474	165.602	1.00	62.11
	4882	OE1	GLU C 177	5.989	55.561	165.935	1.00	66.88
	4883	OE2	GLU C 177	5.448	57.692	165.772	1.00	59.58
15	4884	C	GLU C 177	3.609	55.806	161.469	1.00	31.83
	4885	O	GLU C 177	3.445	54.997	160.567	1.00	34.44
	4886	N	LEU C 178	2.920	56.936	161.537	1.00	29.58
	4887	CA	LEU C 178	1.922	57.227	160.517	1.00	32.80
	4888	CB	LEU C 178	1.256	58.579	160.783	1.00	32.80
20	4889	CG	LEU C 178	0.169	58.899	159.747	1.00	36.92
	4890	CD1	LEU C 178	-0.943	57.873	159.890	1.00	39.85
	4891	CD2	LEU C 178	-0.373	60.304	159.945	1.00	41.35
	4892	C	LEU C 178	2.507	57.230	159.103	1.00	34.82
	4893	O	LEU C 178	1.967	56.593	158.194	1.00	37.07
25	4894	N	ILE C 179	3.602	57.964	158.916	1.00	33.26
	4895	CA	ILE C 179	4.258	58.052	157.616	1.00	29.81
	4896	CB	ILE C 179	5.524	58.954	157.715	1.00	27.58
	4897	CG2	ILE C 179	6.453	58.742	156.518	1.00	22.33
	4898	CG1	ILE C 179	5.084	60.412	157.798	1.00	24.61
30	4899	CD1	ILE C 179	6.174	61.360	158.248	1.00	28.30
	4900	C	ILE C 179	4.616	56.653	157.116	1.00	31.95
	4901	O	ILE C 179	4.460	56.347	155.935	1.00	34.37
	4902	N	GLY C 180	5.078	55.796	158.019	1.00	28.49
	4903	CA	GLY C 180	5.426	54.443	157.624	1.00	28.47
35	4904	C	GLY C 180	4.293	53.678	156.953	1.00	31.30
	4905	O	GLY C 180	4.544	52.796	156.129	1.00	30.57
	4906	N	ASN C 181	3.052	53.994	157.320	1.00	33.14
	4907	CA	ASN C 181	1.877	53.343	156.741	1.00	33.85
	4908	CB	ASN C 181	0.622	53.543	157.607	1.00	33.71
40	4909	CG	ASN C 181	0.741	52.916	158.990	1.00	35.98
	4910	OD1	ASN C 181	1.314	51.841	159.161	1.00	37.44
	4911	ND2	ASN C 181	0.173	53.583	159.983	1.00	29.23
	4912	C	ASN C 181	1.579	53.887	155.350	1.00	34.75

	4913	O	ASN C 181	0.742	53.330	154.650	1.00	38.13
	4914	N	TYR C 182	2.227	54.982	154.952	1.00	31.66
	4915	CA	TYR C 182	1.985	55.529	153.609	1.00	28.77
	4916	CB	TYR C 182	1.770	57.034	153.642	1.00	28.76
5	4917	CG	TYR C 182	0.439	57.491	154.197	1.00	32.33
	4918	CD1	TYR C 182	0.189	57.485	155.571	1.00	31.59
	4919	CE1	TYR C 182	-1.007	57.971	156.085	1.00	34.14
	4920	CD2	TYR C 182	-0.551	57.987	153.348	1.00	33.70
	4921	CE2	TYR C 182	-1.752	58.477	153.851	1.00	35.52
10	4922	CZ	TYR C 182	-1.971	58.468	155.219	1.00	37.64
	4923	OH	TYR C 182	-3.143	58.983	155.719	1.00	44.98
	4924	C	TYR C 182	3.088	55.245	152.590	1.00	29.74
	4925	O	TYR C 182	2.981	55.658	151.437	1.00	33.93
	4926	N	LEU C 183	4.136	54.542	153.004	1.00	26.06
15	4927	CA	LEU C 183	5.235	54.229	152.105	1.00	27.15
	4928	CB	LEU C 183	6.521	54.056	152.914	1.00	20.07
	4929	CG	LEU C 183	6.992	55.221	153.781	1.00	19.89
	4930	CD1	LEU C 183	8.082	54.734	154.708	1.00	12.99
	4931	CD2	LEU C 183	7.482	56.363	152.908	1.00	20.52
20	4932	C	LEU C 183	4.934	52.964	151.302	1.00	29.82
	4933	O	LEU C 183	3.999	52.237	151.612	1.00	32.98
	4934	N	PHE C 184	5.735	52.684	150.282	1.00	30.84
	4935	CA	PHE C 184	5.495	51.510	149.455	1.00	29.54
	4936	CB	PHE C 184	6.476	51.467	148.282	1.00	31.45
25	4937	CG	PHE C 184	6.318	52.607	147.314	1.00	29.11
	4938	CD1	PHE C 184	7.399	53.050	146.561	1.00	30.51
	4939	CD2	PHE C 184	5.102	53.241	147.167	1.00	29.31
	4940	CE1	PHE C 184	7.265	54.112	145.682	1.00	29.06
	4941	CE2	PHE C 184	4.958	54.307	146.287	1.00	33.15
30	4942	CZ	PHE C 184	6.039	54.739	145.549	1.00	33.99
	4943	C	PHE C 184	5.597	50.217	150.232	1.00	34.50
	4944	O	PHE C 184	5.004	49.214	149.853	1.00	41.03
	4945	N	THR C 185	6.369	50.223	151.310	1.00	34.92
	4946	CA	THR C 185	6.527	49.026	152.111	1.00	26.55
35	4947	CB	THR C 185	7.849	49.069	152.864	1.00	32.13
	4948	OG1	THR C 185	7.990	50.353	153.486	1.00	30.89
	4949	CG2	THR C 185	9.017	48.814	151.918	1.00	31.31
	4950	C	THR C 185	5.389	48.797	153.126	1.00	27.03
	4951	O	THR C 185	5.439	47.849	153.897	1.00	26.03
40	4952	N	GLN C 186	4.377	49.660	153.142	1.00	30.35
	4953	CA	GLN C 186	3.254	49.506	154.075	1.00	36.27
	4954	CB	GLN C 186	2.210	50.589	153.838	1.00	38.60
	4955	CG	GLN C 186	1.759	50.637	152.392	1.00	44.27



	4956	CD	GLN C 186	0.423	51.286	152.230	1.00	48.23
	4957	OE1	GLN C 186	-0.601	50.704	152.589	1.00	56.24
	4958	NE2	GLN C 186	0.411	52.505	151.694	1.00	52.86
	4959	C	GLN C 186	2.576	48.153	153.879	1.00	42.97
5	4960	O	GLN C 186	1.960	47.620	154.801	1.00	43.97
	4961	N	HIS C 187	2.697	47.625	152.662	1.00	49.11
	4962	CA	HIS C 187	2.118	46.346	152.267	1.00	52.45
	4963	CB	HIS C 187	2.089	46.212	150.739	1.00	58.05
	4964	CG	HIS C 187	1.334	47.301	150.042	1.00	64.76
10	4965	CD2	HIS C 187	1.724	48.195	149.103	1.00	69.52
	4966	ND1	HIS C 187	0.007	47.571	150.301	1.00	69.82
	4967	CE1	HIS C 187	-0.387	48.586	149.553	1.00	72.94
	4968	NE2	HIS C 187	0.636	48.983	148.816	1.00	74.26
	4969	C	HIS C 187	2.906	45.181	152.815	1.00	52.68
15	4970	O	HIS C 187	2.882	44.103	152.230	1.00	56.51
	4971	N	LEU C 188	3.635	45.401	153.906	1.00	52.26
	4972	CA	LEU C 188	4.425	44.340	154.522	1.00	47.48
	4973	CB	LEU C 188	5.923	44.613	154.424	1.00	46.87
	4974	CG	LEU C 188	6.684	44.546	153.105	1.00	48.02
20	4975	CD1	LEU C 188	8.166	44.766	153.376	1.00	44.05
	4976	CD2	LEU C 188	6.469	43.198	152.443	1.00	49.60
	4977	C	LEU C 188	4.056	44.301	155.975	1.00	50.25
	4978	O	LEU C 188	3.695	45.316	156.551	1.00	52.30
	4979	N	PRO C 189	4.125	43.119	156.594	1.00	55.49
25	4980	CD	PRO C 189	4.529	41.801	156.077	1.00	56.15
	4981	CA	PRO C 189	3.776	43.056	158.016	1.00	55.68
	4982	CB	PRO C 189	4.204	41.641	158.428	1.00	56.18
	4983	CG	PRO C 189	5.120	41.169	157.299	1.00	56.79
	4984	C	PRO C 189	4.518	44.147	158.770	1.00	57.91
30	4985	O	PRO C 189	5.678	44.432	158.475	1.00	58.02
	4986	N	LYS C 190	3.835	44.756	159.732	1.00	58.62
	4987	CA	LYS C 190	4.391	45.841	160.531	1.00	59.99
	4988	CB	LYS C 190	3.492	46.103	161.738	1.00	66.56
	4989	CG	LYS C 190	2.071	46.503	161.401	1.00	75.55
35	4990	CD	LYS C 190	1.969	47.977	161.055	1.00	80.27
	4991	CE	LYS C 190	0.515	48.375	160.833	1.00	85.30
	4992	NZ	LYS C 190	0.363	49.818	160.498	1.00	88.44
	4993	C	LYS C 190	5.826	45.683	161.036	1.00	57.66
	4994	O	LYS C 190	6.650	46.579	160.871	1.00	59.10
40	4995	N	ASP C 191	6.127	44.553	161.659	1.00	54.53
	4996	CA	ASP C 191	7.454	44.347	162.236	1.00	48.27
	4997	CB	ASP C 191	7.365	43.343	163.389	1.00	50.26
	4998	CG	ASP C 191	7.221	41.915	162.897	0.50	55.09

	4999	OD1	ASP	C	191	6.285	41.643	162.109	0.50	58.18
	5000	OD2	ASP	C	191	8.048	41.064	163.295	0.50	57.52
	5001	C	ASP	C	191	8.506	43.876	161.249	1.00	41.26
	5002	O	ASP	C	191	9.586	43.441	161.651	1.00	43.23
5	5003	N	LEU	C	192	8.213	43.965	159.960	1.00	35.50
	5004	CA	LEU	C	192	9.173	43.514	158.955	1.00	33.52
	5005	CB	LEU	C	192	8.695	42.196	158.345	1.00	36.23
	5006	CG	LEU	C	192	8.687	40.945	159.219	1.00	33.76
	5007	CD1	LEU	C	192	7.751	39.926	158.593	1.00	36.75
10	5008	CD2	LEU	C	192	10.102	40.383	159.340	1.00	34.98
	5009	C	LEU	C	192	9.371	44.527	157.840	1.00	28.25
	5010	O	LEU	C	192	10.059	44.257	156.849	1.00	29.01
	5011	N	ARG	C	193	8.763	45.691	157.998	1.00	24.92
	5012	CA	ARG	C	193	8.852	46.729	156.982	1.00	29.02
15	5013	CB	ARG	C	193	7.884	47.841	157.326	1.00	24.96
	5014	CG	ARG	C	193	6.435	47.458	157.056	1.00	34.42
	5015	CD	ARG	C	193	5.520	48.425	157.744	1.00	35.73
	5016	NE	ARG	C	193	4.138	48.314	157.308	1.00	39.32
	5017	CZ	ARG	C	193	3.174	49.117	157.751	1.00	46.47
20	5018	NH1	ARG	C	193	3.476	50.068	158.636	1.00	37.90
	5019	NH2	ARG	C	193	1.922	48.978	157.309	1.00	44.64
	5020	C	ARG	C	193	10.251	47.304	156.733	1.00	30.35
	5021	O	ARG	C	193	10.564	47.679	155.605	1.00	26.18
	5022	N	ASP	C	194	11.085	47.338	157.773	1.00	24.51
25	5023	CA	ASP	C	194	12.432	47.894	157.667	1.00	27.72
	5024	CB	ASP	C	194	12.738	48.799	158.867	1.00	23.30
	5025	CG	ASP	C	194	11.722	49.893	159.048	1.00	25.79
	5026	OD1	ASP	C	194	11.015	50.271	158.071	1.00	20.35
	5027	OD2	ASP	C	194	11.643	50.386	160.186	1.00	32.44
30	5028	C	ASP	C	194	13.547	46.866	157.580	1.00	28.06
	5029	O	ASP	C	194	13.686	46.010	158.447	1.00	30.35
	5030	N	PRO	C	195	14.395	46.976	156.556	1.00	26.27
	5031	CD	PRO	C	195	14.468	48.021	155.527	1.00	27.22
	5032	CA	PRO	C	195	15.494	46.018	156.417	1.00	26.36
35	5033	CB	PRO	C	195	16.260	46.530	155.201	1.00	21.99
	5034	CG	PRO	C	195	15.235	47.324	154.451	1.00	34.10
	5035	C	PRO	C	195	16.378	46.052	157.653	1.00	27.98
	5036	O	PRO	C	195	16.671	47.130	158.180	1.00	25.94
	5037	N	ASP	C	196	16.823	44.884	158.098	1.00	24.12
40	5038	CA	ASP	C	196	17.721	44.824	159.241	1.00	25.36
	5039	CB	ASP	C	196	17.585	43.481	159.947	1.00	26.45
	5040	CG	ASP	C	196	16.204	43.262	160.478	1.00	33.22
	5041	OD1	ASP	C	196	15.354	42.678	159.768	1.00	34.87

	5042	OD2	ASP	C	196	15.957	43.708	161.610	1.00	33.48
	5043	C	ASP	C	196	19.140	44.943	158.694	1.00	25.24
	5044	O	ASP	C	196	20.074	45.356	159.395	1.00	20.54
	5045	N	LEU	C	197	19.273	44.565	157.425	1.00	19.39
5	5046	CA	LEU	C	197	20.546	44.541	156.730	1.00	24.07
	5047	CB	LEU	C	197	21.135	43.125	156.794	1.00	22.73
	5048	CG	LEU	C	197	22.333	42.772	155.900	1.00	27.97
	5049	CD1	LEU	C	197	23.576	43.472	156.436	1.00	27.00
	5050	CD2	LEU	C	197	22.544	41.246	155.851	1.00	26.02
10	5051	C	LEU	C	197	20.356	44.917	155.277	1.00	22.28
	5052	O	LEU	C	197	19.438	44.437	154.638	1.00	31.92
	5053	N	ILE	C	198	21.216	45.781	154.754	1.00	26.20
	5054	CA	ILE	C	198	21.132	46.161	153.350	1.00	22.86
	5055	CB	ILE	C	198	20.883	47.679	153.166	1.00	23.16
15	5056	CG2	ILE	C	198	20.931	48.039	151.686	1.00	18.85
	5057	CG1	ILE	C	198	19.508	48.063	153.713	1.00	21.62
	5058	CD1	ILE	C	198	19.247	49.567	153.720	1.00	16.00
	5059	C	ILE	C	198	22.478	45.774	152.762	1.00	21.51
	5060	O	ILE	C	198	23.515	46.065	153.342	1.00	23.20
20	5061	N	ILE	C	199	22.451	45.092	151.624	1.00	25.25
	5062	CA	ILE	C	199	23.662	44.638	150.957	1.00	21.84
	5063	CB	ILE	C	199	23.556	43.147	150.581	1.00	25.99
	5064	CG2	ILE	C	199	24.788	42.714	149.781	1.00	24.20
	5065	CG1	ILE	C	199	23.382	42.289	151.825	1.00	28.62
25	5066	CD1	ILE	C	199	22.881	40.873	151.530	1.00	27.42
	5067	C	ILE	C	199	23.887	45.380	149.648	1.00	23.23
	5068	O	ILE	C	199	22.951	45.597	148.883	1.00	25.51
	5069	N	ARG	C	200	25.115	45.791	149.375	1.00	28.25
	5070	CA	ARG	C	200	25.362	46.398	148.084	1.00	28.57
30	5071	CB	ARG	C	200	25.674	47.876	148.164	1.00	33.46
	5072	CG	ARG	C	200	25.994	48.399	146.765	1.00	37.72
	5073	CD	ARG	C	200	25.242	49.668	146.414	1.00	33.99
	5074	NE	ARG	C	200	25.428	50.006	145.007	1.00	29.47
	5075	CZ	ARG	C	200	25.058	51.160	144.475	1.00	29.98
35	5076	NH1	ARG	C	200	24.490	52.081	145.241	1.00	30.85
	5077	NH2	ARG	C	200	25.246	51.394	143.188	1.00	33.63
	5078	C	ARG	C	200	26.529	45.683	147.440	1.00	31.01
	5079	O	ARG	C	200	27.579	45.507	148.068	1.00	30.35
	5080	N	THR	C	201	26.324	45.257	146.194	1.00	30.16
40	5081	CA	THR	C	201	27.333	44.551	145.435	1.00	28.51
	5082	CB	THR	C	201	26.717	43.376	144.649	1.00	34.76
	5083	OG1	THR	C	201	25.649	43.849	143.822	1.00	37.16
	5084	CG2	THR	C	201	26.189	42.322	145.592	1.00	34.48

	5085	C	THR C 201	28.045	45.482	144.459	1.00	35.04
	5086	O	THR C 201	27.687	46.659	144.325	1.00	33.67
	5087	N	SER C 202	29.072	44.935	143.806	1.00	38.01
	5088	CA	SER C 202	29.909	45.619	142.813	1.00	37.37
5	5089	CB	SER C 202	29.063	46.183	141.672	1.00	40.22
	5090	OG	SER C 202	29.900	46.513	140.574	1.00	40.85
	5091	C	SER C 202	30.836	46.710	143.332	1.00	38.53
	5092	O	SER C 202	31.278	47.569	142.567	1.00	39.18
	5093	N	GLY C 203	31.117	46.684	144.632	1.00	37.89
10	5094	CA	GLY C 203	32.045	47.637	145.216	1.00	35.59
	5095	C	GLY C 203	31.670	49.090	145.441	1.00	37.34
	5096	O	GLY C 203	32.517	49.854	145.897	1.00	37.41
	5097	N	GLU C 204	30.437	49.491	145.152	1.00	37.78
	5098	CA	GLU C 204	30.054	50.891	145.354	1.00	38.58
15	5099	CB	GLU C 204	28.937	51.284	144.389	1.00	43.16
	5100	CG	GLU C 204	29.324	51.210	142.913	1.00	57.01
	5101	CD	GLU C 204	30.650	51.905	142.595	1.00	61.45
	5102	OE1	GLU C 204	30.830	53.078	142.991	1.00	64.75
	5103	OE2	GLU C 204	31.510	51.273	141.938	1.00	66.61
20	5104	C	GLU C 204	29.614	51.187	146.780	1.00	37.32
	5105	O	GLU C 204	28.776	50.478	147.337	1.00	39.96
	5106	N	LEU C 205	30.182	52.230	147.380	1.00	37.16
	5107	CA	LEU C 205	29.810	52.591	148.747	1.00	32.46
	5108	CB	LEU C 205	31.043	52.845	149.618	1.00	35.23
25	5109	CG	LEU C 205	32.115	51.770	149.774	1.00	37.71
	5110	CD1	LEU C 205	32.850	52.010	151.079	1.00	35.11
	5111	CD2	LEU C 205	31.497	50.394	149.790	1.00	38.62
	5112	C	LEU C 205	28.917	53.817	148.762	1.00	27.22
	5113	O	LEU C 205	29.371	54.942	148.972	1.00	26.48
30	5114	N	ARG C 206	27.639	53.579	148.514	1.00	28.70
	5115	CA	ARG C 206	26.634	54.624	148.506	1.00	33.37
	5116	CB	ARG C 206	26.818	55.535	147.285	1.00	28.37
	5117	CG	ARG C 206	26.640	54.875	145.942	1.00	35.73
	5118	CD	ARG C 206	26.547	55.952	144.848	1.00	40.54
35	5119	NE	ARG C 206	27.812	56.083	144.156	1.00	45.85
	5120	CZ	ARG C 206	28.163	55.327	143.125	1.00	53.44
	5121	NH1	ARG C 206	27.322	54.405	142.662	1.00	54.01
	5122	NH2	ARG C 206	29.369	55.459	142.592	1.00	54.98
	5123	C	ARG C 206	25.315	53.873	148.479	1.00	34.40
40	5124	O	ARG C 206	25.299	52.686	148.176	1.00	39.08
	5125	N	LEU C 207	24.210	54.534	148.807	1.00	37.94
	5126	CA	LEU C 207	22.917	53.838	148.844	1.00	35.15
	5127	CB	LEU C 207	22.158	54.232	150.113	1.00	43.73

	5128	CG	LEU C 207	22.701	53.583	151.389	1.00	46.77
	5129	CD1	LEU C 207	22.138	54.305	152.604	1.00	48.63
	5130	CD2	LEU C 207	22.343	52.084	151.387	1.00	43.20
	5131	C	LEU C 207	22.011	54.034	147.636	1.00	33.96
5	5132	O	LEU C 207	21.064	53.283	147.432	1.00	35.09
	5133	N	SER C 208	22.280	55.057	146.846	1.00	26.70
	5134	CA	SER C 208	21.484	55.292	145.660	1.00	27.73
	5135	CB	SER C 208	21.740	54.176	144.644	1.00	29.65
	5136	OG	SER C 208	23.096	54.172	144.247	1.00	30.96
10	5137	C	SER C 208	19.979	55.453	145.853	1.00	27.23
	5138	O	SER C 208	19.205	54.897	145.085	1.00	22.52
	5139	N	ASN C 209	19.565	56.185	146.883	1.00	23.48
	5140	CA	ASN C 209	18.150	56.452	147.071	1.00	23.14
	5141	CB	ASN C 209	17.648	57.203	145.841	1.00	20.04
15	5142	CG	ASN C 209	16.405	58.025	146.121	1.00	26.37
	5143	OD1	ASN C 209	16.115	58.372	147.262	1.00	22.39
	5144	ND2	ASN C 209	15.672	58.352	145.070	1.00	21.32
	5145	C	ASN C 209	17.296	55.206	147.301	1.00	24.90
	5146	O	ASN C 209	16.125	55.170	146.936	1.00	17.53
20	5147	N	PHE C 210	17.900	54.190	147.903	1.00	22.34
	5148	CA	PHE C 210	17.218	52.949	148.209	1.00	23.23
	5149	CB	PHE C 210	18.143	51.763	147.941	1.00	16.72
	5150	CG	PHE C 210	17.477	50.439	148.157	1.00	19.93
	5151	CD1	PHE C 210	16.350	50.090	147.413	1.00	18.12
25	5152	CD2	PHE C 210	17.956	49.549	149.111	1.00	17.78
	5153	CE1	PHE C 210	15.702	48.864	147.616	1.00	21.11
	5154	CE2	PHE C 210	17.321	48.321	149.323	1.00	24.00
	5155	CZ	PHE C 210	16.187	47.979	148.570	1.00	20.13
	5156	C	PHE C 210	16.740	52.881	149.677	1.00	26.01
30	5157	O	PHE C 210	17.554	52.769	150.594	1.00	27.49
	5158	N	LEU C 211	15.425	52.945	149.883	1.00	21.91
	5159	CA	LEU C 211	14.836	52.864	151.214	1.00	17.98
	5160	CB	LEU C 211	14.939	51.410	151.735	1.00	20.76
	5161	CG	LEU C 211	14.321	50.268	150.888	1.00	18.60
35	5162	CD1	LEU C 211	14.688	48.914	151.464	1.00	24.19
	5163	CD2	LEU C 211	12.801	50.411	150.828	1.00	18.17
	5164	C	LEU C 211	15.491	53.825	152.216	1.00	21.85
	5165	O	LEU C 211	15.903	53.412	153.292	1.00	17.48
	5166	N	PRO C 212	15.592	55.123	151.879	1.00	18.97
40	5167	CD	PRO C 212	15.138	55.860	150.694	1.00	18.49
	5168	CA	PRO C 212	16.224	56.027	152.853	1.00	20.28
	5169	CB	PRO C 212	16.187	57.397	152.151	1.00	10.14
	5170	CG	PRO C 212	15.006	57.288	151.236	1.00	15.15

	5171	C	PRO C 212	15.496	56.031	154.200	1.00	19.88
	5172	O	PRO C 212	16.129	56.043	155.258	1.00	17.10
	5173	N	TRP C 213	14.168	56.020	154.167	1.00	15.36
	5174	CA	TRP C 213	13.427	56.023	155.413	1.00	18.48
5	5175	CB	TRP C 213	11.956	56.349	155.163	1.00	15.00
	5176	CG	TRP C 213	11.133	56.296	156.410	1.00	14.95
	5177	CD2	TRP C 213	10.558	57.409	157.120	1.00	13.26
	5178	CE2	TRP C 213	9.831	56.874	158.204	1.00	13.38
	5179	CE3	TRP C 213	10.587	58.798	156.943	1.00	10.97
10	5180	CD1	TRP C 213	10.752	55.181	157.081	1.00	15.73
	5181	NE1	TRP C 213	9.970	55.520	158.154	1.00	15.93
	5182	CZ2	TRP C 213	9.134	57.677	159.116	1.00	14.95
	5183	CZ3	TRP C 213	9.893	59.596	157.849	1.00	16.49
	5184	CH2	TRP C 213	9.175	59.029	158.925	1.00	17.37
15	5185	C	TRP C 213	13.530	54.689	156.141	1.00	21.20
	5186	O	TRP C 213	14.037	54.611	157.268	1.00	21.60
	5187	N	GLN C 214	13.077	53.632	155.480	1.00	20.72
	5188	CA	GLN C 214	13.071	52.302	156.085	1.00	18.56
	5189	CB	GLN C 214	12.389	51.304	155.140	1.00	20.53
20	5190	CG	GLN C 214	11.000	51.718	154.632	1.00	19.87
	5191	CD	GLN C 214	11.051	52.489	153.317	1.00	24.00
	5192	OE1	GLN C 214	10.128	52.416	152.496	1.00	23.66
	5193	NE2	GLN C 214	12.124	53.235	153.115	1.00	22.54
	5194	C	GLN C 214	14.454	51.772	156.507	1.00	18.39
25	5195	O	GLN C 214	14.561	51.056	157.492	1.00	15.14
	5196	N	GLY C 215	15.511	52.115	155.771	1.00	20.32
	5197	CA	GLY C 215	16.839	51.641	156.142	1.00	14.29
	5198	C	GLY C 215	17.644	52.575	157.059	1.00	19.66
	5199	O	GLY C 215	18.832	52.345	157.286	1.00	17.03
30	5200	N	ALA C 216	17.006	53.601	157.619	1.00	18.83
	5201	CA	ALA C 216	17.716	54.568	158.466	1.00	17.55
	5202	CB	ALA C 216	16.722	55.577	159.096	1.00	14.82
	5203	C	ALA C 216	18.603	53.967	159.543	1.00	25.39
	5204	O	ALA C 216	19.650	54.545	159.862	1.00	25.88
35	5205	N	TYR C 217	18.208	52.817	160.098	1.00	24.30
	5206	CA	TYR C 217	19.001	52.155	161.137	1.00	24.27
	5207	CB	TYR C 217	18.183	51.886	162.404	1.00	25.62
	5208	CG	TYR C 217	17.658	53.123	163.101	1.00	28.31
	5209	CD1	TYR C 217	16.346	53.527	162.927	1.00	20.63
40	5210	CE1	TYR C 217	15.848	54.642	163.568	1.00	24.91
	5211	CD2	TYR C 217	18.474	53.877	163.941	1.00	23.60
	5212	CE2	TYR C 217	17.982	55.005	164.591	1.00	28.44
	5213	CZ	TYR C 217	16.661	55.375	164.399	1.00	28.56

	5214	OH	TYR C 217	16.127	56.446	165.075	1.00	33.70
	5215	C	TYR C 217	19.550	50.821	160.704	1.00	26.66
	5216	O	TYR C 217	19.985	50.039	161.543	1.00	25.50
	5217	N	SER C 218	19.535	50.545	159.414	1.00	25.01
5	5218	CA	SER C 218	20.009	49.259	158.947	1.00	23.76
	5219	CB	SER C 218	19.561	49.025	157.500	1.00	23.40
	5220	OG	SER C 218	18.150	49.005	157.421	1.00	30.19
	5221	C	SER C 218	21.496	49.050	159.006	1.00	24.51
	5222	O	SER C 218	22.279	49.999	158.865	1.00	21.71
10	5223	N	GLU C 219	21.880	47.794	159.221	1.00	18.46
	5224	CA	GLU C 219	23.281	47.422	159.186	1.00	22.83
	5225	CB	GLU C 219	23.509	46.038	159.799	1.00	29.18
	5226	CG	GLU C 219	23.370	45.980	161.323	1.00	27.59
	5227	CD	GLU C 219	24.406	46.830	162.047	1.00	32.10
15	5228	OE1	GLU C 219	25.603	46.801	161.658	1.00	23.10
	5229	OE2	GLU C 219	24.010	47.516	163.016	1.00	34.81
	5230	C	GLU C 219	23.576	47.389	157.682	1.00	24.85
	5231	O	GLU C 219	22.704	47.058	156.876	1.00	25.97
	5232	N	LEU C 220	24.802	47.733	157.308	1.00	28.11
20	5233	CA	LEU C 220	25.182	47.794	155.909	1.00	26.73
	5234	CB	LEU C 220	25.694	49.198	155.557	1.00	24.66
	5235	CG	LEU C 220	24.742	50.364	155.836	1.00	27.44
	5236	CD1	LEU C 220	25.486	51.672	155.670	1.00	27.65
	5237	CD2	LEU C 220	23.557	50.285	154.907	1.00	23.29
25	5238	C	LEU C 220	26.265	46.802	155.604	1.00	30.31
	5239	O	LEU C 220	27.178	46.605	156.395	1.00	32.19
	5240	N	TYR C 221	26.174	46.197	154.431	1.00	29.19
	5241	CA	TYR C 221	27.166	45.232	154.009	1.00	29.64
	5242	CB	TYR C 221	26.603	43.827	154.185	1.00	29.27
30	5243	CG	TYR C 221	27.576	42.761	153.801	1.00	30.79
	5244	CD1	TYR C 221	28.649	42.445	154.621	1.00	34.83
	5245	CE1	TYR C 221	29.596	41.507	154.232	1.00	33.46
	5246	CD2	TYR C 221	27.463	42.114	152.581	1.00	34.52
	5247	CE2	TYR C 221	28.398	41.176	152.181	1.00	38.04
35	5248	CZ	TYR C 221	29.463	40.878	153.008	1.00	37.53
	5249	OH	TYR C 221	30.390	39.955	152.587	1.00	43.39
	5250	C	TYR C 221	27.590	45.477	152.547	1.00	26.87
	5251	O	TYR C 221	26.815	45.268	151.623	1.00	28.38
	5252	N	PHE C 222	28.822	45.933	152.351	1.00	28.01
40	5253	CA	PHE C 222	29.343	46.197	151.009	1.00	28.00
	5254	CB	PHE C 222	30.015	47.570	150.962	1.00	16.62
	5255	CG	PHE C 222	29.103	48.706	151.370	1.00	27.82
	5256	CD1	PHE C 222	28.985	49.087	152.704	1.00	30.97

	5257	CD2	PHE	C	222	28.343	49.379	150.427	1.00	24.76
	5258	CE1	PHE	C	222	28.132	50.113	153.074	1.00	30.05
	5259	CE2	PHE	C	222	27.485	50.412	150.804	1.00	28.26
	5260	CZ	PHE	C	222	27.379	50.776	152.113	1.00	23.79
5	5261	C	PHE	C	222	30.327	45.115	150.588	1.00	30.37
	5262	O	PHE	C	222	31.161	44.673	151.376	1.00	35.12
	5263	N	THR	C	223	30.214	44.673	149.345	1.00	36.00
	5264	CA	THR	C	223	31.090	43.630	148.826	1.00	35.96
	5265	CB	THR	C	223	30.376	42.267	148.807	1.00	36.01
10	5266	OG1	THR	C	223	31.278	41.264	148.330	1.00	36.08
	5267	CG2	THR	C	223	29.163	42.319	147.894	1.00	33.46
	5268	C	THR	C	223	31.490	43.969	147.405	1.00	38.76
	5269	O	THR	C	223	30.704	44.565	146.668	1.00	41.80
	5270	N	ASP	C	224	32.704	43.591	147.014	1.00	39.30
15	5271	CA	ASP	C	224	33.170	43.870	145.664	1.00	37.64
	5272	CB	ASP	C	224	34.691	43.834	145.619	1.00	42.49
	5273	CG	ASP	C	224	35.325	45.056	146.280	1.00	52.24
	5274	OD1	ASP	C	224	36.562	45.068	146.448	1.00	59.55
	5275	OD2	ASP	C	224	34.593	46.011	146.630	1.00	54.97
20	5276	C	ASP	C	224	32.588	42.905	144.643	1.00	38.01
	5277	O	ASP	C	224	32.439	43.248	143.476	1.00	42.48
	5278	N	THR	C	225	32.247	41.704	145.092	1.00	38.04
	5279	CA	THR	C	225	31.679	40.677	144.233	1.00	39.35
	5280	CB	THR	C	225	31.263	39.455	145.093	1.00	38.46
25	5281	OG1	THR	C	225	30.509	38.525	144.310	1.00	43.95
	5282	CG2	THR	C	225	30.424	39.895	146.240	1.00	46.96
	5283	C	THR	C	225	30.488	41.205	143.414	1.00	42.40
	5284	O	THR	C	225	29.572	41.828	143.962	1.00	45.48
	5285	N	LEU	C	226	30.514	40.961	142.101	1.00	37.95
30	5286	CA	LEU	C	226	29.459	41.414	141.192	1.00	35.02
	5287	CB	LEU	C	226	29.896	41.222	139.737	1.00	38.91
	5288	CG	LEU	C	226	31.270	41.770	139.328	1.00	40.63
	5289	CD1	LEU	C	226	31.443	41.645	137.812	1.00	41.48
	5290	CD2	LEU	C	226	31.395	43.219	139.743	1.00	41.07
35	5291	C	LEU	C	226	28.178	40.637	141.450	1.00	32.77
	5292	O	LEU	C	226	28.224	39.470	141.805	1.00	34.74
	5293	N	TRP	C	227	27.028	41.274	141.263	1.00	31.07
	5294	CA	TRP	C	227	25.760	40.603	141.535	1.00	31.17
	5295	CB	TRP	C	227	24.587	41.468	141.090	1.00	26.34
40	5296	CG	TRP	C	227	23.291	40.778	141.278	1.00	27.67
	5297	CD2	TRP	C	227	22.753	40.283	142.509	1.00	27.57
	5298	CE2	TRP	C	227	21.531	39.638	142.203	1.00	28.20
	5299	CE3	TRP	C	227	23.184	40.318	143.840	1.00	27.96



	5300	CD1 TRP C 227	22.399	40.426	140.300	1.00	28.99
	5301	NE1 TRP C 227	21.341	39.739	140.852	1.00	28.25
	5302	CZ2 TRP C 227	20.734	39.032	143.180	1.00	29.13
	5303	CZ3 TRP C 227	22.385	39.714	144.820	1.00	28.45
5	5304	CH2 TRP C 227	21.180	39.083	144.480	1.00	31.16
	5305	C TRP C 227	25.590	39.197	140.951	1.00	34.14
	5306	O TRP C 227	25.104	38.293	141.634	1.00	35.59
	5307	N PRO C 228	25.944	39.005	139.666	1.00	39.70
	5308	CD PRO C 228	26.323	40.045	138.691	1.00	38.99
10	5309	CA PRO C 228	25.822	37.698	139.005	1.00	39.76
	5310	CB PRO C 228	26.437	37.951	137.641	1.00	42.62
	5311	CG PRO C 228	26.026	39.368	137.374	1.00	42.24
	5312	C PRO C 228	26.527	36.572	139.763	1.00	42.62
	5313	O PRO C 228	26.121	35.416	139.677	1.00	41.14
15	5314	N ASP C 229	27.579	36.919	140.504	1.00	41.04
	5315	CA ASP C 229	28.327	35.947	141.295	1.00	42.41
	5316	CB ASP C 229	29.801	36.334	141.347	1.00	40.24
	5317	CG ASP C 229	30.444	36.334	139.986	1.00	43.63
	5318	OD1 ASP C 229	30.046	35.498	139.148	1.00	50.24
20	5319	OD2 ASP C 229	31.356	37.154	139.753	1.00	50.15
	5320	C ASP C 229	27.808	35.810	142.725	1.00	45.81
	5321	O ASP C 229	28.156	34.861	143.430	1.00	47.44
	5322	N PHE C 230	26.989	36.762	143.162	1.00	45.22
	5323	CA PHE C 230	26.451	36.714	144.515	1.00	41.83
25	5324	CB PHE C 230	25.629	37.974	144.818	1.00	36.31
	5325	CG PHE C 230	25.522	38.268	146.276	1.00	32.49
	5326	CD1 PHE C 230	26.548	38.936	146.933	1.00	29.10
	5327	CD2 PHE C 230	24.427	37.818	147.010	1.00	33.92
	5328	CE1 PHE C 230	26.487	39.151	148.310	1.00	32.39
30	5329	CE2 PHE C 230	24.356	38.029	148.384	1.00	32.76
	5330	CZ PHE C 230	25.389	38.695	149.035	1.00	28.19
	5331	C PHE C 230	25.574	35.477	144.636	1.00	38.14
	5332	O PHE C 230	24.575	35.345	143.950	1.00	39.47
	5333	N ASP C 231	25.941	34.575	145.529	1.00	44.51
35	5334	CA ASP C 231	25.198	33.331	145.692	1.00	49.09
	5335	CB ASP C 231	26.021	32.191	145.113	1.00	51.45
	5336	CG ASP C 231	27.435	32.188	145.648	1.00	52.89
	5337	OD1 ASP C 231	27.585	32.426	146.870	1.00	43.89
	5338	OD2 ASP C 231	28.379	31.953	144.857	1.00	51.91
40	5339	C ASP C 231	24.875	33.017	147.145	1.00	50.62
	5340	O ASP C 231	25.120	33.829	148.030	1.00	51.84
	5341	N GLU C 232	24.347	31.822	147.388	1.00	50.44
	5342	CA GLU C 232	23.991	31.426	148.743	1.00	52.01

	5343	CB	GLU C 232	23.490	29.986	148.778	1.00	50.59
	5344	CG	GLU C 232	22.882	29.621	150.122	1.00	52.39
	5345	CD	GLU C 232	22.725	28.130	150.316	1.00	55.37
	5346	OE1	GLU C 232	22.375	27.429	149.337	1.00	52.81
5	5347	OE2	GLU C 232	22.947	27.666	151.457	1.00	56.94
	5348	C	GLU C 232	25.164	31.561	149.703	1.00	51.98
	5349	O	GLU C 232	24.981	31.918	150.864	1.00	55.68
	5350	N	ALA C 233	26.365	31.273	149.222	1.00	50.96
	5351	CA	ALA C 233	27.544	31.376	150.062	1.00	50.84
10	5352	CB	ALA C 233	28.785	30.986	149.275	1.00	50.83
	5353	C	ALA C 233	27.652	32.819	150.518	1.00	53.77
	5354	O	ALA C 233	27.553	33.120	151.710	1.00	56.29
	5355	N	ALA C 234	27.851	33.706	149.545	1.00	53.29
	5356	CA	ALA C 234	27.982	35.136	149.796	1.00	46.76
15	5357	CB	ALA C 234	28.001	35.891	148.479	1.00	40.80
	5358	C	ALA C 234	26.847	35.643	150.687	1.00	42.50
	5359	O	ALA C 234	27.073	36.471	151.572	1.00	36.76
	5360	N	LEU C 235	25.633	35.144	150.468	1.00	38.26
	5361	CA	LEU C 235	24.512	35.579	151.291	1.00	42.55
20	5362	CB	LEU C 235	23.210	34.886	150.892	1.00	34.10
	5363	CG	LEU C 235	22.023	35.239	151.810	1.00	39.56
	5364	CD1	LEU C 235	21.767	36.756	151.757	1.00	34.53
	5365	CD2	LEU C 235	20.767	34.472	151.394	1.00	30.80
	5366	C	LEU C 235	24.815	35.270	152.751	1.00	48.17
25	5367	O	LEU C 235	24.669	36.132	153.622	1.00	49.16
	5368	N	GLN C 236	25.249	34.039	153.013	1.00	50.80
	5369	CA	GLN C 236	25.561	33.623	154.374	1.00	48.18
	5370	CB	GLN C 236	25.852	32.123	154.424	1.00	52.52
	5371	CG	GLN C 236	24.609	31.268	154.284	1.00	54.56
30	5372	CD	GLN C 236	24.905	29.786	154.387	0.50	53.40
	5373	OE1	GLN C 236	25.858	29.286	153.783	0.50	52.88
	5374	NE2	GLN C 236	24.079	29.070	155.144	0.50	48.92
	5375	C	GLN C 236	26.724	34.392	154.973	1.00	44.34
	5376	O	GLN C 236	26.773	34.599	156.181	1.00	39.52
35	5377	N	GLU C 237	27.666	34.818	154.145	1.00	42.59
	5378	CA	GLU C 237	28.781	35.570	154.687	1.00	43.19
	5379	CB	GLU C 237	29.911	35.657	153.681	1.00	42.73
	5380	CG	GLU C 237	31.213	36.119	154.289	1.00	52.44
	5381	CD	GLU C 237	32.410	35.739	153.432	0.50	55.65
40	5382	OE1	GLU C 237	32.422	36.091	152.229	0.50	54.16
	5383	OE2	GLU C 237	33.334	35.086	153.966	0.50	55.37
	5384	C	GLU C 237	28.279	36.964	155.068	1.00	44.75
	5385	O	GLU C 237	28.820	37.604	155.968	1.00	47.59

	5386	N	ALA C 238	27.238	37.429	154.379	1.00	42.54
	5387	CA	ALA C 238	26.646	38.722	154.691	1.00	41.52
	5388	CB	ALA C 238	25.668	39.145	153.615	1.00	37.60
	5389	C	ALA C 238	25.909	38.541	156.007	1.00	42.55
5	5390	O	ALA C 238	25.963	39.405	156.883	1.00	44.16
	5391	N	ILE C 239	25.223	37.409	156.145	1.00	39.07
	5392	CA	ILE C 239	24.482	37.131	157.361	1.00	37.76
	5393	CB	ILE C 239	23.647	35.848	157.244	1.00	37.95
	5394	CG2	ILE C 239	22.974	35.528	158.592	1.00	37.90
10	5395	CG1	ILE C 239	22.593	36.033	156.154	1.00	36.70
	5396	CD1	ILE C 239	21.668	34.865	155.989	1.00	35.32
	5397	C	ILE C 239	25.458	36.974	158.504	1.00	40.90
	5398	O	ILE C 239	25.157	37.320	159.645	1.00	39.54
	5399	N	LEU C 240	26.636	36.454	158.195	1.00	42.81
15	5400	CA	LEU C 240	27.647	36.268	159.220	1.00	43.59
	5401	CB	LEU C 240	28.859	35.543	158.654	1.00	46.08
	5402	CG	LEU C 240	29.834	35.135	159.751	1.00	52.23
	5403	CD1	LEU C 240	29.161	34.098	160.649	1.00	54.06
	5404	CD2	LEU C 240	31.109	34.587	159.127	1.00	53.20
20	5405	C	LEU C 240	28.058	37.637	159.724	1.00	45.00
	5406	O	LEU C 240	27.905	37.936	160.908	1.00	46.99
	5407	N	ALA C 241	28.576	38.469	158.822	1.00	43.48
	5408	CA	ALA C 241	28.991	39.820	159.183	1.00	41.26
	5409	CB	ALA C 241	29.277	40.631	157.932	1.00	41.89
25	5410	C	ALA C 241	27.906	40.503	160.007	1.00	41.76
	5411	O	ALA C 241	28.199	41.143	161.017	1.00	41.71
	5412	N	TYR C 242	26.653	40.348	159.579	1.00	42.00
	5413	CA	TYR C 242	25.518	40.952	160.273	1.00	42.90
	5414	CB	TYR C 242	24.203	40.566	159.599	1.00	35.13
30	5415	CG	TYR C 242	22.973	40.933	160.400	1.00	31.56
	5416	CD1	TYR C 242	22.485	42.233	160.412	1.00	32.86
	5417	CE1	TYR C 242	21.349	42.580	161.168	1.00	30.00
	5418	CD2	TYR C 242	22.305	39.979	161.165	1.00	35.26
	5419	CE2	TYR C 242	21.174	40.313	161.931	1.00	34.61
35	5420	CZ	TYR C 242	20.698	41.618	161.926	1.00	34.12
	5421	OH	TYR C 242	19.571	41.954	162.670	1.00	29.90
	5422	C	TYR C 242	25.477	40.508	161.730	1.00	48.93
	5423	O	TYR C 242	25.187	41.307	162.625	1.00	50.79
	5424	N	ASN C 243	25.758	39.231	161.970	1.00	50.76
40	5425	CA	ASN C 243	25.746	38.726	163.331	1.00	55.04
	5426	CB	ASN C 243	25.606	37.205	163.340	1.00	57.72
	5427	CG	ASN C 243	24.183	36.756	163.041	1.00	62.63
	5428	OD1	ASN C 243	23.848	36.434	161.906	1.00	61.19

	5429	ND2	ASN	C	243	23.334	36.753	164.065	1.00	68.91
	5430	C	ASN	C	243	26.976	39.172	164.110	1.00	54.10
	5431	O	ASN	C	243	26.905	39.395	165.310	1.00	56.01
	5432	N	ARG	C	244	28.101	39.323	163.429	1.00	57.46
5	5433	CA	ARG	C	244	29.303	39.779	164.098	1.00	60.82
	5434	CB	ARG	C	244	30.523	39.589	163.194	1.00	66.28
	5435	CG	ARG	C	244	31.099	38.172	163.205	1.00	72.92
	5436	CD	ARG	C	244	30.079	37.119	162.767	1.00	81.64
	5437	NE	ARG	C	244	30.545	35.754	163.018	1.00	86.88
10	5438	CZ	ARG	C	244	31.626	35.208	162.467	1.00	89.44
	5439	NH1	ARG	C	244	32.372	35.907	161.617	1.00	89.62
	5440	NH2	ARG	C	244	31.969	33.962	162.776	1.00	87.77
	5441	C	ARG	C	244	29.165	41.253	164.493	1.00	63.43
	5442	O	ARG	C	244	30.095	41.844	165.041	1.00	63.84
15	5443	N	ARG	C	245	28.006	41.849	164.229	1.00	63.77
	5444	CA	ARG	C	245	27.804	43.249	164.587	1.00	68.89
	5445	CB	ARG	C	245	26.739	43.901	163.704	1.00	65.75
	5446	CG	ARG	C	245	27.077	43.915	162.217	1.00	65.22
	5447	CD	ARG	C	245	28.413	44.593	161.922	1.00	58.12
20	5448	NE	ARG	C	245	28.756	44.488	160.508	1.00	50.41
	5449	CZ	ARG	C	245	28.099	45.100	159.526	1.00	48.32
	5450	NH1	ARG	C	245	27.054	45.878	159.803	1.00	44.92
	5451	NH2	ARG	C	245	28.480	44.919	158.261	1.00	39.36
	5452	C	ARG	C	245	27.407	43.411	166.046	1.00	75.32
25	5453	O	ARG	C	245	28.040	44.172	166.780	1.00	78.60
	5454	N	HIS	C	246	26.361	42.713	166.477	1.00	80.51
	5455	CA	HIS	C	246	25.948	42.834	167.867	1.00	85.95
	5456	CB	HIS	C	246	24.538	42.253	168.080	1.00	84.82
	5457	CG	HIS	C	246	24.357	40.863	167.560	0.00	84.96
30	5458	CD2	HIS	C	246	24.140	39.691	168.207	0.00	84.82
	5459	ND1	HIS	C	246	24.343	40.564	166.215	0.00	84.82
	5460	CE1	HIS	C	246	24.123	39.271	166.055	0.00	84.81
	5461	NE2	HIS	C	246	23.997	38.720	167.248	0.00	84.81
	5462	C	HIS	C	246	26.966	42.179	168.808	1.00	88.89
35	5463	O	HIS	C	246	26.702	41.152	169.431	1.00	91.32
	5464	N	ARG	C	247	28.143	42.791	168.883	0.00	90.64
	5465	CA	ARG	C	247	29.229	42.329	169.739	0.00	92.32
	5466	CB	ARG	C	247	30.143	41.349	168.992	0.00	91.92
	5467	CG	ARG	C	247	29.678	39.898	169.015	0.00	91.54
40	5468	CD	ARG	C	247	28.544	39.636	168.039	0.00	91.17
	5469	NE	ARG	C	247	27.913	38.340	168.274	0.00	90.90
	5470	CZ	ARG	C	247	28.543	37.172	168.190	0.00	90.76
	5471	NH1	ARG	C	247	29.830	37.129	167.873	0.00	90.69

	5472	NH2	ARG	C	247	27.885	36.046	168.427	0.00	90.69
	5473	C	ARG	C	247	30.029	43.552	170.162	0.00	93.81
	5474	O	ARG	C	247	29.986	43.967	171.321	0.00	93.90
	5475	N	ARG	C	248	30.756	44.126	169.210	0.00	95.72
5	5476	CA	ARG	C	248	31.554	45.315	169.466	0.00	97.55
	5477	CB	ARG	C	248	32.690	45.425	168.446	0.00	97.09
	5478	CG	ARG	C	248	33.833	44.449	168.680	0.00	96.32
	5479	CD	ARG	C	248	34.636	44.821	169.921	0.00	95.70
	5480	NE	ARG	C	248	33.813	44.855	171.127	0.00	95.15
10	5481	CZ	ARG	C	248	34.255	45.216	172.327	0.00	94.87
	5482	NH1	ARG	C	248	35.521	45.576	172.489	0.00	94.68
	5483	NH2	ARG	C	248	33.431	45.219	173.366	0.00	94.68
	5484	C	ARG	C	248	30.661	46.544	169.382	1.00	100.00
	5485	O	ARG	C	248	29.428	46.352	169.269	1.00	100.00
15	5486	OT	ARG	C	248	31.202	47.672	169.438	1.00	100.00
	5487	CB	GLN	D	18	40.282	68.516	143.646	1.00	64.66
	5488	CG	GLN	D	18	40.708	67.124	143.219	1.00	74.17
	5489	CD	GLN	D	18	42.150	67.094	142.755	1.00	77.01
	5490	OE1	GLN	D	18	43.064	67.399	143.523	1.00	78.73
20	5491	NE2	GLN	D	18	42.361	66.735	141.489	1.00	78.58
	5492	C	GLN	D	18	38.568	68.227	145.448	1.00	56.54
	5493	O	GLN	D	18	39.225	67.338	145.993	1.00	55.00
	5494	N	GLN	D	18	38.353	70.044	143.806	1.00	63.95
	5495	CA	GLN	D	18	38.801	68.627	143.990	1.00	62.02
25	5496	N	VAL	D	19	37.606	68.903	146.055	1.00	47.59
	5497	CA	VAL	D	19	37.255	68.689	147.441	1.00	45.47
	5498	CB	VAL	D	19	37.770	69.856	148.295	1.00	47.02
	5499	CG1	VAL	D	19	37.433	69.629	149.738	1.00	48.24
	5500	CG2	VAL	D	19	39.267	70.018	148.093	1.00	50.12
30	5501	C	VAL	D	19	35.738	68.616	147.616	1.00	40.25
	5502	O	VAL	D	19	35.002	69.488	147.128	1.00	35.66
	5503	N	PRO	D	20	35.247	67.568	148.301	1.00	31.88
	5504	CD	PRO	D	20	35.954	66.454	148.950	1.00	28.71
	5505	CA	PRO	D	20	33.797	67.462	148.508	1.00	30.78
35	5506	CB	PRO	D	20	33.664	66.214	149.392	1.00	27.59
	5507	CG	PRO	D	20	35.009	66.095	150.037	1.00	32.37
	5508	C	PRO	D	20	33.346	68.756	149.190	1.00	24.11
	5509	O	PRO	D	20	33.992	69.221	150.110	1.00	29.24
	5510	N	ALA	D	21	32.271	69.357	148.708	1.00	22.88
40	5511	CA	ALA	D	21	31.799	70.610	149.283	1.00	18.72
	5512	CB	ALA	D	21	30.904	71.320	148.306	1.00	18.81
	5513	C	ALA	D	21	31.080	70.493	150.607	1.00	14.71
	5514	O	ALA	D	21	31.137	71.410	151.411	1.00	21.18

	5515	N	HIS	D	22	30.391	69.385	150.836	1.00	16.91
	5516	CA	HIS	D	22	29.630	69.208	152.082	1.00	17.46
	5517	CB	HIS	D	22	28.111	69.356	151.809	1.00	16.54
	5518	CG	HIS	D	22	27.229	69.163	153.013	1.00	14.67
5	5519	CD2	HIS	D	22	27.493	68.728	154.270	1.00	15.37
	5520	ND1	HIS	D	22	25.889	69.491	153.003	1.00	17.83
	5521	CE1	HIS	D	22	25.369	69.274	154.198	1.00	14.81
	5522	NE2	HIS	D	22	26.322	68.814	154.987	1.00	14.09
	5523	C	HIS	D	22	29.953	67.816	152.549	1.00	21.09
10	5524	O	HIS	D	22	29.726	66.846	151.822	1.00	24.14
	5525	N	ILE	D	23	30.504	67.719	153.753	1.00	22.21
	5526	CA	ILE	D	23	30.874	66.427	154.307	1.00	17.23
	5527	CB	ILE	D	23	32.371	66.381	154.631	1.00	18.32
	5528	CG2	ILE	D	23	32.745	64.994	155.168	1.00	18.80
15	5529	CG1	ILE	D	23	33.182	66.695	153.359	1.00	20.87
	5530	CD1	ILE	D	23	34.715	66.583	153.546	1.00	18.95
	5531	C	ILE	D	23	30.090	66.203	155.585	1.00	19.98
	5532	O	ILE	D	23	30.022	67.102	156.428	1.00	18.57
	5533	N	GLY	D	24	29.457	65.032	155.702	1.00	16.66
20	5534	CA	GLY	D	24	28.715	64.707	156.905	1.00	14.42
	5535	C	GLY	D	24	29.628	63.803	157.718	1.00	16.19
	5536	O	GLY	D	24	30.313	62.959	157.156	1.00	17.71
	5537	N	ILE	D	25	29.658	63.979	159.033	1.00	21.57
	5538	CA	ILE	D	25	30.525	63.167	159.877	1.00	19.82
25	5539	CB	ILE	D	25	31.754	63.974	160.407	1.00	24.37
	5540	CG2	ILE	D	25	32.659	63.039	161.203	1.00	23.57
	5541	CG1	ILE	D	25	32.525	64.619	159.239	1.00	24.47
	5542	CD1	ILE	D	25	33.719	65.452	159.662	1.00	26.40
	5543	C	ILE	D	25	29.801	62.628	161.100	1.00	23.04
30	5544	O	ILE	D	25	29.241	63.395	161.888	1.00	18.24
	5545	N	ILE	D	26	29.820	61.307	161.260	1.00	17.22
	5546	CA	ILE	D	26	29.204	60.726	162.428	1.00	20.39
	5547	CB	ILE	D	26	28.427	59.450	162.087	1.00	24.17
	5548	CG2	ILE	D	26	27.969	58.783	163.364	1.00	18.90
35	5549	CG1	ILE	D	26	27.219	59.807	161.206	1.00	24.30
	5550	CD1	ILE	D	26	26.515	58.626	160.566	1.00	21.08
	5551	C	ILE	D	26	30.344	60.427	163.374	1.00	19.28
	5552	O	ILE	D	26	31.141	59.523	163.147	1.00	24.29
	5553	N	MET	D	27	30.420	61.217	164.429	1.00	25.88
40	5554	CA	MET	D	27	31.479	61.107	165.421	1.00	27.96
	5555	CB	MET	D	27	31.621	62.455	166.141	1.00	27.12
	5556	CG	MET	D	27	31.830	63.643	165.178	1.00	26.63
	5557	SD	MET	D	27	31.941	65.319	165.926	1.00	34.21

	5558	CE	MET	D	27	30.390	65.447	166.940	1.00	26.65
	5559	C	MET	D	27	31.196	59.986	166.415	1.00	30.09
	5560	O	MET	D	27	30.351	60.099	167.300	1.00	32.99
	5561	N	ASP	D	28	31.926	58.897	166.280	1.00	30.61
5	5562	CA	ASP	D	28	31.717	57.756	167.151	1.00	30.03
	5563	CB	ASP	D	28	31.143	56.607	166.321	1.00	35.90
	5564	CG	ASP	D	28	29.803	56.146	166.808	1.00	42.50
	5565	OD1	ASP	D	28	29.671	54.948	167.122	1.00	45.31
	5566	OD2	ASP	D	28	28.878	56.981	166.868	1.00	52.85
10	5567	C	ASP	D	28	33.029	57.300	167.757	1.00	27.37
	5568	O	ASP	D	28	34.070	57.435	167.135	1.00	31.02
	5569	N	GLY	D	29	32.987	56.747	168.959	1.00	29.80
	5570	CA	GLY	D	29	34.215	56.219	169.537	1.00	28.39
	5571	C	GLY	D	29	34.846	56.896	170.730	1.00	27.52
15	5572	O	GLY	D	29	35.810	56.361	171.266	1.00	28.60
	5573	N	ASN	D	30	34.335	58.056	171.143	1.00	28.81
	5574	CA	ASN	D	30	34.889	58.771	172.300	1.00	31.68
	5575	CB	ASN	D	30	33.993	59.953	172.700	1.00	21.99
	5576	CG	ASN	D	30	33.885	60.982	171.610	1.00	19.91
20	5577	OD1	ASN	D	30	33.128	61.947	171.713	1.00	33.01
	5578	ND2	ASN	D	30	34.652	60.792	170.554	1.00	18.65
	5579	C	ASN	D	30	35.055	57.844	173.500	1.00	32.08
	5580	O	ASN	D	30	36.123	57.822	174.130	1.00	31.29
	5581	N	GLY	D	31	33.991	57.095	173.805	1.00	28.79
25	5582	CA	GLY	D	31	34.002	56.160	174.915	1.00	27.16
	5583	C	GLY	D	31	35.098	55.107	174.814	1.00	30.93
	5584	O	GLY	D	31	35.906	54.953	175.733	1.00	29.46
	5585	N	ARG	D	32	35.131	54.387	173.699	1.00	29.75
	5586	CA	ARG	D	32	36.129	53.343	173.471	1.00	32.54
30	5587	CB	ARG	D	32	35.944	52.709	172.085	1.00	33.54
	5588	CG	ARG	D	32	34.720	51.811	171.908	1.00	44.29
	5589	CD	ARG	D	32	34.561	51.346	170.435	1.00	44.06
	5590	NE	ARG	D	32	35.621	50.434	169.994	1.00	47.29
	5591	CZ	ARG	D	32	35.811	50.032	168.731	1.00	53.27
35	5592	NH1	ARG	D	32	35.018	50.458	167.751	1.00	48.97
	5593	NH2	ARG	D	32	36.793	49.185	168.443	1.00	53.78
	5594	C	ARG	D	32	37.548	53.899	173.540	1.00	35.30
	5595	O	ARG	D	32	38.480	53.216	173.969	1.00	35.31
	5596	N	TRP	D	33	37.705	55.141	173.094	1.00	35.89
40	5597	CA	TRP	D	33	39.002	55.786	173.050	1.00	33.03
	5598	CB	TRP	D	33	38.895	57.099	172.263	1.00	29.90
	5599	CG	TRP	D	33	40.202	57.783	171.988	1.00	29.98
	5600	CD2	TRP	D	33	40.814	58.814	172.777	1.00	21.98

	5601	CE2	TRP	D	33	41.995	59.214	172.103	1.00	26.43
	5602	CE3	TRP	D	33	40.474	59.447	173.980	1.00	28.18
	5603	CD1	TRP	D	33	41.028	57.590	170.901	1.00	31.31
	5604	NE1	TRP	D	33	42.105	58.449	170.964	1.00	22.33
5	5605	CZ2	TRP	D	33	42.837	60.229	172.598	1.00	21.68
	5606	CZ3	TRP	D	33	41.315	60.457	174.472	1.00	22.03
	5607	CH2	TRP	D	33	42.478	60.835	173.775	1.00	15.61
	5608	C	TRP	D	33	39.527	56.040	174.459	1.00	36.01
	5609	O	TRP	D	33	40.701	55.771	174.755	1.00	30.76
10	5610	N	ALA	D	34	38.664	56.556	175.324	1.00	32.99
	5611	CA	ALA	D	34	39.073	56.833	176.686	1.00	36.24
	5612	CB	ALA	D	34	37.991	57.587	177.408	1.00	31.89
	5613	C	ALA	D	34	39.386	55.521	177.414	1.00	40.64
	5614	O	ALA	D	34	40.408	55.403	178.103	1.00	39.29
15	5615	N	LYS	D	35	38.520	54.533	177.237	1.00	36.51
	5616	CA	LYS	D	35	38.711	53.255	177.896	1.00	40.50
	5617	CB	LYS	D	35	37.609	52.279	177.497	1.00	39.81
	5618	CG	LYS	D	35	37.712	50.929	178.182	1.00	47.28
	5619	CD	LYS	D	35	36.548	50.035	177.780	1.00	55.64
20	5620	CE	LYS	D	35	36.699	48.618	178.311	1.00	63.06
	5621	NZ	LYS	D	35	35.568	47.743	177.869	1.00	66.31
	5622	C	LYS	D	35	40.078	52.650	177.598	1.00	40.69
	5623	O	LYS	D	35	40.687	52.031	178.464	1.00	43.63
	5624	N	LYS	D	36	40.566	52.822	176.378	1.00	40.05
25	5625	CA	LYS	D	36	41.871	52.282	176.030	1.00	38.83
	5626	CB	LYS	D	36	42.140	52.450	174.535	1.00	40.91
	5627	CG	LYS	D	36	41.344	51.526	173.636	1.00	46.86
	5628	CD	LYS	D	36	41.681	51.747	172.169	1.00	46.17
	5629	CE	LYS	D	36	41.075	50.634	171.324	1.00	50.26
30	5630	NZ	LYS	D	36	41.120	50.940	169.864	1.00	54.06
	5631	C	LYS	D	36	42.965	53.002	176.812	1.00	39.14
	5632	O	LYS	D	36	44.002	52.423	177.102	1.00	42.27
	5633	N	ARG	D	37	42.716	54.269	177.137	1.00	35.55
	5634	CA	ARG	D	37	43.653	55.122	177.858	1.00	32.12
35	5635	CB	ARG	D	37	43.424	56.598	177.478	1.00	34.81
	5636	CG	ARG	D	37	43.211	56.933	175.972	1.00	40.77
	5637	CD	ARG	D	37	44.492	56.832	175.235	1.00	35.37
	5638	NE	ARG	D	37	44.593	57.426	173.895	1.00	29.13
	5639	CZ	ARG	D	37	44.072	56.914	172.783	1.00	32.13
40	5640	NH1	ARG	D	37	43.332	55.818	172.806	1.00	29.45
	5641	NH2	ARG	D	37	44.460	57.382	171.606	1.00	35.04
	5642	C	ARG	D	37	43.424	54.985	179.363	1.00	32.41
	5643	O	ARG	D	37	43.939	55.780	180.151	1.00	33.63



	5644	N	MET	D	38	42.617	54.007	179.754	1.00	34.44
	5645	CA	MET	D	38	42.288	53.765	181.166	1.00	39.65
	5646	CB	MET	D	38	43.549	53.393	181.984	1.00	38.08
	5647	CG	MET	D	38	44.224	52.088	181.572	0.50	38.24
5	5648	SD	MET	D	38	43.102	50.668	181.608	0.50	46.24
	5649	CE	MET	D	38	43.651	49.767	180.178	0.50	36.27
	5650	C	MET	D	38	41.619	54.969	181.823	1.00	41.48
	5651	O	MET	D	38	41.675	55.111	183.044	1.00	43.02
	5652	N	GLN	D	39	40.971	55.821	181.027	1.00	41.09
10	5653	CA	GLN	D	39	40.322	57.027	181.563	1.00	42.38
	5654	CB	GLN	D	39	40.830	58.274	180.814	1.00	37.85
	5655	CG	GLN	D	39	42.344	58.513	180.892	1.00	43.03
	5656	CD	GLN	D	39	42.857	58.658	182.328	1.00	50.02
	5657	OE1	GLN	D	39	42.348	59.471	183.101	1.00	47.42
15	5658	NE2	GLN	D	39	43.875	57.869	182.683	1.00	50.54
	5659	C	GLN	D	39	38.803	56.970	181.462	1.00	40.82
	5660	O	GLN	D	39	38.268	56.237	180.644	1.00	47.44
	5661	N	PRO	D	40	38.084	57.743	182.293	1.00	43.17
	5662	CD	PRO	D	40	38.541	58.753	183.260	1.00	40.77
20	5663	CA	PRO	D	40	36.616	57.726	182.224	1.00	44.96
	5664	CB	PRO	D	40	36.208	58.673	183.348	1.00	39.92
	5665	CG	PRO	D	40	37.318	59.651	183.363	1.00	42.00
	5666	C	PRO	D	40	36.142	58.209	180.849	1.00	49.02
	5667	O	PRO	D	40	36.912	58.821	180.106	1.00	50.71
25	5668	N	ARG	D	41	34.882	57.942	180.512	1.00	50.18
	5669	CA	ARG	D	41	34.337	58.332	179.214	1.00	50.29
	5670	CB	ARG	D	41	32.897	57.833	179.077	1.00	57.65
	5671	CG	ARG	D	41	32.317	57.940	177.672	1.00	68.97
	5672	CD	ARG	D	41	30.827	57.618	177.686	1.00	78.38
30	5673	NE	ARG	D	41	30.176	57.841	176.395	1.00	84.71
	5674	CZ	ARG	D	41	28.867	58.044	176.251	1.00	87.80
	5675	NH1	ARG	D	41	28.073	58.058	177.318	1.00	87.20
	5676	NH2	ARG	D	41	28.346	58.222	175.040	1.00	88.07
	5677	C	ARG	D	41	34.390	59.838	178.958	1.00	48.81
35	5678	O	ARG	D	41	34.626	60.266	177.827	1.00	43.83
	5679	N	VAL	D	42	34.169	60.638	180.000	1.00	47.72
	5680	CA	VAL	D	42	34.213	62.101	179.876	1.00	46.51
	5681	CB	VAL	D	42	34.087	62.774	181.257	1.00	50.10
	5682	CG1	VAL	D	42	34.695	64.162	181.220	1.00	53.63
40	5683	CG2	VAL	D	42	32.619	62.849	181.662	1.00	52.92
	5684	C	VAL	D	42	35.528	62.544	179.220	1.00	44.08
	5685	O	VAL	D	42	35.568	63.501	178.446	1.00	37.88
	5686	N	PHE	D	43	36.598	61.828	179.545	1.00	38.31

	5687	CA	PHE	D	43	37.922	62.087	178.998	1.00	35.04
	5688	CB	PHE	D	43	38.906	61.091	179.605	1.00	35.83
	5689	CG	PHE	D	43	40.315	61.277	179.156	1.00	33.59
	5690	CD1	PHE	D	43	41.138	62.215	179.778	1.00	31.31
5	5691	CD2	PHE	D	43	40.838	60.480	178.143	1.00	28.19
	5692	CE1	PHE	D	43	42.473	62.354	179.395	1.00	32.31
	5693	CE2	PHE	D	43	42.168	60.609	177.752	1.00	35.46
	5694	CZ	PHE	D	43	42.990	61.552	178.384	1.00	35.27
	5695	C	PHE	D	43	37.917	61.948	177.469	1.00	34.72
10	5696	O	PHE	D	43	38.667	62.636	176.769	1.00	35.15
	5697	N	GLY	D	44	37.074	61.052	176.957	1.00	36.82
	5698	CA	GLY	D	44	36.977	60.853	175.516	1.00	30.19
	5699	C	GLY	D	44	36.201	61.977	174.833	1.00	28.57
	5700	O	GLY	D	44	36.519	62.357	173.711	1.00	26.49
15	5701	N	HIS	D	45	35.185	62.517	175.502	1.00	25.50
	5702	CA	HIS	D	45	34.400	63.602	174.919	1.00	32.93
	5703	CB	HIS	D	45	33.099	63.810	175.703	1.00	34.24
	5704	CG	HIS	D	45	32.148	62.667	175.551	1.00	44.34
	5705	CD2	HIS	D	45	31.769	61.972	174.450	1.00	40.10
20	5706	ND1	HIS	D	45	31.578	62.020	176.628	1.00	46.15
	5707	CE1	HIS	D	45	30.901	60.969	176.198	1.00	46.13
	5708	NE2	HIS	D	45	31.004	60.917	174.881	1.00	47.34
	5709	C	HIS	D	45	35.199	64.883	174.842	1.00	34.03
	5710	O	HIS	D	45	35.013	65.680	173.912	1.00	35.60
25	5711	N	LYS	D	46	36.093	65.091	175.808	1.00	32.96
	5712	CA	LYS	D	46	36.939	66.285	175.763	1.00	33.82
	5713	CB	LYS	D	46	37.844	66.376	177.001	1.00	39.76
	5714	CG	LYS	D	46	37.112	66.382	178.327	1.00	48.98
	5715	CD	LYS	D	46	37.183	67.738	178.987	1.00	53.12
30	5716	CE	LYS	D	46	36.568	67.677	180.371	1.00	55.85
	5717	NZ	LYS	D	46	36.366	69.045	180.927	1.00	63.27
	5718	C	LYS	D	46	37.816	66.133	174.517	1.00	26.47
	5719	O	LYS	D	46	37.946	67.042	173.716	1.00	26.90
	5720	N	ALA	D	47	38.402	64.953	174.370	1.00	25.12
35	5721	CA	ALA	D	47	39.268	64.659	173.254	1.00	25.00
	5722	CB	ALA	D	47	39.854	63.241	173.405	1.00	27.88
	5723	C	ALA	D	47	38.484	64.787	171.959	1.00	26.19
	5724	O	ALA	D	47	39.034	65.206	170.948	1.00	27.14
	5725	N	GLY	D	48	37.200	64.430	171.993	1.00	27.45
40	5726	CA	GLY	D	48	36.360	64.548	170.804	1.00	19.71
	5727	C	GLY	D	48	36.218	66.006	170.380	1.00	20.83
	5728	O	GLY	D	48	36.256	66.317	169.187	1.00	21.89
	5729	N	MET	D	49	36.060	66.908	171.342	1.00	18.54

	5730	CA	MET	D	49	35.954	68.333	170.997	1.00	29.00
	5731	CB	MET	D	49	35.702	69.198	172.237	1.00	27.05
	5732	CG	MET	D	49	34.247	69.256	172.752	1.00	39.13
	5733	SD	MET	D	49	34.048	70.614	173.960	0.50	32.80
5	5734	CE	MET	D	49	34.664	69.821	175.356	1.00	38.11
	5735	C	MET	D	49	37.254	68.808	170.322	1.00	32.79
	5736	O	MET	D	49	37.229	69.554	169.321	1.00	28.54
	5737	N	GLU	D	50	38.396	68.377	170.865	1.00	30.21
	5738	CA	GLU	D	50	39.671	68.779	170.270	1.00	29.49
10	5739	CB	GLU	D	50	40.862	68.246	171.075	1.00	32.79
	5740	CG	GLU	D	50	41.176	69.019	172.365	1.00	42.05
	5741	CD	GLU	D	50	41.543	70.478	172.105	1.00	44.82
	5742	OE1	GLU	D	50	42.023	70.790	170.992	1.00	47.15
	5743	OE2	GLU	D	50	41.367	71.310	173.016	1.00	46.90
15	5744	C	GLU	D	50	39.732	68.256	168.843	1.00	24.96
	5745	O	GLU	D	50	40.168	68.956	167.940	1.00	25.71
	5746	N	ALA	D	51	39.296	67.019	168.635	1.00	23.33
	5747	CA	ALA	D	51	39.306	66.463	167.291	1.00	26.68
	5748	CB	ALA	D	51	38.812	65.033	167.320	1.00	29.11
20	5749	C	ALA	D	51	38.423	67.317	166.369	1.00	26.04
	5750	O	ALA	D	51	38.790	67.570	165.218	1.00	28.89
	5751	N	LEU	D	52	37.269	67.769	166.872	1.00	28.07
	5752	CA	LEU	D	52	36.367	68.606	166.068	1.00	24.07
	5753	CB	LEU	D	52	35.077	68.939	166.834	1.00	25.52
25	5754	CG	LEU	D	52	34.010	69.731	166.058	1.00	26.86
	5755	CD1	LEU	D	52	33.613	68.998	164.772	1.00	23.83
	5756	CD2	LEU	D	52	32.794	69.918	166.940	1.00	27.95
	5757	C	LEU	D	52	37.077	69.896	165.690	1.00	19.98
	5758	O	LEU	D	52	37.116	70.269	164.526	1.00	20.58
30	5759	N	GLN	D	53	37.660	70.566	166.677	1.00	22.57
	5760	CA	GLN	D	53	38.377	71.812	166.420	1.00	23.07
	5761	CB	GLN	D	53	39.120	72.281	167.675	1.00	26.87
	5762	CG	GLN	D	53	39.624	73.727	167.594	1.00	28.27
	5763	CD	GLN	D	53	38.479	74.721	167.672	1.00	35.21
35	5764	OE1	GLN	D	53	37.303	74.335	167.692	1.00	30.64
	5765	NE2	GLN	D	53	38.811	76.006	167.715	1.00	33.88
	5766	C	GLN	D	53	39.381	71.636	165.286	1.00	20.78
	5767	O	GLN	D	53	39.379	72.407	164.334	1.00	25.59
	5768	N	THR	D	54	40.229	70.614	165.368	1.00	26.46
40	5769	CA	THR	D	54	41.224	70.425	164.311	1.00	27.55
	5770	CB	THR	D	54	42.437	69.475	164.737	1.00	32.84
	5771	OG1	THR	D	54	42.558	68.375	163.831	1.00	40.52
	5772	CG2	THR	D	54	42.292	68.967	166.143	1.00	25.21

	5773	C	THR D	54	40.648	69.965	163.001	1.00	26.33
	5774	O	THR D	54	41.202	70.275	161.953	1.00	26.71
	5775	N	VAL D	55	39.530	69.245	163.028	1.00	28.05
	5776	CA	VAL D	55	38.950	68.805	161.764	1.00	22.48
5	5777	CB	VAL D	55	37.988	67.621	161.944	1.00	23.03
	5778	CG1	VAL D	55	37.190	67.415	160.665	1.00	16.34
	5779	CG2	VAL D	55	38.782	66.354	162.257	1.00	23.82
	5780	C	VAL D	55	38.216	69.944	161.081	1.00	24.32
	5781	O	VAL D	55	38.241	70.059	159.839	1.00	23.32
10	5782	N	THR D	56	37.571	70.813	161.857	1.00	22.58
	5783	CA	THR D	56	36.880	71.877	161.172	1.00	24.61
	5784	CB	THR D	56	35.653	72.464	161.994	1.00	19.78
	5785	OG1	THR D	56	35.892	73.813	162.373	1.00	29.42
	5786	CG2	THR D	56	35.356	71.660	163.194	1.00	12.09
15	5787	C	THR D	56	37.880	72.947	160.697	1.00	26.37
	5788	O	THR D	56	37.698	73.517	159.613	1.00	24.90
	5789	N	LYS D	57	38.960	73.181	161.447	1.00	25.44
	5790	CA	LYS D	57	39.952	74.178	160.996	1.00	27.63
	5791	CB	LYS D	57	41.065	74.360	162.023	1.00	28.00
20	5792	CG	LYS D	57	40.715	75.339	163.111	1.00	35.69
	5793	CD	LYS D	57	41.611	75.183	164.326	1.00	42.72
	5794	CE	LYS D	57	43.075	75.411	164.014	1.00	47.19
	5795	NZ	LYS D	57	43.849	75.390	165.286	1.00	51.03
	5796	C	LYS D	57	40.565	73.718	159.690	1.00	24.90
25	5797	O	LYS D	57	40.704	74.500	158.764	1.00	27.61
	5798	N	ALA D	58	40.916	72.436	159.630	1.00	21.59
	5799	CA	ALA D	58	41.497	71.846	158.442	1.00	28.70
	5800	CB	ALA D	58	41.996	70.424	158.751	1.00	27.62
	5801	C	ALA D	58	40.522	71.809	157.260	1.00	32.44
30	5802	O	ALA D	58	40.910	72.102	156.121	1.00	34.79
	5803	N	ALA D	59	39.266	71.433	157.507	1.00	31.33
	5804	CA	ALA D	59	38.297	71.380	156.410	1.00	23.48
	5805	CB	ALA D	59	36.940	70.884	156.898	1.00	24.37
	5806	C	ALA D	59	38.165	72.780	155.837	1.00	21.59
35	5807	O	ALA D	59	38.096	72.941	154.624	1.00	21.47
	5808	N	ASN D	60	38.133	73.785	156.713	1.00	21.46
	5809	CA	ASN D	60	38.020	75.188	156.283	1.00	25.82
	5810	CB	ASN D	60	37.976	76.112	157.508	1.00	23.52
	5811	CG	ASN D	60	37.704	77.581	157.152	1.00	29.73
40	5812	OD1	ASN D	60	36.879	77.900	156.293	1.00	27.05
	5813	ND2	ASN D	60	38.380	78.482	157.855	1.00	32.23
	5814	C	ASN D	60	39.203	75.561	155.390	1.00	29.16
	5815	O	ASN D	60	39.030	76.215	154.365	1.00	33.60

	5816	N	LYS	D	61	40.405	75.137	155.773	1.00	34.38
	5817	CA	LYS	D	61	41.599	75.436	154.980	1.00	35.55
	5818	CB	LYS	D	61	42.881	75.110	155.754	1.00	43.25
	5819	CG	LYS	D	61	43.148	76.101	156.876	1.00	62.00
5	5820	CD	LYS	D	61	44.385	75.773	157.709	1.00	70.68
	5821	CE	LYS	D	61	44.535	76.796	158.849	1.00	76.65
	5822	NZ	LYS	D	61	45.577	76.442	159.865	1.00	80.29
	5823	C	LYS	D	61	41.617	74.698	153.662	1.00	31.92
	5824	O	LYS	D	61	42.062	75.254	152.662	1.00	33.97
10	5825	N	LEU	D	62	41.136	73.455	153.654	1.00	28.38
	5826	CA	LEU	D	62	41.130	72.651	152.430	1.00	25.45
	5827	CB	LEU	D	62	40.950	71.160	152.767	1.00	27.25
	5828	CG	LEU	D	62	42.115	70.462	153.482	1.00	34.62
	5829	CD1	LEU	D	62	41.701	69.079	153.980	1.00	31.58
15	5830	CD2	LEU	D	62	43.296	70.341	152.529	1.00	33.78
	5831	C	LEU	D	62	40.098	73.070	151.382	1.00	26.71
	5832	O	LEU	D	62	40.155	72.608	150.238	1.00	31.57
	5833	N	GLY	D	63	39.166	73.948	151.742	1.00	23.99
	5834	CA	GLY	D	63	38.164	74.350	150.766	1.00	24.81
20	5835	C	GLY	D	63	36.764	73.741	150.952	1.00	28.60
	5836	O	GLY	D	63	35.890	73.961	150.121	1.00	24.49
	5837	N	VAL	D	64	36.535	73.000	152.042	1.00	28.19
	5838	CA	VAL	D	64	35.227	72.385	152.298	1.00	26.72
	5839	CB	VAL	D	64	35.305	71.368	153.465	1.00	25.98
25	5840	CG1	VAL	D	64	33.900	70.833	153.813	1.00	18.91
	5841	CG2	VAL	D	64	36.231	70.228	153.074	1.00	25.27
	5842	C	VAL	D	64	34.234	73.490	152.635	1.00	22.94
	5843	O	VAL	D	64	34.560	74.399	153.372	1.00	23.43
	5844	N	LYS	D	65	33.034	73.416	152.073	1.00	21.87
30	5845	CA	LYS	D	65	32.030	74.444	152.296	1.00	22.60
	5846	CB	LYS	D	65	31.123	74.574	151.075	1.00	26.62
	5847	CG	LYS	D	65	31.846	74.984	149.811	1.00	31.34
	5848	CD	LYS	D	65	32.575	76.319	150.002	1.00	36.68
	5849	CE	LYS	D	65	33.171	76.813	148.677	1.00	46.28
35	5850	NZ	LYS	D	65	33.882	78.131	148.824	1.00	51.34
	5851	C	LYS	D	65	31.174	74.214	153.519	1.00	21.40
	5852	O	LYS	D	65	30.822	75.159	154.209	1.00	20.51
	5853	N	VAL	D	66	30.842	72.954	153.783	1.00	20.16
	5854	CA	VAL	D	66	30.002	72.622	154.919	1.00	16.40
40	5855	CB	VAL	D	66	28.513	72.450	154.465	1.00	20.80
	5856	CG1	VAL	D	66	27.611	72.204	155.658	1.00	17.44
	5857	CG2	VAL	D	66	28.053	73.666	153.692	1.00	12.74
	5858	C	VAL	D	66	30.406	71.296	155.548	1.00	17.35

	5859	O	VAL	D	66	30.732	70.359	154.830	1.00	18.65
	5860	N	ILE	D	67	30.446	71.229	156.873	1.00	13.25
	5861	CA	ILE	D	67	30.645	69.941	157.512	1.00	18.92
	5862	CB	ILE	D	67	31.986	69.746	158.353	1.00	26.53
5	5863	CG2	ILE	D	67	33.230	69.759	157.446	1.00	21.38
	5864	CG1	ILE	D	67	32.113	70.788	159.448	1.00	31.25
	5865	CD1	ILE	D	67	33.298	70.495	160.367	1.00	31.73
	5866	C	ILE	D	67	29.438	69.833	158.453	1.00	22.96
	5867	O	ILE	D	67	29.175	70.739	159.253	1.00	20.09
10	5868	N	THR	D	68	28.650	68.767	158.289	1.00	17.21
	5869	CA	THR	D	68	27.513	68.532	159.161	1.00	18.54
	5870	CB	THR	D	68	26.248	68.142	158.390	1.00	23.46
	5871	OG1	THR	D	68	25.866	69.243	157.560	1.00	24.20
	5872	CG2	THR	D	68	25.109	67.807	159.366	1.00	9.03
15	5873	C	THR	D	68	27.982	67.407	160.061	1.00	18.17
	5874	O	THR	D	68	28.266	66.284	159.630	1.00	21.64
	5875	N	VAL	D	69	28.069	67.739	161.331	1.00	17.60
	5876	CA	VAL	D	69	28.600	66.838	162.310	1.00	17.25
	5877	CB	AVAL	D	69	29.740	67.579	163.058	0.50	18.30
20	7718	CB	BVAL	D	69	29.789	67.518	163.005	0.50	16.30
	5878	CG1AVAL	D	69	29.881	67.055	164.448	0.50	21.30	
	7719	CG1BVAL	D	69	29.316	68.492	164.084	0.50	7.03	
	5879	CG2AVAL	D	69	31.051	67.466	162.276	0.50	6.35	
	7720	CG2BVAL	D	69	30.710	66.479	163.505	0.50	12.12	
25	5880	C	VAL	D	69	27.537	66.319	163.314	1.00	20.32
	5881	O	VAL	D	69	26.774	67.077	163.881	1.00	20.76
	5882	N	TYR	D	70	27.526	65.017	163.544	1.00	20.88
	5883	CA	TYR	D	70	26.525	64.381	164.395	1.00	21.38
	5884	CB	TYR	D	70	25.771	63.380	163.501	1.00	24.61
30	5885	CG	TYR	D	70	24.610	62.579	164.067	1.00	19.51
	5886	CD1	TYR	D	70	23.611	63.173	164.837	1.00	23.23
	5887	CE1	TYR	D	70	22.470	62.476	165.191	1.00	19.62
	5888	CD2	TYR	D	70	24.431	61.250	163.675	1.00	29.18
	5889	CE2	TYR	D	70	23.294	60.544	164.020	1.00	29.01
35	5890	CZ	TYR	D	70	22.319	61.163	164.780	1.00	30.73
	5891	OH	TYR	D	70	21.210	60.439	165.132	1.00	43.11
	5892	C	TYR	D	70	27.108	63.699	165.616	1.00	24.05
	5893	O	TYR	D	70	27.894	62.756	165.493	1.00	22.26
	5894	N	ALA	D	71	26.687	64.171	166.789	1.00	38.30
40	5895	CA	ALA	D	71	27.138	63.652	168.079	1.00	52.13
	5896	CB	ALA	D	71	26.638	64.568	169.176	1.00	54.94
	5897	C	ALA	D	71	26.743	62.194	168.396	1.00	62.43
	5898	O	ALA	D	71	27.295	61.245	167.821	1.00	61.48

	5899	N	PHE D	72	25.806	62.017	169.332	1.00	72.70
	5900	CA	PHE D	72	25.361	60.673	169.714	1.00	82.28
	5901	CB	PHE D	72	24.225	60.747	170.756	1.00	89.06
	5902	CG	PHE D	72	23.871	59.406	171.402	1.00	95.63
5	5903	CD1	PHE D	72	23.268	58.381	170.662	1.00	96.57
	5904	CD2	PHE D	72	24.126	59.181	172.761	1.00	97.69
	5905	CE1	PHE D	72	22.924	57.160	171.259	1.00	95.11
	5906	CE2	PHE D	72	23.785	57.962	173.369	1.00	97.98
	5907	CZ	PHE D	72	23.183	56.953	172.614	1.00	97.03
10	5908	C	PHE D	72	24.874	59.993	168.441	1.00	85.41
	5909	O	PHE D	72	24.469	60.668	167.493	1.00	86.55
	5910	N	SER D	73	24.915	58.663	168.421	1.00	87.73
	5911	CA	SER D	73	24.496	57.904	167.247	1.00	86.19
	5912	CB	SER D	73	25.443	58.222	166.100	1.00	86.48
15	5913	OG	SER D	73	26.767	58.336	166.598	1.00	88.15
	5914	C	SER D	73	24.504	56.405	167.520	1.00	86.94
	5915	O	SER D	73	25.563	55.774	167.517	1.00	86.05
	5916	N	THR D	78	24.981	54.823	178.842	0.30	93.96
	5917	CA	THR D	78	23.811	55.692	178.842	0.30	94.11
20	5918	CB	THR D	78	22.680	55.101	177.973	0.30	93.10
	5919	OG1	THR D	78	22.345	53.792	178.446	0.30	92.02
	5920	CG2	THR D	78	23.118	55.013	176.519	0.30	91.79
	5921	C	THR D	78	23.285	55.910	180.258	0.30	95.37
	5922	O	THR D	78	22.582	55.064	180.811	0.30	95.17
25	5923	N	ARG D	79	23.638	57.053	180.838	1.00	96.68
	5924	CA	ARG D	79	23.216	57.407	182.192	1.00	98.40
	5925	CB	ARG D	79	24.285	56.965	183.199	1.00	97.66
	5926	CG	ARG D	79	24.599	55.479	183.150	0.30	98.06
	5927	CD	ARG D	79	25.584	55.076	184.236	0.30	98.28
30	5928	NE	ARG D	79	25.901	53.651	184.176	0.30	97.22
	5929	CZ	ARG D	79	26.676	53.018	185.050	0.30	96.66
	5930	NH1	ARG D	79	27.219	53.683	186.061	0.30	95.97
	5931	NH2	ARG D	79	26.912	51.721	184.911	0.30	96.02
	5932	C	ARG D	79	22.988	58.925	182.310	1.00	100.00
35	5933	O	ARG D	79	23.766	59.717	181.764	1.00	100.00
	5934	N	PRO D	80	21.916	59.349	183.023	1.00	100.00
	5935	CD	PRO D	80	20.882	58.480	183.625	1.00	100.00
	5936	CA	PRO D	80	21.571	60.768	183.223	1.00	100.00
	5937	CB	PRO D	80	20.507	60.708	184.318	1.00	98.82
40	5938	CG	PRO D	80	19.753	59.468	183.940	1.00	99.83
	5939	C	PRO D	80	22.733	61.714	183.577	1.00	100.00
	5940	O	PRO D	80	23.022	62.646	182.814	1.00	100.00
	5941	N	ASP D	81	23.388	61.485	184.720	1.00	100.00

	5942	CA	ASP	D	81	24.511	62.331	185.138	1.00100.00
	5943	CB	ASP	D	81	24.954	61.994	186.565	1.00 99.71
	5944	CG	ASP	D	81	24.092	62.677	187.614	1.00100.00
	5945	OD1	ASP	D	81	22.893	62.335	187.719	1.00100.00
5	5946	OD2	ASP	D	81	24.615	63.563	188.328	1.00100.00
	5947	C	ASP	D	81	25.700	62.223	184.192	1.00100.00
	5948	O	ASP	D	81	26.788	61.783	184.576	1.00100.00
	5949	N	GLN	D	82	25.455	62.647	182.953	1.00100.00
	5950	CA	GLN	D	82	26.419	62.648	181.862	1.00 98.67
10	5951	CB	GLN	D	82	27.158	61.310	181.777	1.00 99.01
	5952	CG	GLN	D	82	28.110	61.215	180.594	1.00 99.73
	5953	CD	GLN	D	82	28.797	59.867	180.490	1.00100.00
	5954	OE1	GLN	D	82	29.443	59.568	179.487	1.00 99.90
	5955	NE2	GLN	D	82	28.666	59.046	181.529	1.00100.00
15	5956	C	GLN	D	82	25.610	62.873	180.590	1.00 98.00
	5957	O	GLN	D	82	25.466	64.005	180.129	1.00 97.88
	5958	N	GLU	D	83	25.069	61.791	180.037	0.00 97.36
	5959	CA	GLU	D	83	24.264	61.868	178.823	0.00 96.70
	5960	CB	GLU	D	83	23.509	60.549	178.614	0.00 96.78
20	5961	CG	GLU	D	83	22.913	60.363	177.222	0.00 96.85
	5962	CD	GLU	D	83	21.578	61.060	177.043	0.00 96.89
	5963	OE1	GLU	D	83	21.063	61.072	175.906	0.00 96.90
	5964	OE2	GLU	D	83	21.039	61.587	178.037	0.00 96.90
	5965	C	GLU	D	83	23.286	63.034	178.955	0.00 96.17
25	5966	O	GLU	D	83	22.723	63.505	177.967	0.00 96.17
	5967	N	VAL	D	84	23.102	63.495	180.189	0.00 95.50
	5968	CA	VAL	D	84	22.218	64.614	180.487	0.00 94.74
	5969	CB	VAL	D	84	20.949	64.140	181.225	0.00 94.76
	5970	CG1	VAL	D	84	19.955	65.280	181.339	0.00 94.68
30	5971	CG2	VAL	D	84	20.331	62.964	180.495	0.00 94.68
	5972	C	VAL	D	84	22.942	65.629	181.374	0.00 94.32
	5973	O	VAL	D	84	22.411	66.700	181.665	0.00 94.17
	5974	N	LYS	D	85	24.158	65.292	181.799	1.00 93.40
	5975	CA	LYS	D	85	24.937	66.181	182.660	1.00 93.90
35	5976	CB	LYS	D	85	25.348	65.453	183.940	1.00 95.53
	5977	CG	LYS	D	85	24.545	65.829	185.179	1.00 98.00
	5978	CD	LYS	D	85	24.849	67.252	185.640	1.00 97.99
	5979	CE	LYS	D	85	24.155	67.568	186.961	1.00 99.48
	5980	NZ	LYS	D	85	24.458	68.949	187.451	1.00100.00
40	5981	C	LYS	D	85	26.184	66.756	182.000	1.00 94.14
	5982	O	LYS	D	85	26.397	67.971	182.005	1.00 93.55
	5983	N	PHE	D	86	27.015	65.882	181.445	1.00 93.91
	5984	CA	PHE	D	86	28.242	66.326	180.801	1.00 92.51



	5985	CB	PHE D	86	29.297	65.226	180.837	1.00	95.39
	5986	CG	PHE D	86	30.625	65.705	181.322	1.00	98.40
	5987	CD1	PHE D	86	30.909	65.731	182.682	1.00	100.00
	5988	CD2	PHE D	86	31.570	66.197	180.426	1.00	99.94
5	5989	CE1	PHE D	86	32.119	66.244	183.151	1.00	100.00
	5990	CE2	PHE D	86	32.785	66.716	180.877	1.00	100.00
	5991	CZ	PHE D	86	33.062	66.741	182.245	1.00	100.00
	5992	C	PHE D	86	28.033	66.774	179.365	1.00	90.60
	5993	O	PHE D	86	28.595	67.779	178.933	1.00	92.28
10	5994	N	ILE D	87	27.228	66.023	178.626	1.00	87.01
	5995	CA	ILE D	87	26.957	66.355	177.236	1.00	84.47
	5996	CB	ILE D	87	26.473	65.101	176.454	1.00	87.95
	5997	CG2	ILE D	87	26.487	65.378	174.940	1.00	89.09
	5998	CG1	ILE D	87	27.408	63.917	176.766	1.00	87.77
15	5999	CD1	ILE D	87	27.044	62.616	176.064	1.00	88.91
	6000	C	ILE D	87	25.930	67.493	177.152	1.00	81.17
	6001	O	ILE D	87	25.460	67.854	176.069	1.00	81.59
	6002	N	MET D	88	25.572	68.050	178.306	1.00	75.61
	6003	CA	MET D	88	24.654	69.175	178.322	1.00	70.76
20	6004	CB	MET D	88	23.523	68.979	179.360	1.00	70.10
	6005	CG	AMET D	88	22.590	67.846	178.954	0.50	72.40
	7721	CG	BMET D	88	23.846	69.471	180.801	0.50	67.58
	6006	SD	AMET D	88	22.387	67.684	177.127	0.50	71.78
	7722	SD	BMET D	88	22.466	69.716	182.013	0.50	68.85
25	6007	CE	AMET D	88	21.596	66.038	177.023	0.50	71.91
	7723	CE	BMET D	88	22.496	71.472	182.154	0.50	58.97
	6008	C	MET D	88	25.514	70.387	178.641	1.00	67.14
	6009	O	MET D	88	25.089	71.535	178.497	1.00	65.60
	6010	N	ASN D	89	26.751	70.109	179.037	1.00	63.12
30	6011	CA	ASN D	89	27.715	71.156	179.357	1.00	61.74
	6012	CB	ASN D	89	28.343	70.906	180.728	1.00	62.41
	6013	CG	ASN D	89	29.196	72.074	181.196	1.00	68.74
	6014	OD1	ASN D	89	28.678	73.153	181.514	1.00	68.37
	6015	ND2	ASN D	89	30.515	71.876	181.215	1.00	69.47
35	6016	C	ASN D	89	28.814	71.238	178.290	1.00	58.21
	6017	O	ASN D	89	29.571	72.211	178.238	1.00	54.23
	6018	N	LEU D	90	28.898	70.225	177.432	1.00	54.65
	6019	CA	LEU D	90	29.905	70.238	176.372	1.00	50.53
	6020	CB	LEU D	90	29.842	68.950	175.534	1.00	49.38
40	6021	CG	LEU D	90	30.420	67.676	176.167	1.00	52.71
	6022	CD1	LEU D	90	30.133	66.449	175.275	1.00	47.90
	6023	CD2	LEU D	90	31.930	67.862	176.381	1.00	51.41
	6024	C	LEU D	90	29.702	71.460	175.472	1.00	44.28

	6025	O	LEU	D	90	30.667	72.119	175.087	1.00	40.67
	6026	N	PRO	D	91	28.441	71.771	175.119	1.00	40.86
	6027	CD	PRO	D	91	27.232	70.929	175.136	1.00	40.90
	6028	CA	PRO	D	91	28.227	72.939	174.264	1.00	40.05
5	6029	CB	PRO	D	91	26.725	72.901	174.004	1.00	39.04
	6030	CG	PRO	D	91	26.470	71.438	173.905	1.00	35.14
	6031	C	PRO	D	91	28.673	74.218	174.935	1.00	39.02
	6032	O	PRO	D	91	29.174	75.123	174.285	1.00	41.93
	6033	N	VAL	D	92	28.497	74.296	176.244	1.00	38.20
10	6034	CA	VAL	D	92	28.906	75.491	176.950	1.00	37.45
	6035	CB	VAL	D	92	28.434	75.451	178.425	1.00	37.04
	6036	CG1	VAL	D	92	28.359	76.866	178.988	1.00	30.49
	6037	CG2	VAL	D	92	27.076	74.762	178.508	1.00	39.79
	6038	C	VAL	D	92	30.436	75.590	176.882	1.00	37.83
15	6039	O	VAL	D	92	30.982	76.648	176.547	1.00	34.15
	6040	N	GLU	D	93	31.119	74.486	177.189	1.00	39.62
	6041	CA	GLU	D	93	32.589	74.441	177.156	1.00	44.61
	6042	CB	GLU	D	93	33.115	73.070	177.612	1.00	49.36
	6043	CG	GLU	D	93	33.334	72.914	179.112	1.00	60.54
20	6044	CD	GLU	D	93	33.824	71.518	179.491	1.00	66.56
	6045	OE1	GLU	D	93	34.868	71.080	178.950	1.00	66.48
	6046	OE2	GLU	D	93	33.161	70.858	180.330	1.00	71.74
	6047	C	GLU	D	93	33.109	74.718	175.745	1.00	43.85
	6048	O	GLU	D	93	34.105	75.427	175.554	1.00	43.53
25	6049	N	PHE	D	94	32.432	74.147	174.757	1.00	40.25
	6050	CA	PHE	D	94	32.820	74.354	173.377	1.00	41.92
	6051	CB	PHE	D	94	31.875	73.601	172.437	1.00	44.47
	6052	CG	PHE	D	94	32.299	73.646	171.005	1.00	40.18
	6053	CD1	PHE	D	94	33.453	72.967	170.588	1.00	38.25
30	6054	CD2	PHE	D	94	31.592	74.411	170.086	1.00	39.02
	6055	CE1	PHE	D	94	33.900	73.056	169.273	1.00	32.89
	6056	CE2	PHE	D	94	32.033	74.507	168.767	1.00	39.32
	6057	CZ	PHE	D	94	33.193	73.828	168.364	1.00	25.20
	6058	C	PHE	D	94	32.760	75.840	173.068	1.00	42.55
35	6059	O	PHE	D	94	33.710	76.408	172.527	1.00	47.20
	6060	N	TYR	D	95	31.642	76.466	173.423	1.00	40.00
	6061	CA	TYR	D	95	31.449	77.891	173.170	1.00	40.46
	6062	CB	TYR	D	95	30.066	78.344	173.659	1.00	42.86
	6063	CG	TYR	D	95	29.886	79.850	173.641	1.00	45.63
40	6064	CD1	TYR	D	95	29.873	80.562	172.434	1.00	47.08
	6065	CE1	TYR	D	95	29.738	81.948	172.413	1.00	45.11
	6066	CD2	TYR	D	95	29.756	80.571	174.824	1.00	49.03
	6067	CE2	TYR	D	95	29.616	81.967	174.811	1.00	49.07

	6068	CZ	TYR	D	95	29.607	82.643	173.603	1.00	46.75
	6069	OH	TYR	D	95	29.438	84.009	173.582	1.00	51.83
	6070	C	TYR	D	95	32.511	78.760	173.827	1.00	40.67
	6071	O	TYR	D	95	32.950	79.757	173.257	1.00	38.43
5	6072	N	ASP	D	96	32.919	78.383	175.032	1.00	43.38
	6073	CA	ASP	D	96	33.902	79.165	175.766	1.00	45.21
	6074	CB	ASP	D	96	33.813	78.879	177.271	1.00	50.93
	6075	CG	ASP	D	96	32.514	79.361	177.887	1.00	53.39
	6076	OD1	ASP	D	96	32.159	80.534	177.658	1.00	58.40
10	6077	OD2	ASP	D	96	31.856	78.573	178.604	1.00	53.50
	6078	C	ASP	D	96	35.332	78.945	175.349	1.00	44.63
	6079	O	ASP	D	96	36.118	79.886	175.343	1.00	48.66
	6080	N	ASN	D	97	35.667	77.710	174.984	1.00	43.04
	6081	CA	ASN	D	97	37.048	77.373	174.656	1.00	39.60
15	6082	CB	ASN	D	97	37.477	76.188	175.530	1.00	46.02
	6083	CG	ASN	D	97	37.190	76.422	177.020	1.00	51.86
	6084	OD1	ASN	D	97	37.664	77.403	177.615	1.00	49.35
	6085	ND2	ASN	D	97	36.414	75.518	177.624	1.00	50.90
	6086	C	ASN	D	97	37.448	77.086	173.215	1.00	38.11
20	6087	O	ASN	D	97	38.635	76.924	172.928	1.00	39.09
	6088	N	TYR	D	98	36.491	77.006	172.302	1.00	33.09
	6089	CA	TYR	D	98	36.851	76.726	170.928	1.00	28.38
	6090	CB	TYR	D	98	36.484	75.286	170.568	1.00	32.06
	6091	CG	TYR	D	98	37.197	74.247	171.395	1.00	32.88
25	6092	CD1	TYR	D	98	36.692	73.845	172.633	1.00	32.59
	6093	CE1	TYR	D	98	37.365	72.892	173.410	1.00	32.71
	6094	CD2	TYR	D	98	38.398	73.676	170.951	1.00	32.41
	6095	CE2	TYR	D	98	39.079	72.728	171.720	1.00	32.88
	6096	CZ	TYR	D	98	38.555	72.341	172.943	1.00	35.46
30	6097	OH	TYR	D	98	39.209	71.399	173.694	1.00	38.04
	6098	C	TYR	D	98	36.206	77.675	169.925	1.00	29.48
	6099	O	TYR	D	98	36.806	77.988	168.889	1.00	26.15
	6100	N	VAL	D	99	34.997	78.139	170.242	1.00	25.69
	6101	CA	VAL	D	99	34.253	79.030	169.355	1.00	27.56
35	6102	CB	VAL	D	99	32.830	79.313	169.946	1.00	28.92
	6103	CG1	VAL	D	99	32.128	80.414	169.180	1.00	19.79
	6104	CG2	VAL	D	99	31.986	78.016	169.874	1.00	27.21
	6105	C	VAL	D	99	34.956	80.344	168.967	1.00	28.53
	6106	O	VAL	D	99	34.933	80.742	167.794	1.00	29.56
40	6107	N	PRO	D	100	35.589	81.034	169.931	1.00	26.69
	6108	CD	PRO	D	100	35.565	80.917	171.400	1.00	23.46
	6109	CA	PRO	D	100	36.235	82.277	169.497	1.00	27.12
	6110	CB	PRO	D	100	36.786	82.883	170.807	1.00	30.36

	6111	CG	PRO D 100	36.725	81.768	171.812	1.00	35.22
	6112	C	PRO D 100	37.290	82.055	168.421	1.00	24.63
	6113	O	PRO D 100	37.397	82.852	167.490	1.00	30.46
	6114	N	GLU D 101	38.044	80.961	168.527	1.00	23.03
5	6115	CA	GLU D 101	39.056	80.635	167.523	1.00	21.98
	6116	CB	GLU D 101	39.950	79.468	167.985	1.00	23.49
	6117	CG	GLU D 101	40.975	79.076	166.902	1.00	30.94
	6118	CD	GLU D 101	41.895	77.935	167.314	1.00	40.80
	6119	OE1	GLU D 101	41.578	77.231	168.310	1.00	41.04
10	6120	OE2	GLU D 101	42.933	77.738	166.626	1.00	40.11
	6121	C	GLU D 101	38.384	80.267	166.185	1.00	24.49
	6122	O	GLU D 101	38.870	80.637	165.103	1.00	25.73
	6123	N	LEU D 102	37.279	79.520	166.248	1.00	22.56
	6124	CA	LEU D 102	36.553	79.177	165.020	1.00	21.86
15	6125	CB	LEU D 102	35.358	78.257	165.312	1.00	22.88
	6126	CG	LEU D 102	35.748	76.831	165.689	1.00	27.46
	6127	CD1	LEU D 102	34.508	75.984	165.947	1.00	19.44
	6128	CD2	LEU D 102	36.581	76.248	164.530	1.00	30.85
	6129	C	LEU D 102	36.052	80.482	164.411	1.00	17.85
20	6130	O	LEU D 102	36.072	80.669	163.180	1.00	15.76
	6131	N	HIS D 103	35.623	81.400	165.271	1.00	16.69
	6132	CA	HIS D 103	35.131	82.662	164.754	1.00	27.18
	6133	CB	HIS D 103	34.510	83.485	165.872	1.00	22.97
	6134	CG	HIS D 103	34.019	84.824	165.424	1.00	28.33
25	6135	CD2	HIS D 103	34.157	86.056	165.974	1.00	27.91
	6136	ND1	HIS D 103	33.195	84.981	164.331	1.00	15.98
	6137	CE1	HIS D 103	32.833	86.247	164.237	1.00	24.92
	6138	NE2	HIS D 103	33.401	86.921	165.221	1.00	24.90
	6139	C	HIS D 103	36.271	83.446	164.080	1.00	26.61
30	6140	O	HIS D 103	36.104	83.999	162.987	1.00	29.47
	6141	N	ALA D 104	37.425	83.482	164.737	1.00	26.98
	6142	CA	ALA D 104	38.583	84.176	164.184	1.00	26.49
	6143	CB	ALA D 104	39.778	84.110	165.176	1.00	22.46
	6144	C	ALA D 104	38.941	83.506	162.856	1.00	27.99
35	6145	O	ALA D 104	39.559	84.118	161.995	1.00	29.20
	6146	N	ASN D 105	38.543	82.249	162.676	1.00	26.05
	6147	CA	ASN D 105	38.853	81.572	161.423	1.00	23.54
	6148	CB	ASN D 105	39.096	80.094	161.672	1.00	33.79
	6149	CG	ASN D 105	40.508	79.815	162.132	1.00	37.79
40	6150	OD1	ASN D 105	41.358	79.404	161.341	1.00	45.56
	6151	ND2	ASN D 105	40.772	80.051	163.414	1.00	40.73
	6152	C	ASN D 105	37.794	81.741	160.350	1.00	22.57
	6153	O	ASN D 105	37.839	81.068	159.319	1.00	25.33

	6154	N	ASN D 106	36.845	82.643	160.584	1.00	21.46
	6155	CA	ASN D 106	35.768	82.901	159.628	1.00	19.56
	6156	CB	ASN D 106	36.365	83.369	158.285	1.00	16.33
	6157	CG	ASN D 106	35.336	84.049	157.370	1.00	22.87
5	6158	OD1	ASN D 106	35.480	84.041	156.133	1.00	23.64
	6159	ND2	ASN D 106	34.310	84.649	157.965	1.00	6.84
	6160	C	ASN D 106	34.859	81.666	159.417	1.00	17.72
	6161	O	ASN D 106	34.358	81.462	158.325	1.00	17.99
	6162	N	VAL D 107	34.671	80.852	160.458	1.00	19.40
10	6163	CA	VAL D 107	33.788	79.683	160.401	1.00	24.55
	6164	CB	VAL D 107	34.337	78.494	161.249	1.00	25.54
	6165	CG1	VAL D 107	33.322	77.341	161.273	1.00	21.76
	6166	CG2	VAL D 107	35.662	77.995	160.657	1.00	19.97
	6167	C	VAL D 107	32.379	80.044	160.920	1.00	23.70
15	6168	O	VAL D 107	32.218	80.620	161.986	1.00	23.47
	6169	N	LYS D 108	31.359	79.717	160.148	1.00	21.64
	6170	CA	LYS D 108	29.985	80.012	160.547	1.00	22.62
	6171	CB	LYS D 108	29.151	80.380	159.327	1.00	16.51
	6172	CG	LYS D 108	27.708	80.734	159.611	1.00	17.92
20	6173	CD	LYS D 108	27.063	80.926	158.269	1.00	24.87
	6174	CE	LYS D 108	25.735	81.639	158.349	1.00	39.06
	6175	NZ	LYS D 108	25.311	82.029	156.958	1.00	45.06
	6176	C	LYS D 108	29.424	78.752	161.204	1.00	23.04
	6177	O	LYS D 108	29.564	77.653	160.669	1.00	22.08
25	6178	N	ILE D 109	28.795	78.928	162.362	1.00	23.35
	6179	CA	ILE D 109	28.246	77.826	163.120	1.00	22.53
	6180	CB	ILE D 109	28.777	77.859	164.570	1.00	21.99
	6181	CG2	ILE D 109	28.293	76.632	165.355	1.00	27.12
	6182	CG1	ILE D 109	30.308	77.851	164.562	1.00	23.29
30	6183	CD1	ILE D 109	30.957	77.968	165.949	1.00	20.18
	6184	C	ILE D 109	26.716	77.834	163.121	1.00	24.38
	6185	O	ILE D 109	26.100	78.857	163.406	1.00	22.27
	6186	N	GLN D 110	26.127	76.687	162.769	1.00	20.15
	6187	CA	GLN D 110	24.666	76.510	162.741	1.00	26.37
35	6188	CB	GLN D 110	24.107	76.571	161.304	1.00	20.04
	6189	CG	GLN D 110	24.335	77.904	160.623	1.00	29.36
	6190	CD	GLN D 110	23.591	78.048	159.308	1.00	33.34
	6191	OE1	GLN D 110	23.630	77.161	158.445	1.00	30.67
	6192	NE2	GLN D 110	22.914	79.184	159.141	1.00	37.42
40	6193	C	GLN D 110	24.288	75.169	163.354	1.00	21.62
	6194	O	GLN D 110	25.141	74.334	163.616	1.00	25.07
	6195	N	MET D 111	23.002	74.953	163.570	1.00	26.97
	6196	CA	MET D 111	22.553	73.696	164.152	1.00	33.18

	6197	CB	MET	D	111	22.259	73.900	165.618	0.50	37.80
	6198	CG	AMET	D	111	22.320	75.346	165.990	0.50	49.46
	7724	CG	BMET	D	111	21.399	75.116	165.902	0.50	55.88
	6199	SD	AMET	D	111	23.960	75.712	166.521	0.50	56.46
5	7725	SD	BMET	D	111	20.945	75.301	167.643	0.50	73.72
	6200	CE	AMET	D	111	23.680	75.629	168.121	0.50	58.87
	7726	CE	BMET	D	111	22.344	74.568	168.407	0.50	65.35
	6201	C	MET	D	111	21.303	73.175	163.486	1.00	28.09
	6202	O	MET	D	111	20.538	73.935	162.911	1.00	29.71
10	6203	N	ILE	D	112	21.116	71.867	163.544	1.00	23.99
	6204	CA	ILE	D	112	19.905	71.250	163.017	1.00	21.53
	6205	CB	ILE	D	112	20.096	70.551	161.617	1.00	23.39
	6206	CG2	ILE	D	112	20.263	71.581	160.497	1.00	25.19
	6207	CG1	ILE	D	112	21.284	69.618	161.637	1.00	16.54
15	6208	CD1	ILE	D	112	21.404	68.813	160.324	1.00	21.42
	6209	C	ILE	D	112	19.528	70.221	164.085	1.00	21.51
	6210	O	ILE	D	112	20.401	69.622	164.751	1.00	23.96
	6211	N	GLY	D	113	18.231	70.029	164.259	1.00	16.88
	6212	CA	GLY	D	113	17.754	69.113	165.273	1.00	22.10
20	6213	C	GLY	D	113	16.773	69.878	166.132	1.00	25.32
	6214	O	GLY	D	113	16.567	71.076	165.944	1.00	26.11
	6215	N	GLU	D	114	16.165	69.204	167.089	1.00	28.28
	6216	CA	GLU	D	114	15.197	69.868	167.942	1.00	33.26
	6217	CB	GLU	D	114	14.087	68.864	168.292	1.00	35.95
25	6218	CG	GLU	D	114	13.578	68.170	167.019	1.00	40.98
	6219	CD	GLU	D	114	12.413	67.218	167.240	1.00	51.22
	6220	OE1	GLU	D	114	12.222	66.297	166.409	1.00	49.28
	6221	OE2	GLU	D	114	11.674	67.398	168.227	1.00	58.49
	6222	C	GLU	D	114	15.922	70.424	169.164	1.00	33.78
30	6223	O	GLU	D	114	15.781	69.931	170.285	1.00	33.23
	6224	N	THR	D	115	16.702	71.473	168.907	1.00	39.26
	6225	CA	THR	D	115	17.513	72.161	169.909	1.00	42.70
	6226	CB	THR	D	115	18.438	73.220	169.240	1.00	45.35
	6227	OG1	THR	D	115	19.086	72.650	168.096	1.00	47.52
35	6228	CG2	THR	D	115	19.514	73.662	170.216	0.00	45.00
	6229	C	THR	D	115	16.740	72.843	171.052	1.00	41.85
	6230	O	THR	D	115	17.326	73.121	172.093	1.00	41.22
	6231	N	ASP	D	116	15.448	73.113	170.853	1.00	46.47
	6232	CA	ASP	D	116	14.592	73.733	171.882	1.00	50.85
40	6233	CB	ASP	D	116	13.115	73.719	171.488	1.00	54.34
	6234	CG	ASP	D	116	12.851	74.376	170.195	1.00	60.82
	6235	OD1	ASP	D	116	13.100	75.592	170.104	1.00	70.09
	6236	OD2	ASP	D	116	12.385	73.674	169.273	1.00	68.92

	6237	C	ASP D 116	14.634	72.910	173.159	1.00	50.97
	6238	O	ASP D 116	14.804	73.435	174.264	1.00	53.93
	6239	N	ARG D 117	14.423	71.612	172.968	1.00	45.97
	6240	CA	ARG D 117	14.352	70.629	174.034	1.00	44.53
5	6241	CB	ARG D 117	14.018	69.265	173.452	1.00	44.97
	6242	CG	ARG D 117	12.756	69.191	172.623	1.00	53.45
	6243	CD	ARG D 117	12.751	67.815	171.994	1.00	66.67
	6244	NE	ARG D 117	11.464	67.380	171.473	1.00	76.38
	6245	CZ	ARG D 117	11.275	66.187	170.914	1.00	83.43
10	6246	NH1	ARG D 117	12.298	65.341	170.818	1.00	85.60
	6247	NH2	ARG D 117	10.076	65.835	170.454	1.00	85.14
	6248	C	ARG D 117	15.579	70.472	174.893	1.00	40.49
	6249	O	ARG D 117	15.501	69.886	175.973	1.00	45.83
	6250	N	LEU D 118	16.714	70.971	174.433	1.00	32.16
15	6251	CA	LEU D 118	17.923	70.816	175.220	1.00	28.95
	6252	CB	LEU D 118	19.150	71.194	174.384	1.00	37.07
	6253	CG	LEU D 118	19.556	70.318	173.202	1.00	31.39
	6254	CD1	LEU D 118	20.491	71.081	172.320	1.00	31.59
	6255	CD2	LEU D 118	20.217	69.042	173.722	1.00	41.68
20	6256	C	LEU D 118	17.890	71.676	176.467	1.00	28.79
	6257	O	LEU D 118	17.110	72.631	176.563	1.00	28.51
	6258	N	PRO D 119	18.729	71.340	177.458	1.00	24.23
	6259	CD	PRO D 119	19.713	70.239	177.503	1.00	26.67
	6260	CA	PRO D 119	18.745	72.154	178.677	1.00	24.99
25	6261	CB	PRO D 119	19.950	71.618	179.452	1.00	22.23
	6262	CG	PRO D 119	20.067	70.159	178.981	1.00	24.19
	6263	C	PRO D 119	18.951	73.632	178.271	1.00	33.78
	6264	O	PRO D 119	19.741	73.941	177.365	1.00	34.14
	6265	N	LYS D 120	18.236	74.531	178.940	1.00	34.03
30	6266	CA	LYS D 120	18.321	75.964	178.680	1.00	34.61
	6267	CB	LYS D 120	17.665	76.717	179.834	1.00	29.48
	6268	CG	LYS D 120	17.758	78.220	179.777	1.00	33.41
	6269	CD	LYS D 120	16.913	78.822	180.895	1.00	34.46
	6270	CE	LYS D 120	16.846	80.347	180.815	1.00	31.91
35	6271	NZ	LYS D 120	18.088	80.952	181.329	1.00	36.84
	6272	C	LYS D 120	19.759	76.462	178.507	1.00	35.11
	6273	O	LYS D 120	20.114	77.052	177.486	1.00	30.88
	6274	N	GLN D 121	20.586	76.217	179.509	1.00	33.41
	6275	CA	GLN D 121	21.956	76.687	179.448	1.00	38.90
40	6276	CB	GLN D 121	22.705	76.310	180.729	1.00	42.39
	6277	CG	GLN D 121	23.733	77.352	181.126	1.00	58.56
	6278	CD	GLN D 121	24.298	77.143	182.519	1.00	63.84
	6279	OE1	GLN D 121	25.031	76.184	182.774	1.00	66.26

	6280	NE2	GLN	D	121	23.956	78.048	183.432	1.00	64.53
	6281	C	GLN	D	121	22.715	76.187	178.217	1.00	36.31
	6282	O	GLN	D	121	23.515	76.936	177.641	1.00	30.61
	6283	N	THR	D	122	22.475	74.942	177.802	1.00	32.04
5	6284	CA	THR	D	122	23.188	74.450	176.636	1.00	31.84
	6285	CB	THR	D	122	23.341	72.888	176.642	1.00	29.05
	6286	OG1	THR	D	122	23.125	72.351	175.330	1.00	32.17
	6287	CG2	THR	D	122	22.440	72.257	177.644	1.00	31.53
	6288	C	THR	D	122	22.584	75.013	175.350	1.00	29.85
10	6289	O	THR	D	122	23.315	75.265	174.395	1.00	28.65
	6290	N	PHE	D	123	21.277	75.280	175.346	1.00	28.52
	6291	CA	PHE	D	123	20.642	75.887	174.176	1.00	28.12
	6292	CB	PHE	D	123	19.116	75.935	174.312	1.00	20.94
	6293	CG	PHE	D	123	18.406	76.598	173.142	1.00	22.82
15	6294	CD1	PHE	D	123	18.567	76.120	171.840	1.00	24.48
	6295	CD2	PHE	D	123	17.554	77.680	173.346	1.00	26.82
	6296	CE1	PHE	D	123	17.879	76.716	170.744	1.00	25.40
	6297	CE2	PHE	D	123	16.863	78.289	172.270	1.00	30.29
	6298	CZ	PHE	D	123	17.023	77.805	170.967	1.00	26.50
20	6299	C	PHE	D	123	21.152	77.321	174.009	1.00	29.47
	6300	O	PHE	D	123	21.369	77.774	172.895	1.00	28.65
	6301	N	GLU	D	124	21.349	78.026	175.116	1.00	27.66
	6302	CA	GLU	D	124	21.803	79.413	175.061	1.00	30.12
	6303	CB	GLU	D	124	21.620	80.095	176.424	1.00	27.32
25	6304	CG	GLU	D	124	20.157	80.436	176.752	1.00	37.67
	6305	CD	GLU	D	124	19.913	80.721	178.245	1.00	38.51
	6306	OE1	GLU	D	124	18.805	81.175	178.576	1.00	47.24
	6307	OE2	GLU	D	124	20.814	80.494	179.085	1.00	42.03
	6308	C	GLU	D	124	23.250	79.547	174.612	1.00	28.73
30	6309	O	GLU	D	124	23.606	80.510	173.920	1.00	27.73
	6310	N	ALA	D	125	24.079	78.590	175.004	1.00	21.84
	6311	CA	ALA	D	125	25.482	78.614	174.615	1.00	29.29
	6312	CB	ALA	D	125	26.250	77.473	175.308	1.00	26.80
	6313	C	ALA	D	125	25.538	78.449	173.088	1.00	30.84
35	6314	O	ALA	D	125	26.245	79.181	172.394	1.00	30.47
	6315	N	LEU	D	126	24.765	77.498	172.575	1.00	25.53
	6316	CA	LEU	D	126	24.727	77.247	171.143	1.00	30.19
	6317	CB	LEU	D	126	23.946	75.961	170.844	1.00	26.30
	6318	CG	LEU	D	126	24.472	74.596	171.311	1.00	29.33
40	6319	CD1	LEU	D	126	23.331	73.600	171.246	1.00	31.05
	6320	CD2	LEU	D	126	25.652	74.130	170.459	1.00	26.95
	6321	C	LEU	D	126	24.111	78.419	170.362	1.00	28.46
	6322	O	LEU	D	126	24.585	78.761	169.279	1.00	23.25



	6323	N	THR D 127	23.063	79.052	170.871	1.00	27.05
	6324	CA	THR D 127	22.551	80.140	170.066	1.00	27.90
	6325	CB	THR D 127	21.041	80.556	170.418	1.00	27.06
	6326	OG1	THR D 127	20.958	81.926	170.833	1.00	35.13
5	6327	CG2	THR D 127	20.454	79.676	171.420	1.00	21.79
	6328	C	THR D 127	23.563	81.301	170.093	1.00	26.46
	6329	O	THR D 127	23.664	82.030	169.116	1.00	23.58
	6330	N	LYS D 128	24.346	81.430	171.167	1.00	26.47
	6331	CA	LYS D 128	25.380	82.481	171.229	1.00	32.02
10	6332	CB	LYS D 128	25.991	82.595	172.630	1.00	31.89
	6333	CG	LYS D 128	25.264	83.605	173.520	1.00	44.66
	6334	CD	LYS D 128	25.337	83.291	175.029	1.00	47.77
	6335	CE	LYS D 128	26.724	83.493	175.644	1.00	53.01
	6336	NZ	LYS D 128	26.691	83.334	177.148	1.00	54.75
15	6337	C	LYS D 128	26.505	82.218	170.219	1.00	33.07
	6338	O	LYS D 128	27.033	83.164	169.629	1.00	29.97
	6339	N	ALA D 129	26.865	80.941	170.023	1.00	28.13
	6340	CA	ALA D 129	27.915	80.571	169.069	1.00	24.05
	6341	CB	ALA D 129	28.246	79.076	169.180	1.00	25.93
20	6342	C	ALA D 129	27.397	80.888	167.677	1.00	25.07
	6343	O	ALA D 129	28.144	81.349	166.804	1.00	25.24
	6344	N	GLU D 130	26.099	80.669	167.491	1.00	22.73
	6345	CA	GLU D 130	25.425	80.926	166.215	1.00	27.17
	6346	CB	GLU D 130	24.012	80.326	166.256	1.00	28.21
25	6347	CG	GLU D 130	23.059	80.828	165.208	1.00	40.58
	6348	CD	GLU D 130	21.668	80.190	165.322	1.00	47.70
	6349	OE1	GLU D 130	21.072	80.209	166.422	1.00	43.19
	6350	OE2	GLU D 130	21.169	79.677	164.299	1.00	52.76
	6351	C	GLU D 130	25.382	82.418	165.884	1.00	23.91
30	6352	O	GLU D 130	25.766	82.816	164.787	1.00	23.20
	6353	N	GLU D 131	24.936	83.231	166.841	1.00	25.05
	6354	CA	GLU D 131	24.842	84.683	166.682	1.00	25.16
	6355	CB	GLU D 131	24.163	85.319	167.909	1.00	25.72
	6356	CG	GLU D 131	22.721	84.861	168.157	1.00	29.70
35	6357	CD	GLU D 131	22.099	85.488	169.409	1.00	39.30
	6358	OE1	GLU D 131	22.854	85.842	170.347	1.00	44.27
	6359	OE2	GLU D 131	20.852	85.612	169.473	1.00	39.01
	6360	C	GLU D 131	26.226	85.320	166.486	1.00	24.72
	6361	O	GLU D 131	26.389	86.228	165.677	1.00	24.32
40	6362	N	LEU D 132	27.215	84.839	167.228	1.00	17.71
	6363	CA	LEU D 132	28.572	85.363	167.126	1.00	17.77
	6364	CB	LEU D 132	29.497	84.592	168.059	1.00	14.97
	6365	CG	LEU D 132	31.005	84.804	167.848	1.00	24.89

	6366	CD1	LEU D 132	31.379	86.207	168.244	1.00	24.98
	6367	CD2	LEU D 132	31.797	83.806	168.681	1.00	27.75
	6368	C	LEU D 132	29.111	85.235	165.702	1.00	20.37
	6369	O	LEU D 132	29.611	86.195	165.108	1.00	20.67
5	6370	N	THR D 133	28.963	84.042	165.148	1.00	19.77
	6371	CA	THR D 133	29.486	83.736	163.818	1.00	18.73
	6372	CB	THR D 133	30.011	82.299	163.780	1.00	16.84
	6373	OG1	THR D 133	28.882	81.408	163.868	1.00	13.92
	6374	CG2	THR D 133	30.979	82.026	164.954	1.00	10.46
10	6375	C	THR D 133	28.545	83.837	162.621	1.00	20.01
	6376	O	THR D 133	28.930	83.419	161.525	1.00	20.03
	6377	N	LYS D 134	27.341	84.376	162.787	1.00	18.88
	6378	CA	LYS D 134	26.409	84.378	161.658	1.00	19.54
	6379	CB	LYS D 134	25.009	84.805	162.109	1.00	22.86
15	6380	CG	LYS D 134	24.830	86.276	162.211	1.00	23.60
	6381	CD	LYS D 134	23.398	86.621	162.537	1.00	33.14
	6382	CE	LYS D 134	23.174	88.129	162.457	1.00	40.99
	6383	NZ	LYS D 134	21.792	88.507	162.883	1.00	50.08
	6384	C	LYS D 134	26.783	85.181	160.423	1.00	24.55
20	6385	O	LYS D 134	26.185	84.990	159.379	1.00	24.86
	6386	N	ASN D 135	27.742	86.096	160.511	1.00	24.86
	6387	CA	ASN D 135	28.097	86.838	159.306	1.00	22.66
	6388	CB	ASN D 135	28.394	88.299	159.657	1.00	26.58
	6389	CG	ASN D 135	27.227	88.979	160.368	1.00	27.10
25	6390	OD1	ASN D 135	26.114	89.079	159.829	1.00	25.80
	6391	ND2	ASN D 135	27.476	89.446	161.579	1.00	20.76
	6392	C	ASN D 135	29.312	86.206	158.618	1.00	22.49
	6393	O	ASN D 135	29.723	86.648	157.543	1.00	22.11
	6394	N	ASN D 136	29.872	85.160	159.225	1.00	19.16
30	6395	CA	ASN D 136	31.063	84.536	158.670	1.00	21.81
	6396	CB	ASN D 136	31.627	83.534	159.679	1.00	19.92
	6397	CG	ASN D 136	32.053	84.216	160.990	1.00	20.34
	6398	OD1	ASN D 136	31.895	85.429	161.145	1.00	19.19
	6399	ND2	ASN D 136	32.585	83.441	161.927	1.00	17.34
35	6400	C	ASN D 136	30.806	83.915	157.297	1.00	26.68
	6401	O	ASN D 136	29.738	83.352	157.048	1.00	24.00
	6402	N	THR D 137	31.790	84.050	156.408	1.00	22.30
	6403	CA	THR D 137	31.682	83.578	155.032	1.00	18.92
	6404	CB	THR D 137	32.045	84.705	154.087	1.00	21.20
40	6405	OG1	THR D 137	33.371	85.134	154.389	1.00	22.97
	6406	CG2	THR D 137	31.082	85.874	154.250	1.00	13.36
	6407	C	THR D 137	32.552	82.375	154.684	1.00	21.55
	6408	O	THR D 137	32.685	82.005	153.515	1.00	22.33

	6409	N	GLY D 138	33.166	81.774	155.697	1.00	21.17
	6410	CA	GLY D 138	33.979	80.610	155.448	1.00	18.14
	6411	C	GLY D 138	33.148	79.342	155.611	1.00	21.80
	6412	O	GLY D 138	31.932	79.337	155.413	1.00	22.64
5	6413	N	LEU D 139	33.820	78.264	155.976	1.00	20.58
	6414	CA	LEU D 139	33.187	76.972	156.166	1.00	22.34
	6415	CB	LEU D 139	34.209	76.000	156.714	1.00	20.47
	6416	CG	LEU D 139	33.669	74.667	157.227	1.00	21.25
	6417	CD1	LEU D 139	33.415	73.744	156.045	1.00	21.11
10	6418	CD2	LEU D 139	34.701	74.047	158.155	1.00	25.80
	6419	C	LEU D 139	32.000	77.013	157.128	1.00	22.16
	6420	O	LEU D 139	32.031	77.731	158.113	1.00	21.45
	6421	N	ILE D 140	30.953	76.244	156.839	1.00	20.57
	6422	CA	ILE D 140	29.830	76.193	157.757	1.00	20.25
15	6423	CB	ILE D 140	28.474	76.179	157.016	1.00	24.03
	6424	CG2	ILE D 140	27.322	76.003	158.033	1.00	15.11
	6425	CG1	ILE D 140	28.298	77.481	156.227	1.00	16.17
	6426	CD1	ILE D 140	27.157	77.399	155.182	1.00	13.85
	6427	C	ILE D 140	29.932	74.931	158.629	1.00	20.15
20	6428	O	ILE D 140	29.902	73.814	158.123	1.00	24.51
	6429	N	LEU D 141	30.094	75.121	159.935	1.00	20.54
	6430	CA	LEU D 141	30.138	74.010	160.875	1.00	18.41
	6431	CB	LEU D 141	31.063	74.312	162.064	1.00	17.23
	6432	CG	LEU D 141	30.887	73.284	163.192	1.00	17.99
25	6433	CD1	LEU D 141	31.325	71.872	162.736	1.00	14.42
	6434	CD2	LEU D 141	31.672	73.733	164.393	1.00	20.42
	6435	C	LEU D 141	28.698	73.843	161.367	1.00	18.36
	6436	O	LEU D 141	28.214	74.648	162.157	1.00	16.02
	6437	N	ASN D 142	28.049	72.783	160.887	1.00	19.50
30	6438	CA	ASN D 142	26.649	72.443	161.154	1.00	18.69
	6439	CB	ASN D 142	26.029	72.079	159.798	1.00	24.28
	6440	CG	ASN D 142	24.536	72.109	159.801	1.00	22.44
	6441	OD1	ASN D 142	23.915	72.918	160.487	1.00	32.14
	6442	ND2	ASN D 142	23.936	71.231	159.011	1.00	28.86
35	6443	C	ASN D 142	26.482	71.288	162.168	1.00	20.22
	6444	O	ASN D 142	26.693	70.113	161.844	1.00	19.68
	6445	N	PHE D 143	26.109	71.636	163.395	1.00	22.96
	6446	CA	PHE D 143	25.925	70.663	164.486	1.00	25.78
	6447	CB	PHE D 143	26.035	71.359	165.837	1.00	25.92
40	6448	CG	PHE D 143	27.428	71.525	166.331	1.00	31.48
	6449	CD1	PHE D 143	28.028	72.787	166.341	1.00	30.63
	6450	CD2	PHE D 143	28.144	70.419	166.807	1.00	28.50
	6451	CE1	PHE D 143	29.326	72.957	166.818	1.00	36.42

	6452	CE2	PHE	D	143	29.440	70.563	167.286	1.00	26.38
	6453	CZ	PHE	D	143	30.042	71.841	167.294	1.00	38.44
	6454	C	PHE	D	143	24.565	69.983	164.469	1.00	27.52
	6455	O	PHE	D	143	23.538	70.669	164.566	1.00	28.38
5	6456	N	ALA	D	144	24.531	68.655	164.364	1.00	21.54
	6457	CA	ALA	D	144	23.235	67.976	164.389	1.00	21.94
	6458	CB	ALA	D	144	23.236	66.765	163.475	1.00	17.78
	6459	C	ALA	D	144	23.023	67.567	165.843	1.00	21.99
	6460	O	ALA	D	144	23.631	66.618	166.327	1.00	26.54
10	6461	N	LEU	D	145	22.179	68.304	166.551	1.00	23.96
	6462	CA	LEU	D	145	21.940	68.013	167.961	1.00	25.61
	6463	CB	LEU	D	145	22.314	69.208	168.822	1.00	26.98
	6464	CG	LEU	D	145	23.785	69.589	168.814	1.00	38.09
	6465	CD1	LEU	D	145	23.921	71.047	169.272	1.00	39.20
15	6466	CD2	LEU	D	145	24.563	68.630	169.700	1.00	34.71
	6467	C	LEU	D	145	20.492	67.701	168.197	1.00	22.77
	6468	O	LEU	D	145	19.622	68.415	167.708	1.00	26.95
	6469	N	ASN	D	146	20.244	66.658	168.980	1.00	22.25
	6470	CA	ASN	D	146	18.884	66.230	169.272	1.00	25.33
20	6471	CB	ASN	D	146	18.178	67.256	170.153	1.00	29.63
	6472	CG	ASN	D	146	16.971	66.675	170.840	1.00	43.70
	6473	OD1	ASN	D	146	17.053	65.594	171.428	1.00	50.94
	6474	ND2	ASN	D	146	15.840	67.371	170.766	1.00	41.84
	6475	C	ASN	D	146	18.192	66.109	167.921	1.00	23.53
25	6476	O	ASN	D	146	17.076	66.584	167.710	1.00	27.41
	6477	N	TYR	D	147	18.900	65.447	167.017	1.00	22.04
	6478	CA	TYR	D	147	18.495	65.244	165.640	1.00	20.69
	6479	CB	TYR	D	147	19.600	65.801	164.716	1.00	20.53
	6480	CG	TYR	D	147	19.428	65.455	163.254	1.00	20.57
30	6481	CD1	TYR	D	147	18.768	66.309	162.386	1.00	19.76
	6482	CE1	TYR	D	147	18.526	65.939	161.058	1.00	22.66
	6483	CD2	TYR	D	147	19.849	64.220	162.761	1.00	20.64
	6484	CE2	TYR	D	147	19.604	63.842	161.458	1.00	19.20
	6485	CZ	TYR	D	147	18.943	64.698	160.609	1.00	17.64
35	6486	OH	TYR	D	147	18.681	64.286	159.321	1.00	19.96
	6487	C	TYR	D	147	18.265	63.782	165.281	1.00	22.58
	6488	O	TYR	D	147	18.978	62.885	165.762	1.00	19.95
	6489	N	GLY	D	148	17.292	63.560	164.399	1.00	18.68
	6490	CA	GLY	D	148	17.017	62.223	163.893	1.00	13.67
40	6491	C	GLY	D	148	16.435	62.421	162.500	1.00	21.59
	6492	O	GLY	D	148	15.582	63.296	162.326	1.00	21.87
	6493	N	GLY	D	149	16.877	61.631	161.514	1.00	18.63
	6494	CA	GLY	D	149	16.367	61.770	160.155	1.00	13.84

	6495	C	GLY D 149	14.855	61.655	160.022	1.00	15.60
	6496	O	GLY D 149	14.183	62.550	159.517	1.00	16.35
	6497	N	ARG D 150	14.314	60.535	160.472	1.00	19.92
	6498	CA	ARG D 150	12.888	60.301	160.391	1.00	15.99
5	6499	CB	ARG D 150	12.561	58.981	161.050	1.00	19.76
	6500	CG	ARG D 150	13.010	57.811	160.211	1.00	24.93
	6501	CD	ARG D 150	12.711	56.535	160.929	1.00	20.13
	6502	NE	ARG D 150	13.166	55.404	160.143	1.00	27.47
	6503	CZ	ARG D 150	13.034	54.151	160.533	1.00	31.21
10	6504	NH1	ARG D 150	12.452	53.893	161.697	1.00	30.61
	6505	NH2	ARG D 150	13.509	53.170	159.781	1.00	31.04
	6506	C	ARG D 150	12.081	61.405	161.013	1.00	18.37
	6507	O	ARG D 150	11.117	61.874	160.414	1.00	19.44
	6508	N	ALA D 151	12.477	61.833	162.209	1.00	18.82
15	6509	CA	ALA D 151	11.775	62.914	162.894	1.00	17.12
	6510	CB	ALA D 151	12.318	63.089	164.332	1.00	11.31
	6511	C	ALA D 151	11.913	64.218	162.102	1.00	20.05
	6512	O	ALA D 151	10.992	65.032	162.072	1.00	26.28
	6513	N	GLU D 152	13.054	64.430	161.453	1.00	21.44
20	6514	CA	GLU D 152	13.216	65.652	160.676	1.00	23.41
	6515	CB	GLU D 152	14.649	65.811	160.182	1.00	21.14
	6516	CG	GLU D 152	14.751	66.717	158.987	1.00	17.02
	6517	CD	GLU D 152	16.151	66.758	158.411	1.00	27.32
	6518	OE1	GLU D 152	16.772	65.674	158.238	1.00	26.50
25	6519	OE2	GLU D 152	16.625	67.875	158.122	1.00	19.43
	6520	C	GLU D 152	12.251	65.646	159.489	1.00	24.57
	6521	O	GLU D 152	11.592	66.649	159.205	1.00	24.08
	6522	N	ILE D 153	12.173	64.519	158.795	1.00	21.70
	6523	CA	ILE D 153	11.260	64.391	157.656	1.00	20.37
30	6524	CB	ILE D 153	11.445	63.038	156.953	1.00	20.53
	6525	CG2	ILE D 153	10.260	62.762	155.999	1.00	21.01
	6526	CG1	ILE D 153	12.807	63.019	156.250	1.00	22.02
	6527	CD1	ILE D 153	13.263	61.649	155.813	1.00	18.51
	6528	C	ILE D 153	9.808	64.487	158.148	1.00	25.14
35	6529	O	ILE D 153	8.962	65.057	157.463	1.00	22.66
	6530	N	THR D 154	9.531	63.928	159.332	1.00	23.57
	6531	CA	THR D 154	8.183	63.965	159.893	1.00	27.44
	6532	CB	THR D 154	8.091	63.184	161.209	1.00	25.28
	6533	OG1	THR D 154	8.426	61.809	160.979	1.00	25.04
40	6534	CG2	THR D 154	6.673	63.258	161.759	1.00	22.63
	6535	C	THR D 154	7.750	65.403	160.147	1.00	27.83
	6536	O	THR D 154	6.652	65.813	159.761	1.00	30.10
	6537	N	GLN D 155	8.620	66.169	160.785	1.00	27.18

	6538	CA	GLN D 155	8.335	67.567	161.069	1.00	28.89
	6539	CB	GLN D 155	9.443	68.173	161.921	1.00	25.88
	6540	CG	GLN D 155	9.613	69.690	161.784	1.00	45.96
	6541	CD	GLN D 155	10.522	70.105	160.615	1.00	51.71
5	6542	OE1	GLN D 155	10.738	71.295	160.385	1.00	62.31
	6543	NE2	GLN D 155	11.057	69.126	159.882	1.00	50.83
	6544	C	GLN D 155	8.126	68.407	159.817	1.00	30.25
	6545	O	GLN D 155	7.328	69.340	159.842	1.00	33.72
	6546	N	ALA D 156	8.821	68.092	158.725	1.00	30.18
10	6547	CA	ALA D 156	8.652	68.863	157.486	1.00	30.91
	6548	CB	ALA D 156	9.804	68.609	156.531	1.00	21.97
	6549	C	ALA D 156	7.342	68.472	156.802	1.00	35.69
	6550	O	ALA D 156	6.736	69.264	156.078	1.00	35.93
	6551	N	LEU D 157	6.940	67.224	157.009	1.00	38.87
15	6552	CA	LEU D 157	5.719	66.684	156.437	1.00	41.87
	6553	CB	LEU D 157	5.649	65.192	156.714	1.00	52.00
	6554	CG	LEU D 157	4.548	64.373	156.048	1.00	62.30
	6555	CD1	LEU D 157	3.180	64.819	156.503	1.00	62.70
	6556	CD2	LEU D 157	4.680	64.525	154.562	1.00	67.25
20	6557	C	LEU D 157	4.559	67.384	157.121	1.00	45.20
	6558	O	LEU D 157	3.540	67.679	156.504	1.00	43.90
	6559	N	LYS D 158	4.737	67.653	158.406	1.00	40.28
	6560	CA	LYS D 158	3.733	68.316	159.190	1.00	37.58
	6561	CB	LYS D 158	4.126	68.275	160.654	1.00	39.97
25	6562	CG	LYS D 158	3.185	68.983	161.581	1.00	41.48
	6563	CD	LYS D 158	3.574	68.689	163.023	1.00	50.91
	6564	CE	LYS D 158	3.773	67.190	163.237	1.00	52.99
	6565	NZ	LYS D 158	4.269	66.856	164.599	1.00	62.94
	6566	C	LYS D 158	3.580	69.748	158.735	1.00	40.28
30	6567	O	LYS D 158	2.475	70.166	158.404	1.00	49.43
	6568	N	LEU D 159	4.672	70.512	158.716	1.00	39.64
	6569	CA	LEU D 159	4.603	71.911	158.274	1.00	34.30
	6570	CB	LEU D 159	5.989	72.569	158.313	1.00	32.82
	6571	CG	LEU D 159	6.660	72.642	159.693	1.00	41.25
35	6572	CD1	LEU D 159	8.022	73.310	159.582	1.00	40.36
	6573	CD2	LEU D 159	5.779	73.401	160.662	1.00	34.01
	6574	C	LEU D 159	4.011	72.048	156.866	1.00	32.57
	6575	O	LEU D 159	3.216	72.940	156.630	1.00	33.77
	6576	N	ILE D 160	4.391	71.164	155.941	1.00	31.87
40	6577	CA	ILE D 160	3.883	71.209	154.575	1.00	33.66
	6578	CB	ILE D 160	4.600	70.182	153.678	1.00	36.05
	6579	CG2	ILE D 160	3.892	70.058	152.326	1.00	29.17
	6580	CG1	ILE D 160	6.069	70.590	153.488	1.00	39.93

	6581	CD1	ILE D 160	6.866	69.606	152.632	1.00	33.67
	6582	C	ILE D 160	2.372	70.940	154.511	1.00	41.17
	6583	O	ILE D 160	1.650	71.590	153.751	1.00	38.67
	6584	N	SER D 161	1.908	69.978	155.303	1.00	43.47
5	6585	CA	SER D 161	0.492	69.619	155.343	1.00	48.71
	6586	CB	SER D 161	0.284	68.352	156.166	1.00	44.85
	6587	OG	SER D 161	0.264	68.672	157.547	1.00	49.90
	6588	C	SER D 161	-0.301	70.771	155.968	1.00	48.48
	6589	O	SER D 161	-1.393	71.096	155.519	1.00	49.42
10	6590	N	GLN D 162	0.265	71.384	157.001	1.00	49.59
	6591	CA	GLN D 162	-0.357	72.517	157.667	1.00	50.30
	6592	CB	GLN D 162	0.470	72.926	158.880	1.00	49.62
	6593	CG	GLN D 162	-0.064	74.133	159.626	1.00	48.65
	6594	CD	GLN D 162	-1.459	73.910	160.166	1.00	53.10
15	6595	OE1	GLN D 162	-2.425	74.501	159.681	1.00	56.82
	6596	NE2	GLN D 162	-1.575	73.048	161.170	1.00	49.66
	6597	C	GLN D 162	-0.471	73.713	156.713	1.00	55.08
	6598	O	GLN D 162	-1.314	74.593	156.906	1.00	55.78
	6599	N	ASP D 163	0.396	73.762	155.703	1.00	54.53
20	6600	CA	ASP D 163	0.347	74.843	154.735	1.00	52.44
	6601	CB	ASP D 163	1.724	75.114	154.115	1.00	52.00
	6602	CG	ASP D 163	2.602	75.989	155.001	1.00	52.83
	6603	OD1	ASP D 163	2.062	76.614	155.935	1.00	51.25
	6604	OD2	ASP D 163	3.828	76.070	154.760	1.00	55.47
25	6605	C	ASP D 163	-0.648	74.464	153.657	1.00	51.75
	6606	O	ASP D 163	-1.190	75.324	152.981	1.00	55.59
	6607	N	VAL D 164	-0.892	73.170	153.495	1.00	52.69
	6608	CA	VAL D 164	-1.857	72.713	152.505	1.00	50.12
	6609	CB	VAL D 164	-1.771	71.199	152.291	1.00	49.56
30	6610	CG1	VAL D 164	-3.101	70.670	151.741	1.00	50.84
	6611	CG2	VAL D 164	-0.641	70.892	151.317	1.00	40.50
	6612	C	VAL D 164	-3.252	73.078	153.000	1.00	53.23
	6613	O	VAL D 164	-4.129	73.419	152.202	1.00	50.59
	6614	N	LEU D 165	-3.445	72.996	154.316	1.00	52.98
35	6615	CA	LEU D 165	-4.715	73.361	154.928	1.00	56.08
	6616	CB	LEU D 165	-4.666	73.178	156.448	1.00	56.15
	6617	CG	LEU D 165	-5.271	71.920	157.069	1.00	55.67
	6618	CD1	LEU D 165	-5.268	72.052	158.583	1.00	48.94
	6619	CD2	LEU D 165	-6.699	71.740	156.564	1.00	52.81
40	6620	C	LEU D 165	-4.965	74.835	154.617	1.00	57.49
	6621	O	LEU D 165	-5.928	75.180	153.939	1.00	63.46
	6622	N	ASP D 166	-4.085	75.696	155.115	1.00	53.12
	6623	CA	ASP D 166	-4.182	77.133	154.900	1.00	52.07

	6624	CB	ASP D 166	-3.090	77.824	155.714	1.00	55.44
	6625	CG	ASP D 166	-3.142	77.439	157.185	1.00	62.26
	6626	OD1	ASP D 166	-3.602	76.315	157.474	1.00	66.60
	6627	OD2	ASP D 166	-2.721	78.240	158.049	1.00	65.46
5	6628	C	ASP D 166	-4.057	77.501	153.416	1.00	51.35
	6629	O	ASP D 166	-3.769	78.638	153.070	1.00	50.61
	6630	N	ALA D 167	-4.276	76.523	152.545	1.00	53.45
	6631	CA	ALA D 167	-4.195	76.728	151.103	1.00	56.80
	6632	CB	ALA D 167	-5.508	77.319	150.579	1.00	57.61
10	6633	C	ALA D 167	-3.016	77.595	150.666	1.00	56.32
	6634	O	ALA D 167	-3.052	78.199	149.591	1.00	58.85
	6635	N	LYS D 168	-1.982	77.669	151.502	1.00	54.28
	6636	CA	LYS D 168	-0.774	78.428	151.163	1.00	53.06
	6637	CB	LYS D 168	0.113	78.641	152.395	1.00	56.19
15	6638	CG	LYS D 168	-0.492	79.481	153.508	1.00	57.21
	6639	CD	LYS D 168	0.567	79.802	154.555	1.00	59.95
	6640	CE	LYS D 168	0.023	80.691	155.656	1.00	62.54
	6641	NZ	LYS D 168	1.107	81.117	156.575	1.00	67.36
	6642	C	LYS D 168	0.020	77.628	150.118	1.00	50.90
20	6643	O	LYS D 168	0.928	78.150	149.470	1.00	49.04
	6644	N	ILE D 169	-0.331	76.350	149.986	1.00	48.21
	6645	CA	ILE D 169	0.293	75.446	149.034	1.00	52.90
	6646	CB	ILE D 169	1.392	74.574	149.666	1.00	54.58
	6647	CG2	ILE D 169	2.177	73.887	148.569	1.00	55.85
25	6648	CG1	ILE D 169	2.329	75.404	150.532	1.00	55.75
	6649	CD1	ILE D 169	3.307	74.552	151.309	1.00	56.29
	6650	C	ILE D 169	-0.791	74.471	148.613	1.00	56.46
	6651	O	ILE D 169	-1.719	74.214	149.371	1.00	57.60
	6652	N	ASN D 170	-0.666	73.917	147.413	1.00	62.71
30	6653	CA	ASN D 170	-1.634	72.936	146.928	1.00	68.38
	6654	CB	ASN D 170	-2.058	73.246	145.487	1.00	71.15
	6655	CG	ASN D 170	-2.492	74.680	145.307	1.00	73.98
	6656	OD1	ASN D 170	-3.444	75.138	145.944	1.00	76.40
	6657	ND2	ASN D 170	-1.790	75.407	144.443	1.00	75.65
35	6658	C	ASN D 170	-0.913	71.601	146.955	1.00	67.55
	6659	O	ASN D 170	0.303	71.555	146.794	1.00	69.38
	6660	N	PRO D 171	-1.646	70.500	147.163	1.00	66.12
	6661	CD	PRO D 171	-3.092	70.391	147.413	1.00	67.34
	6662	CA	PRO D 171	-1.005	69.185	147.194	1.00	64.56
40	6663	CB	PRO D 171	-2.124	68.273	147.694	1.00	65.89
	6664	CG	PRO D 171	-3.350	68.928	147.148	1.00	67.80
	6665	C	PRO D 171	-0.460	68.796	145.807	1.00	63.97
	6666	O	PRO D 171	0.096	67.709	145.609	1.00	65.12



	6667	N	GLY D 172	-0.627	69.702	144.849	1.00	63.16
	6668	CA	GLY D 172	-0.130	69.467	143.504	1.00	56.96
	6669	C	GLY D 172	1.245	70.104	143.369	1.00	55.03
	6670	O	GLY D 172	1.943	69.910	142.370	1.00	53.56
5	6671	N	ASP D 173	1.632	70.876	144.382	1.00	49.47
	6672	CA	ASP D 173	2.932	71.528	144.390	1.00	50.66
	6673	CB	ASP D 173	2.784	73.007	144.724	1.00	55.68
	6674	CG	ASP D 173	2.058	73.759	143.650	1.00	60.41
	6675	OD1	ASP D 173	0.934	74.242	143.918	1.00	63.52
10	6676	OD2	ASP D 173	2.615	73.853	142.533	1.00	61.67
	6677	C	ASP D 173	3.865	70.876	145.402	1.00	47.81
	6678	O	ASP D 173	4.794	71.505	145.902	1.00	43.64
	6679	N	ILE D 174	3.598	69.615	145.713	1.00	46.84
	6680	CA	ILE D 174	4.423	68.879	146.653	1.00	42.36
15	6681	CB	ILE D 174	3.563	67.986	147.552	1.00	45.80
	6682	CG2	ILE D 174	4.427	66.949	148.251	1.00	40.41
	6683	CG1	ILE D 174	2.822	68.865	148.567	1.00	45.30
	6684	CD1	ILE D 174	1.700	68.155	149.269	1.00	48.42
	6685	C	ILE D 174	5.382	68.053	145.830	1.00	41.18
20	6686	O	ILE D 174	4.992	67.119	145.128	1.00	41.38
	6687	N	THR D 175	6.651	68.420	145.921	1.00	37.90
	6688	CA	THR D 175	7.708	67.765	145.175	1.00	34.96
	6689	CB	THR D 175	8.176	68.665	144.038	1.00	38.58
	6690	OG1	THR D 175	8.641	69.905	144.592	1.00	39.98
25	6691	CG2	THR D 175	7.036	68.961	143.087	1.00	40.23
	6692	C	THR D 175	8.897	67.549	146.088	1.00	35.44
	6693	O	THR D 175	8.896	68.000	147.238	1.00	33.36
	6694	N	GLU D 176	9.924	66.886	145.559	1.00	32.56
	6695	CA	GLU D 176	11.124	66.629	146.330	1.00	31.14
30	6696	CB	GLU D 176	12.068	65.728	145.532	1.00	32.97
	6697	CG	GLU D 176	11.470	64.348	145.267	1.00	35.70
	6698	CD	GLU D 176	12.348	63.443	144.413	1.00	36.58
	6699	OE1	GLU D 176	13.591	63.607	144.409	1.00	32.30
	6700	OE2	GLU D 176	11.786	62.542	143.757	1.00	37.92
35	6701	C	GLU D 176	11.802	67.948	146.695	1.00	30.62
	6702	O	GLU D 176	12.331	68.106	147.799	1.00	27.19
	6703	N	GLU D 177	11.767	68.903	145.774	1.00	27.71
	6704	CA	GLU D 177	12.385	70.194	146.011	1.00	27.73
	6705	CB	GLU D 177	12.389	71.037	144.734	1.00	29.83
40	6706	CG	GLU D 177	11.413	70.564	143.661	1.00	44.22
	6707	CD	GLU D 177	11.839	69.270	142.985	0.50	40.88
	6708	OE1	GLU D 177	12.972	69.222	142.477	0.50	50.02
	6709	OE2	GLU D 177	11.047	68.305	142.950	0.50	42.65

	6710	C	GLU D 177	11.663	70.921	147.119	1.00	27.28
	6711	O	GLU D 177	12.293	71.584	147.942	1.00	33.11
	6712	N	LEU D 178	10.338	70.784	147.151	1.00	34.79
	6713	CA	LEU D 178	9.522	71.428	148.185	1.00	32.68
5	6714	CB	LEU D 178	8.033	71.166	147.957	1.00	34.89
	6715	CG	LEU D 178	7.194	71.674	149.133	1.00	39.05
	6716	CD1	LEU D 178	7.182	73.203	149.090	1.00	41.04
	6717	CD2	LEU D 178	5.775	71.124	149.069	1.00	46.39
	6718	C	LEU D 178	9.903	70.867	149.547	1.00	29.47
10	6719	O	LEU D 178	10.198	71.610	150.474	1.00	29.75
	6720	N	ILE D 179	9.868	69.547	149.662	1.00	26.59
	6721	CA	ILE D 179	10.225	68.888	150.908	1.00	26.34
	6722	CB	ILE D 179	10.226	67.371	150.695	1.00	28.63
	6723	CG2	ILE D 179	11.024	66.667	151.800	1.00	24.19
15	6724	CG1	ILE D 179	8.775	66.899	150.600	1.00	18.48
	6725	CD1	ILE D 179	8.605	65.477	150.172	1.00	23.64
	6726	C	ILE D 179	11.596	69.377	151.398	1.00	29.22
	6727	O	ILE D 179	11.774	69.668	152.583	1.00	26.63
	6728	N	GLY D 180	12.548	69.491	150.467	1.00	30.68
20	6729	CA	GLY D 180	13.886	69.964	150.788	1.00	25.15
	6730	C	GLY D 180	13.886	71.343	151.418	1.00	29.42
	6731	O	GLY D 180	14.731	71.643	152.263	1.00	32.18
	6732	N	ASN D 181	12.945	72.196	151.019	1.00	31.62
	6733	CA	ASN D 181	12.859	73.544	151.598	1.00	29.93
25	6734	CB	ASN D 181	11.981	74.476	150.746	1.00	33.51
	6735	CG	ASN D 181	12.604	74.823	149.401	1.00	35.64
	6736	OD1	ASN D 181	13.804	75.071	149.292	1.00	38.43
	6737	ND2	ASN D 181	11.774	74.869	148.374	1.00	33.30
	6738	C	ASN D 181	12.289	73.529	153.013	1.00	27.12
30	6739	O	ASN D 181	12.292	74.558	153.698	1.00	28.47
	6740	N	TYR D 182	11.798	72.381	153.464	1.00	25.25
	6741	CA	TYR D 182	11.237	72.302	154.817	1.00	26.02
	6742	CB	TYR D 182	9.831	71.710	154.789	1.00	28.60
	6743	CG	TYR D 182	8.784	72.672	154.306	1.00	33.10
35	6744	CD1	TYR D 182	8.650	72.970	152.950	1.00	29.25
	6745	CE1	TYR D 182	7.662	73.859	152.505	1.00	35.53
	6746	CD2	TYR D 182	7.915	73.285	155.209	1.00	34.84
	6747	CE2	TYR D 182	6.930	74.167	154.782	1.00	36.53
	6748	CZ	TYR D 182	6.803	74.450	153.424	1.00	36.40
40	6749	OH	TYR D 182	5.802	75.306	152.999	1.00	39.60
	6750	C	TYR D 182	12.081	71.501	155.801	1.00	27.90
	6751	O	TYR D 182	11.812	71.525	157.004	1.00	27.28
	6752	N	LEU D 183	13.076	70.778	155.287	1.00	25.87

	6753	CA	LEU D 183	13.980	69.993	156.132	1.00	23.83
	6754	CB	LEU D 183	14.842	69.065	155.266	1.00	20.70
	6755	CG	LEU D 183	14.122	68.016	154.403	1.00	18.66
	6756	CD1	LEU D 183	15.127	67.260	153.566	1.00	18.93
5	6757	CD2	LEU D 183	13.399	67.036	155.297	1.00	21.63
	6758	C	LEU D 183	14.873	70.977	156.908	1.00	25.18
	6759	O	LEU D 183	15.032	72.136	156.501	1.00	26.11
	6760	N	PHE D 184	15.448	70.519	158.016	1.00	25.59
	6761	CA	PHE D 184	16.306	71.358	158.844	1.00	24.30
10	6762	CB	PHE D 184	16.844	70.556	160.044	1.00	24.70
	6763	CG	PHE D 184	15.783	70.110	161.011	1.00	28.32
	6764	CD1	PHE D 184	16.038	69.066	161.899	1.00	26.96
	6765	CD2	PHE D 184	14.542	70.740	161.062	1.00	23.15
	6766	CE1	PHE D 184	15.076	68.657	162.828	1.00	22.90
15	6767	CE2	PHE D 184	13.586	70.337	161.983	1.00	30.47
	6768	CZ	PHE D 184	13.861	69.284	162.873	1.00	22.78
	6769	C	PHE D 184	17.489	71.942	158.079	1.00	25.25
	6770	O	PHE D 184	18.024	72.969	158.474	1.00	24.79
	6771	N	THR D 185	17.908	71.281	157.001	1.00	24.63
20	6772	CA	THR D 185	19.043	71.757	156.224	1.00	23.06
	6773	CB	THR D 185	19.696	70.602	155.436	1.00	24.93
	6774	OG1	THR D 185	18.681	69.833	154.780	1.00	25.13
	6775	CG2	THR D 185	20.516	69.697	156.369	1.00	22.31
	6776	C	THR D 185	18.700	72.877	155.233	1.00	27.85
25	6777	O	THR D 185	19.556	73.279	154.416	1.00	23.35
	6778	N	GLN D 186	17.470	73.386	155.322	1.00	18.96
	6779	CA	GLN D 186	16.997	74.432	154.413	1.00	27.47
	6780	CB	GLN D 186	15.505	74.758	154.673	1.00	20.77
	6781	CG	GLN D 186	15.244	75.373	156.060	1.00	32.84
30	6782	CD	GLN D 186	13.757	75.558	156.395	1.00	30.97
	6783	OE1	GLN D 186	13.173	76.598	156.112	1.00	35.43
	6784	NE2	GLN D 186	13.153	74.545	157.006	1.00	31.24
	6785	C	GLN D 186	17.798	75.722	154.510	1.00	27.95
	6786	O	GLN D 186	17.883	76.462	153.554	1.00	24.73
35	6787	N	HIS D 187	18.369	75.992	155.673	1.00	34.72
	6788	CA	HIS D 187	19.124	77.223	155.866	1.00	37.76
	6789	CB	HIS D 187	19.229	77.543	157.356	1.00	41.89
	6790	CG	HIS D 187	17.901	77.580	158.052	1.00	49.74
	6791	CD2	HIS D 187	17.444	76.914	159.141	1.00	54.37
40	6792	ND1	HIS D 187	16.849	78.356	157.611	1.00	51.79
	6793	CE1	HIS D 187	15.803	78.167	158.396	1.00	53.08
	6794	NE2	HIS D 187	16.137	77.297	159.333	1.00	55.02
	6795	C	HIS D 187	20.497	77.200	155.223	1.00	36.51

	6796	O	HIS D 187	21.178	78.216	155.195	1.00	41.92
	6797	N	LEU D 188	20.910	76.051	154.703	1.00	32.46
	6798	CA	LEU D 188	22.191	75.996	154.021	1.00	36.08
	6799	CB	LEU D 188	22.766	74.573	154.001	1.00	25.49
5	6800	CG	LEU D 188	23.120	73.855	155.307	1.00	28.83
	6801	CD1	LEU D 188	23.458	72.390	154.980	1.00	22.87
	6802	CD2	LEU D 188	24.277	74.555	156.010	1.00	22.25
	6803	C	LEU D 188	21.920	76.438	152.580	1.00	37.12
	6804	O	LEU D 188	20.817	76.244	152.070	1.00	35.72
10	6805	N	PRO D 189	22.914	77.062	151.914	1.00	37.70
	6806	CD	PRO D 189	24.217	77.523	152.411	1.00	30.53
	6807	CA	PRO D 189	22.696	77.485	150.525	1.00	36.87
	6808	CB	PRO D 189	24.084	77.943	150.060	1.00	32.08
	6809	CG	PRO D 189	25.039	77.467	151.151	1.00	38.74
15	6810	C	PRO D 189	22.170	76.294	149.730	1.00	39.26
	6811	O	PRO D 189	22.597	75.161	149.946	1.00	39.87
	6812	N	LYS D 190	21.235	76.561	148.826	1.00	41.29
	6813	CA	LYS D 190	20.598	75.534	148.004	1.00	39.38
	6814	CB	LYS D 190	19.860	76.189	146.832	1.00	45.61
20	6815	CG	LYS D 190	18.589	76.946	147.196	1.00	57.43
	6816	CD	LYS D 190	17.346	76.059	147.037	1.00	66.22
	6817	CE	LYS D 190	16.046	76.855	147.212	1.00	66.40
	6818	NZ	LYS D 190	14.834	76.014	146.973	1.00	67.46
	6819	C	LYS D 190	21.488	74.431	147.455	1.00	37.09
25	6820	O	LYS D 190	21.193	73.253	147.630	1.00	41.50
	6821	N	ASP D 191	22.563	74.803	146.777	1.00	31.88
	6822	CA	ASP D 191	23.461	73.822	146.169	1.00	32.39
	6823	CB	ASP D 191	24.374	74.524	145.172	1.00	33.91
	6824	CG	ASP D 191	25.167	75.633	145.822	1.00	48.53
30	6825	OD1	ASP D 191	24.536	76.496	146.483	1.00	52.08
	6826	OD2	ASP D 191	26.413	75.644	145.686	1.00	57.67
	6827	C	ASP D 191	24.327	73.043	147.165	1.00	30.24
	6828	O	ASP D 191	24.982	72.063	146.786	1.00	31.21
	6829	N	LEU D 192	24.326	73.469	148.428	1.00	28.09
35	6830	CA	LEU D 192	25.130	72.826	149.474	1.00	29.65
	6831	CB	LEU D 192	25.966	73.898	150.180	1.00	22.62
	6832	CG	LEU D 192	26.911	74.671	149.244	1.00	23.88
	6833	CD1	LEU D 192	27.560	75.803	149.996	1.00	27.62
	6834	CD2	LEU D 192	27.966	73.741	148.687	1.00	17.51
40	6835	C	LEU D 192	24.348	72.027	150.535	1.00	28.79
	6836	O	LEU D 192	24.928	71.601	151.539	1.00	29.73
	6837	N	ARG D 193	23.053	71.812	150.313	1.00	22.56
	6838	CA	ARG D 193	22.216	71.113	151.298	1.00	24.28

	6839	CB	ARG D 193	20.736	71.295	150.951	1.00	24.81
	6840	CG	ARG D 193	20.208	72.642	151.338	1.00	22.97
	6841	CD	ARG D 193	19.041	73.039	150.490	1.00	28.82
	6842	NE	ARG D 193	18.451	74.273	150.993	1.00	33.57
5	6843	CZ	ARG D 193	17.208	74.663	150.731	1.00	33.23
	6844	NH1	ARG D 193	16.423	73.912	149.960	1.00	28.48
	6845	NH2	ARG D 193	16.743	75.782	151.272	1.00	28.13
	6846	C	ARG D 193	22.488	69.634	151.519	1.00	21.67
	6847	O	ARG D 193	22.467	69.150	152.656	1.00	23.31
10	6848	N	ASP D 194	22.757	68.930	150.435	1.00	18.03
	6849	CA	ASP D 194	23.015	67.512	150.491	1.00	25.41
	6850	CB	ASP D 194	22.403	66.869	149.247	1.00	20.54
	6851	CG	ASP D 194	20.899	67.088	149.170	1.00	28.50
	6852	OD1	ASP D 194	20.281	67.497	150.185	1.00	28.94
15	6853	OD2	ASP D 194	20.333	66.838	148.091	1.00	35.78
	6854	C	ASP D 194	24.496	67.154	150.613	1.00	24.26
	6855	O	ASP D 194	25.323	67.649	149.872	1.00	27.57
	6856	N	PRO D 195	24.843	66.275	151.558	1.00	25.62
	6857	CD	PRO D 195	23.992	65.685	152.606	1.00	21.60
20	6858	CA	PRO D 195	26.248	65.883	151.730	1.00	22.87
	6859	CB	PRO D 195	26.208	64.962	152.945	1.00	21.20
	6860	CG	PRO D 195	24.985	65.421	153.695	1.00	27.26
	6861	C	PRO D 195	26.795	65.142	150.523	1.00	23.25
	6862	O	PRO D 195	26.147	64.246	150.004	1.00	27.41
25	6863	N	ASP D 196	27.988	65.498	150.072	1.00	21.62
	6864	CA	ASP D 196	28.578	64.775	148.956	1.00	20.52
	6865	CB	ASP D 196	29.644	65.623	148.269	1.00	27.06
	6866	CG	ASP D 196	29.073	66.868	147.663	1.00	26.11
	6867	OD1	ASP D 196	29.120	67.941	148.321	1.00	21.26
30	6868	OD2	ASP D 196	28.552	66.750	146.531	1.00	36.91
	6869	C	ASP D 196	29.231	63.505	149.480	1.00	20.41
	6870	O	ASP D 196	29.271	62.494	148.792	1.00	21.30
	6871	N	LEU D 197	29.731	63.573	150.712	1.00	19.60
	6872	CA	LEU D 197	30.432	62.456	151.354	1.00	20.66
35	6873	CB	LEU D 197	31.955	62.715	151.338	1.00	18.94
	6874	CG	LEU D 197	32.863	61.789	152.156	1.00	23.54
	6875	CD1	LEU D 197	32.949	60.375	151.498	1.00	16.11
	6876	CD2	LEU D 197	34.245	62.424	152.237	1.00	16.20
	6877	C	LEU D 197	29.976	62.356	152.803	1.00	17.57
40	6878	O	LEU D 197	29.797	63.375	153.453	1.00	18.10
	6879	N	ILE D 198	29.774	61.142	153.304	1.00	13.50
	6880	CA	ILE D 198	29.375	60.980	154.700	1.00	16.74
	6881	CB	ILE D 198	27.937	60.390	154.865	1.00	20.54

	6882	CG2	ILE	D	198	27.672	60.067	156.332	1.00	12.72
	6883	CG1	ILE	D	198	26.885	61.424	154.401	1.00	16.97
	6884	CD1	ILE	D	198	25.440	60.972	154.561	1.00	11.89
	6885	C	ILE	D	198	30.406	60.048	155.272	1.00	18.48
5	6886	O	ILE	D	198	30.698	59.002	154.698	1.00	19.94
	6887	N	ILE	D	199	30.975	60.447	156.397	1.00	17.92
	6888	CA	ILE	D	199	32.028	59.693	157.043	1.00	14.34
	6889	CB	ILE	D	199	33.232	60.617	157.371	1.00	18.46
	6890	CG2	ILE	D	199	34.173	59.949	158.382	1.00	20.95
10	6891	CG1	ILE	D	199	33.972	60.982	156.080	1.00	23.97
	6892	CD1	ILE	D	199	34.997	62.114	156.234	1.00	14.85
	6893	C	ILE	D	199	31.516	59.126	158.328	1.00	14.12
	6894	O	ILE	D	199	30.902	59.831	159.123	1.00	15.36
	6895	N	ARG	D	200	31.784	57.851	158.537	1.00	16.72
15	6896	CA	ARG	D	200	31.371	57.192	159.755	1.00	21.83
	6897	CB	ARG	D	200	30.374	56.082	159.417	1.00	24.24
	6898	CG	ARG	D	200	29.915	55.315	160.628	1.00	33.20
	6899	CD	ARG	D	200	28.465	55.546	160.963	1.00	34.40
	6900	NE	ARG	D	200	28.252	55.308	162.388	1.00	36.16
20	6901	CZ	ARG	D	200	27.067	55.078	162.940	1.00	38.07
	6902	NH1	ARG	D	200	25.974	55.046	162.183	1.00	36.26
	6903	NH2	ARG	D	200	26.978	54.881	164.245	1.00	33.37
	6904	C	ARG	D	200	32.643	56.639	160.420	1.00	20.17
	6905	O	ARG	D	200	33.416	55.939	159.792	1.00	28.60
25	6906	N	THR	D	201	32.886	56.993	161.672	1.00	24.69
	6907	CA	THR	D	201	34.073	56.514	162.366	1.00	24.02
	6908	CB	THR	D	201	34.783	57.660	163.114	1.00	21.09
	6909	OG1	THR	D	201	33.908	58.235	164.084	1.00	26.37
	6910	CG2	THR	D	201	35.188	58.748	162.141	1.00	21.46
30	6911	C	THR	D	201	33.773	55.399	163.358	1.00	29.57
	6912	O	THR	D	201	32.605	55.091	163.618	1.00	28.76
	6913	N	SER	D	202	34.838	54.773	163.876	1.00	32.30
	6914	CA	SER	D	202	34.734	53.717	164.881	1.00	30.72
	6915	CB	SER	D	202	33.826	54.189	166.028	1.00	32.36
35	6916	OG	SER	D	202	33.807	53.266	167.102	1.00	42.75
	6917	C	SER	D	202	34.260	52.346	164.395	1.00	31.16
	6918	O	SER	D	202	33.685	51.575	165.158	1.00	35.05
	6919	N	GLY	D	203	34.475	52.044	163.129	1.00	31.01
	6920	CA	GLY	D	203	34.090	50.739	162.622	1.00	28.42
40	6921	C	GLY	D	203	32.622	50.388	162.517	1.00	27.89
	6922	O	GLY	D	203	32.286	49.247	162.241	1.00	34.96
	6923	N	GLU	D	204	31.743	51.352	162.725	1.00	32.71
	6924	CA	GLU	D	204	30.313	51.110	162.621	1.00	32.01

	6925	CB	GLU D 204	29.550	52.207	163.360	1.00	38.54
	6926	CG	GLU D 204	29.673	52.127	164.861	1.00	50.00
	6927	CD	GLU D 204	29.435	50.719	165.371	1.00	55.94
	6928	OE1	GLU D 204	28.454	50.087	164.919	1.00	60.50
5	6929	OE2	GLU D 204	30.223	50.241	166.219	1.00	60.12
	6930	C	GLU D 204	29.914	51.114	161.148	1.00	28.99
	6931	O	GLU D 204	30.197	52.067	160.436	1.00	33.53
	6932	N	LEU D 205	29.281	50.045	160.688	1.00	27.12
	6933	CA	LEU D 205	28.851	49.962	159.302	1.00	28.21
10	6934	CB	LEU D 205	29.314	48.639	158.681	1.00	34.86
	6935	CG	LEU D 205	30.613	48.543	157.849	1.00	40.22
	6936	CD1	LEU D 205	30.273	48.538	156.357	1.00	39.68
	6937	CD2	LEU D 205	31.564	49.692	158.172	1.00	37.50
	6938	C	LEU D 205	27.339	50.074	159.252	1.00	27.93
15	6939	O	LEU D 205	26.646	49.145	158.864	1.00	33.73
	6940	N	ARG D 206	26.828	51.216	159.681	1.00	29.79
	6941	CA	ARG D 206	25.398	51.467	159.673	1.00	30.19
	6942	CB	ARG D 206	24.767	50.931	160.950	1.00	30.10
	6943	CG	ARG D 206	25.227	51.612	162.198	1.00	34.91
20	6944	CD	ARG D 206	24.366	51.211	163.353	1.00	34.39
	6945	NE	ARG D 206	24.790	49.943	163.901	1.00	45.41
	6946	CZ	ARG D 206	25.557	49.822	164.977	1.00	52.92
	6947	NH1	ARG D 206	25.971	50.908	165.618	1.00	54.52
	6948	NH2	ARG D 206	25.906	48.614	165.408	1.00	56.84
25	6949	C	ARG D 206	25.197	52.973	159.542	1.00	33.05
	6950	O	ARG D 206	26.104	53.761	159.827	1.00	33.47
	6951	N	LEU D 207	23.999	53.385	159.158	1.00	35.91
	6952	CA	LEU D 207	23.713	54.803	158.913	1.00	37.61
	6953	CB	LEU D 207	22.821	54.878	157.659	1.00	45.71
30	6954	CG	LEU D 207	22.238	53.504	157.242	1.00	41.56
	6955	CD1	LEU D 207	21.609	52.854	158.467	1.00	37.60
	6956	CD2	LEU D 207	21.181	53.642	156.104	1.00	39.02
	6957	C	LEU D 207	23.123	55.670	160.049	1.00	37.51
	6958	O	LEU D 207	23.120	56.911	159.967	1.00	38.35
35	6959	N	SER D 208	22.628	55.017	161.092	1.00	24.15
	6960	CA	SER D 208	22.028	55.671	162.253	1.00	20.91
	6961	CB	SER D 208	23.115	56.049	163.246	1.00	18.47
	6962	OG	SER D 208	23.784	54.888	163.659	1.00	21.46
	6963	C	SER D 208	21.070	56.855	162.108	1.00	22.71
40	6964	O	SER D 208	21.095	57.784	162.916	1.00	22.82
	6965	N	ASN D 209	20.222	56.835	161.094	1.00	21.42
	6966	CA	ASN D 209	19.231	57.893	160.961	1.00	17.48
	6967	CB	ASN D 209	18.299	57.809	162.188	1.00	16.20

	6968	CG	ASN	D	209	16.963	58.515	161.987	1.00	19.86
	6969	OD1	ASN	D	209	16.486	58.700	160.868	1.00	14.67
	6970	ND2	ASN	D	209	16.347	58.895	163.092	1.00	17.14
	6971	C	ASN	D	209	19.852	59.296	160.824	1.00	17.04
5	6972	O	ASN	D	209	19.303	60.280	161.302	1.00	14.34
	6973	N	PHE	D	210	21.001	59.368	160.170	1.00	18.04
	6974	CA	PHE	D	210	21.684	60.638	159.921	1.00	16.36
	6975	CB	PHE	D	210	23.180	60.484	160.149	1.00	19.10
	6976	CG	PHE	D	210	23.956	61.764	159.969	1.00	21.10
10	6977	CD1	PHE	D	210	23.655	62.874	160.727	1.00	14.31
	6978	CD2	PHE	D	210	24.995	61.840	159.046	1.00	19.80
	6979	CE1	PHE	D	210	24.374	64.059	160.577	1.00	19.27
	6980	CE2	PHE	D	210	25.729	63.025	158.885	1.00	23.51
	6981	CZ	PHE	D	210	25.417	64.131	159.649	1.00	15.26
15	6982	C	PHE	D	210	21.446	61.061	158.470	1.00	15.01
	6983	O	PHE	D	210	21.847	60.364	157.552	1.00	18.32
	6984	N	LEU	D	211	20.776	62.193	158.282	1.00	17.17
	6985	CA	LEU	D	211	20.481	62.733	156.952	1.00	15.46
	6986	CB	LEU	D	211	21.732	63.443	156.385	1.00	12.81
20	6987	CG	LEU	D	211	22.345	64.548	157.290	1.00	16.60
	6988	CD1	LEU	D	211	23.595	65.129	156.641	1.00	18.96
	6989	CD2	LEU	D	211	21.342	65.654	157.563	1.00	8.25
	6990	C	LEU	D	211	19.931	61.734	155.924	1.00	18.70
	6991	O	LEU	D	211	20.428	61.659	154.805	1.00	18.32
25	6992	N	PRO	D	212	18.889	60.955	156.289	1.00	17.80
	6993	CD	PRO	D	212	18.225	60.881	157.595	1.00	17.20
	6994	CA	PRO	D	212	18.294	59.979	155.364	1.00	18.97
	6995	CB	PRO	D	212	17.088	59.420	156.148	1.00	19.76
	6996	CG	PRO	D	212	16.818	60.432	157.181	1.00	24.29
30	6997	C	PRO	D	212	17.892	60.573	154.015	1.00	15.44
	6998	O	PRO	D	212	18.221	60.033	152.945	1.00	13.00
	6999	N	TRP	D	213	17.182	61.681	154.053	1.00	12.04
	7000	CA	TRP	D	213	16.798	62.323	152.797	1.00	15.79
	7001	CB	TRP	D	213	15.773	63.416	153.060	1.00	12.12
35	7002	CG	TRP	D	213	15.361	64.156	151.845	1.00	16.46
	7003	CD2	TRP	D	213	14.125	64.013	151.149	1.00	19.97
	7004	CE2	TRP	D	213	14.126	64.962	150.091	1.00	20.58
	7005	CE3	TRP	D	213	13.012	63.182	151.315	1.00	14.88
	7006	CD1	TRP	D	213	16.056	65.151	151.198	1.00	15.78
40	7007	NE1	TRP	D	213	15.317	65.641	150.148	1.00	20.92
	7008	CZ2	TRP	D	213	13.059	65.096	149.210	1.00	20.31
	7009	CZ3	TRP	D	213	11.943	63.318	150.435	1.00	25.52
	7010	CH2	TRP	D	213	11.975	64.268	149.394	1.00	22.12



	7011	C	TRP D 213	17.990	62.939	152.047	1.00	16.94
	7012	O	TRP D 213	18.302	62.553	150.904	1.00	18.63
	7013	N	GLN D 214	18.644	63.895	152.702	1.00	15.86
	7014	CA	GLN D 214	19.784	64.618	152.133	1.00	17.05
5	7015	CB	GLN D 214	20.291	65.666	153.133	1.00	14.93
	7016	CG	GLN D 214	19.230	66.625	153.701	1.00	13.05
	7017	CD	GLN D 214	18.662	66.150	155.059	1.00	16.53
	7018	OE1	GLN D 214	18.228	66.953	155.894	1.00	18.57
	7019	NE2	GLN D 214	18.653	64.851	155.265	1.00	9.63
10	7020	C	GLN D 214	20.959	63.727	151.677	1.00	16.49
	7021	O	GLN D 214	21.602	64.030	150.681	1.00	17.95
	7022	N	GLY D 215	21.212	62.627	152.388	1.00	19.08
	7023	CA	GLY D 215	22.299	61.719	152.040	1.00	13.31
	7024	C	GLY D 215	21.923	60.554	151.138	1.00	17.46
15	7025	O	GLY D 215	22.719	59.658	150.946	1.00	18.16
	7026	N	ALA D 216	20.723	60.568	150.567	1.00	20.06
	7027	CA	ALA D 216	20.258	59.483	149.683	1.00	22.36
	7028	CB	ALA D 216	18.900	59.879	149.004	1.00	23.76
	7029	C	ALA D 216	21.255	59.051	148.612	1.00	21.72
20	7030	O	ALA D 216	21.317	57.869	148.282	1.00	22.39
	7031	N	TYR D 217	22.030	59.987	148.064	1.00	18.33
	7032	CA	TYR D 217	23.027	59.635	147.040	1.00	19.11
	7033	CB	TYR D 217	22.819	60.435	145.747	1.00	21.81
	7034	CG	TYR D 217	21.451	60.325	145.118	1.00	22.69
25	7035	CD1	TYR D 217	20.462	61.260	145.396	1.00	25.39
	7036	CE1	TYR D 217	19.212	61.194	144.778	1.00	25.57
	7037	CD2	TYR D 217	21.159	59.308	144.213	1.00	22.79
	7038	CE2	TYR D 217	19.902	59.233	143.588	1.00	23.27
	7039	CZ	TYR D 217	18.946	60.184	143.874	1.00	25.67
30	7040	OH	TYR D 217	17.739	60.172	143.211	1.00	35.64
	7041	C	TYR D 217	24.466	59.863	147.456	1.00	20.67
	7042	O	TYR D 217	25.361	59.741	146.638	1.00	23.26
	7043	N	SER D 218	24.706	60.212	148.708	1.00	21.01
	7044	CA	SER D 218	26.066	60.473	149.147	1.00	19.51
35	7045	CB	SER D 218	26.065	60.930	150.604	1.00	19.16
	7046	OG	SER D 218	25.191	62.021	150.786	1.00	23.90
	7047	C	SER D 218	27.026	59.299	149.046	1.00	20.95
	7048	O	SER D 218	26.631	58.144	149.163	1.00	20.49
	7049	N	GLU D 219	28.304	59.613	148.856	1.00	24.47
40	7050	CA	GLU D 219	29.354	58.591	148.844	1.00	19.81
	7051	CB	GLU D 219	30.671	59.156	148.295	1.00	26.14
	7052	CG	GLU D 219	30.713	59.345	146.795	1.00	29.57
	7053	CD	GLU D 219	30.492	58.039	146.051	1.00	36.54

	7054	OE1	GLU	D	219	31.111	57.021	146.460	1.00	31.78
	7055	OE2	GLU	D	219	29.707	58.037	145.066	1.00	41.97
	7056	C	GLU	D	219	29.538	58.289	150.324	1.00	17.55
	7057	O	GLU	D	219	29.529	59.195	151.139	1.00	17.42
5	7058	N	LEU	D	220	29.676	57.027	150.684	1.00	18.74
	7059	CA	LEU	D	220	29.855	56.703	152.087	1.00	22.81
	7060	CB	LEU	D	220	28.875	55.617	152.525	1.00	13.34
	7061	CG	LEU	D	220	27.379	55.894	152.291	1.00	22.63
	7062	CD1	LEU	D	220	26.553	54.656	152.648	1.00	19.93
10	7063	CD2	LEU	D	220	26.933	57.072	153.102	1.00	14.34
	7064	C	LEU	D	220	31.298	56.239	152.317	1.00	28.88
	7065	O	LEU	D	220	31.900	55.551	151.482	1.00	27.20
	7066	N	TYR	D	221	31.845	56.634	153.457	1.00	24.42
	7067	CA	TYR	D	221	33.199	56.276	153.803	1.00	28.17
15	7068	CB	TYR	D	221	34.122	57.473	153.571	1.00	29.00
	7069	CG	TYR	D	221	35.531	57.233	154.018	1.00	29.40
	7070	CD1	TYR	D	221	36.424	56.494	153.239	1.00	29.58
	7071	CE1	TYR	D	221	37.724	56.267	153.677	1.00	27.31
	7072	CD2	TYR	D	221	35.971	57.728	155.232	1.00	26.93
20	7073	CE2	TYR	D	221	37.251	57.510	155.672	1.00	24.96
	7074	CZ	TYR	D	221	38.124	56.787	154.908	1.00	28.52
	7075	OH	TYR	D	221	39.395	56.587	155.399	1.00	34.32
	7076	C	TYR	D	221	33.213	55.855	155.265	1.00	30.35
	7077	O	TYR	D	221	32.855	56.631	156.155	1.00	32.66
25	7078	N	PHE	D	222	33.599	54.607	155.495	1.00	31.08
	7079	CA	PHE	D	222	33.673	54.040	156.834	1.00	28.64
	7080	CB	PHE	D	222	32.930	52.698	156.887	1.00	25.60
	7081	CG	PHE	D	222	31.496	52.785	156.452	1.00	21.34
	7082	CD1	PHE	D	222	31.155	52.666	155.109	1.00	18.25
30	7083	CD2	PHE	D	222	30.495	53.043	157.381	1.00	21.90
	7084	CE1	PHE	D	222	29.829	52.804	154.696	1.00	24.31
	7085	CE2	PHE	D	222	29.164	53.188	156.980	1.00	18.83
	7086	CZ	PHE	D	222	28.832	53.067	155.635	1.00	22.46
	7087	C	PHE	D	222	35.131	53.826	157.217	1.00	28.93
35	7088	O	PHE	D	222	35.942	53.423	156.387	1.00	32.66
	7089	N	THR	D	223	35.460	54.124	158.465	1.00	25.87
	7090	CA	THR	D	223	36.802	53.935	158.961	1.00	26.29
	7091	CB	THR	D	223	37.659	55.236	158.883	1.00	30.16
	7092	OG1	THR	D	223	38.978	54.941	159.359	1.00	29.78
40	7093	CG2	THR	D	223	37.066	56.367	159.756	1.00	18.85
	7094	C	THR	D	223	36.755	53.437	160.415	1.00	32.41
	7095	O	THR	D	223	35.822	53.760	161.187	1.00	25.13
	7096	N	ASP	D	224	37.784	52.666	160.764	1.00	29.74

	7097	CA	ASP D 224	37.948	52.062	162.079	1.00	33.20
	7098	CB	ASP D 224	38.962	50.911	161.998	1.00	42.51
	7099	CG	ASP D 224	38.400	49.664	161.331	1.00	46.84
	7100	OD1	ASP D 224	39.186	48.962	160.657	1.00	52.91
5	7101	OD2	ASP D 224	37.191	49.379	161.492	1.00	47.15
	7102	C	ASP D 224	38.446	53.036	163.130	1.00	33.73
	7103	O	ASP D 224	38.233	52.816	164.322	1.00	32.16
	7104	N	THR D 225	39.111	54.106	162.704	1.00	31.40
	7105	CA	THR D 225	39.662	55.035	163.678	1.00	35.46
10	7106	CB	THR D 225	40.603	56.100	163.025	1.00	39.76
	7107	OG1	THR D 225	40.137	57.422	163.323	1.00	39.15
	7108	CG2	THR D 225	40.706	55.881	161.539	1.00	36.37
	7109	C	THR D 225	38.613	55.700	164.529	1.00	31.49
	7110	O	THR D 225	37.546	56.087	164.056	1.00	35.25
15	7111	N	LEU D 226	38.932	55.786	165.814	1.00	29.16
	7112	CA	LEU D 226	38.051	56.357	166.808	1.00	24.42
	7113	CB	LEU D 226	38.576	55.984	168.199	1.00	18.97
	7114	CG	LEU D 226	38.771	54.457	168.336	1.00	26.39
	7115	CD1	LEU D 226	39.359	54.129	169.703	1.00	26.25
20	7116	CD2	LEU D 226	37.432	53.721	168.152	1.00	20.69
	7117	C	LEU D 226	37.996	57.854	166.564	1.00	24.79
	7118	O	LEU D 226	38.951	58.435	166.069	1.00	27.08
	7119	N	TRP D 227	36.874	58.477	166.893	1.00	23.87
	7120	CA	TRP D 227	36.721	59.899	166.615	1.00	20.57
25	7121	CB	TRP D 227	35.375	60.445	167.131	1.00	13.60
	7122	CG	TRP D 227	35.254	61.943	166.935	1.00	12.14
	7123	CD2	TRP D 227	35.339	62.661	165.692	1.00	11.92
	7124	CE2	TRP D 227	35.264	64.035	165.995	1.00	10.28
	7125	CE3	TRP D 227	35.468	62.273	164.351	1.00	15.22
30	7126	CD1	TRP D 227	35.124	62.882	167.905	1.00	15.67
	7127	NE1	TRP D 227	35.127	64.147	167.352	1.00	19.49
	7128	CZ2	TRP D 227	35.316	65.027	165.009	1.00	11.20
	7129	CZ3	TRP D 227	35.512	63.264	163.367	1.00	10.34
	7130	CH2	TRP D 227	35.439	64.623	163.706	1.00	16.75
35	7131	C	TRP D 227	37.835	60.766	167.146	1.00	19.03
	7132	O	TRP D 227	38.332	61.610	166.422	1.00	27.38
	7133	N	PRO D 228	38.228	60.591	168.418	1.00	21.50
	7134	CD	PRO D 228	37.695	59.668	169.434	1.00	22.76
	7135	CA	PRO D 228	39.308	61.414	168.988	1.00	21.58
40	7136	CB	PRO D 228	39.442	60.869	170.417	1.00	20.20
	7137	CG	PRO D 228	38.058	60.387	170.720	1.00	22.04
	7138	C	PRO D 228	40.632	61.316	168.195	1.00	22.98
	7139	O	PRO D 228	41.467	62.201	168.297	1.00	30.74

	7140	N	ASP	D	229	40.824	60.246	167.416	1.00	20.17
	7141	CA	ASP	D	229	42.035	60.104	166.609	1.00	21.29
	7142	CB	ASP	D	229	42.502	58.647	166.549	1.00	24.77
	7143	CG	ASP	D	229	42.863	58.104	167.906	1.00	27.75
5	7144	OD1	ASP	D	229	43.463	58.855	168.701	1.00	29.56
	7145	OD2	ASP	D	229	42.559	56.929	168.179	1.00	32.82
	7146	C	ASP	D	229	41.865	60.611	165.181	1.00	26.12
	7147	O	ASP	D	229	42.836	60.645	164.405	1.00	27.93
	7148	N	PHE	D	230	40.642	61.005	164.830	1.00	26.40
10	7149	CA	PHE	D	230	40.347	61.516	163.493	1.00	22.38
	7150	CB	PHE	D	230	38.827	61.551	163.263	1.00	23.41
	7151	CG	PHE	D	230	38.444	61.540	161.822	1.00	17.64
	7152	CD1	PHE	D	230	38.222	60.337	161.167	1.00	15.30
	7153	CD2	PHE	D	230	38.421	62.717	161.093	1.00	19.65
15	7154	CE1	PHE	D	230	37.988	60.309	159.791	1.00	19.33
	7155	CE2	PHE	D	230	38.187	62.699	159.710	1.00	22.14
	7156	CZ	PHE	D	230	37.974	61.500	159.062	1.00	15.64
	7157	C	PHE	D	230	40.932	62.930	163.375	1.00	22.33
	7158	O	PHE	D	230	40.521	63.838	164.081	1.00	28.03
20	7159	N	ASP	D	231	41.902	63.100	162.483	1.00	30.17
	7160	CA	ASP	D	231	42.567	64.385	162.287	1.00	33.02
	7161	CB	ASP	D	231	43.990	64.318	162.819	1.00	33.61
	7162	CG	ASP	D	231	44.717	63.083	162.337	1.00	38.73
	7163	OD1	ASP	D	231	44.377	62.601	161.231	1.00	40.74
25	7164	OD2	ASP	D	231	45.625	62.601	163.052	1.00	40.53
	7165	C	ASP	D	231	42.605	64.768	160.814	1.00	32.19
	7166	O	ASP	D	231	41.925	64.151	159.984	1.00	31.75
	7167	N	GLU	D	232	43.406	65.779	160.483	1.00	31.53
	7168	CA	GLU	D	232	43.474	66.228	159.103	1.00	29.37
30	7169	CB	GLU	D	232	44.446	67.385	158.954	1.00	31.76
	7170	CG	GLU	D	232	44.321	68.068	157.599	1.00	34.26
	7171	CD	GLU	D	232	45.340	69.175	157.392	1.00	34.92
	7172	OE1	GLU	D	232	45.716	69.849	158.381	1.00	32.21
	7173	OE2	GLU	D	232	45.755	69.370	156.228	1.00	38.93
35	7174	C	GLU	D	232	43.900	65.083	158.209	1.00	31.10
	7175	O	GLU	D	232	43.387	64.921	157.098	1.00	33.84
	7176	N	ALA	D	233	44.831	64.274	158.698	1.00	25.93
	7177	CA	ALA	D	233	45.295	63.142	157.913	1.00	30.20
	7178	CB	ALA	D	233	46.390	62.373	158.681	1.00	28.08
40	7179	C	ALA	D	233	44.124	62.210	157.557	1.00	30.69
	7180	O	ALA	D	233	43.923	61.866	156.387	1.00	30.65
	7181	N	ALA	D	234	43.350	61.808	158.561	1.00	29.30
	7182	CA	ALA	D	234	42.207	60.934	158.318	1.00	29.35

	7183	CB	ALA D 234	41.533	60.567	159.643	1.00	24.48
	7184	C	ALA D 234	41.217	61.616	157.366	1.00	30.07
	7185	O	ALA D 234	40.672	60.975	156.467	1.00	33.59
	7186	N	LEU D 235	41.018	62.921	157.539	1.00	29.20
5	7187	CA	LEU D 235	40.105	63.668	156.675	1.00	31.50
	7188	CB	LEU D 235	39.914	65.106	157.218	1.00	26.47
	7189	CG	LEU D 235	38.936	66.096	156.564	1.00	33.34
	7190	CD1	LEU D 235	39.543	66.686	155.358	1.00	43.67
	7191	CD2	LEU D 235	37.631	65.421	156.205	1.00	28.91
10	7192	C	LEU D 235	40.604	63.679	155.222	1.00	33.39
	7193	O	LEU D 235	39.808	63.501	154.288	1.00	35.23
	7194	N	GLN D 236	41.909	63.864	155.013	1.00	36.23
	7195	CA	GLN D 236	42.432	63.874	153.632	1.00	39.04
	7196	CB	GLN D 236	43.880	64.394	153.568	1.00	36.85
15	7197	CG	GLN D 236	43.976	65.889	153.860	1.00	43.23
	7198	CD	GLN D 236	45.228	66.554	153.312	1.00	51.65
	7199	OE1	GLN D 236	46.288	66.559	153.952	1.00	57.67
	7200	NE2	GLN D 236	45.113	67.123	152.119	1.00	53.71
	7201	C	GLN D 236	42.337	62.506	152.973	1.00	36.24
20	7202	O	GLN D 236	42.191	62.416	151.749	1.00	35.71
	7203	N	GLU D 237	42.412	61.444	153.776	1.00	37.49
	7204	CA	GLU D 237	42.292	60.084	153.246	1.00	40.65
	7205	CB	GLU D 237	42.682	59.034	154.283	1.00	45.39
	7206	CG	GLU D 237	44.163	58.861	154.488	1.00	57.80
25	7207	CD	GLU D 237	44.470	57.746	155.473	1.00	67.03
	7208	OE1	GLU D 237	43.972	56.616	155.251	1.00	71.07
	7209	OE2	GLU D 237	45.204	57.999	156.462	1.00	67.17
	7210	C	GLU D 237	40.839	59.855	152.845	1.00	38.95
	7211	O	GLU D 237	40.558	59.189	151.848	1.00	37.70
30	7212	N	ALA D 238	39.905	60.393	153.623	1.00	34.11
	7213	CA	ALA D 238	38.507	60.220	153.255	1.00	29.45
	7214	CB	ALA D 238	37.602	60.768	154.339	1.00	26.87
	7215	C	ALA D 238	38.316	60.988	151.947	1.00	28.15
	7216	O	ALA D 238	37.778	60.462	150.966	1.00	28.83
35	7217	N	ILE D 239	38.772	62.237	151.924	1.00	28.49
	7218	CA	ILE D 239	38.642	63.037	150.723	1.00	28.02
	7219	CB	ILE D 239	39.260	64.390	150.907	1.00	27.19
	7220	CG2	ILE D 239	39.369	65.079	149.552	1.00	18.94
	7221	CG1	ILE D 239	38.448	65.176	151.939	1.00	25.23
40	7222	CD1	ILE D 239	39.014	66.541	152.254	1.00	26.37
	7223	C	ILE D 239	39.313	62.354	149.539	1.00	37.00
	7224	O	ILE D 239	38.803	62.402	148.416	1.00	39.32
	7225	N	LEU D 240	40.454	61.710	149.794	1.00	39.14

	7226	CA	LEU D 240	41.186	61.013	148.743	1.00	41.30
	7227	CB	LEU D 240	42.513	60.480	149.279	1.00	48.81
	7228	CG	LEU D 240	43.448	59.840	148.254	1.00	48.36
	7229	CD1	LEU D 240	43.935	60.902	147.270	1.00	52.77
5	7230	CD2	LEU D 240	44.617	59.195	148.980	1.00	52.54
	7231	C	LEU D 240	40.354	59.860	148.207	1.00	38.95
	7232	O	LEU D 240	40.218	59.698	146.991	1.00	40.40
	7233	N	ALA D 241	39.809	59.052	149.113	1.00	35.76
	7234	CA	ALA D 241	38.959	57.934	148.706	1.00	39.83
10	7235	CB	ALA D 241	38.469	57.149	149.931	1.00	34.80
	7236	C	ALA D 241	37.761	58.474	147.918	1.00	38.65
	7237	O	ALA D 241	37.354	57.887	146.921	1.00	44.66
	7238	N	TYR D 242	37.202	59.593	148.369	1.00	37.78
	7239	CA	TYR D 242	36.065	60.204	147.700	1.00	37.01
15	7240	CB	TYR D 242	35.650	61.476	148.424	1.00	30.63
	7241	CG	TYR D 242	34.652	62.300	147.646	1.00	28.13
	7242	CD1	TYR D 242	33.292	62.048	147.741	1.00	30.93
	7243	CE1	TYR D 242	32.366	62.823	147.052	1.00	31.95
	7244	CD2	TYR D 242	35.072	63.349	146.832	1.00	32.54
20	7245	CE2	TYR D 242	34.161	64.130	146.136	1.00	35.49
	7246	CZ	TYR D 242	32.804	63.862	146.252	1.00	36.61
	7247	OH	TYR D 242	31.888	64.643	145.584	1.00	37.48
	7248	C	TYR D 242	36.405	60.542	146.246	1.00	44.22
	7249	O	TYR D 242	35.595	60.324	145.333	1.00	42.91
25	7250	N	ASN D 243	37.597	61.088	146.032	1.00	46.14
	7251	CA	ASN D 243	38.024	61.444	144.681	1.00	47.89
	7252	CB	ASN D 243	39.320	62.253	144.720	1.00	48.01
	7253	CG	ASN D 243	39.078	63.723	145.003	1.00	50.35
	7254	OD1	ASN D 243	39.816	64.355	145.758	1.00	51.70
30	7255	ND2	ASN D 243	38.040	64.278	144.389	1.00	50.60
	7256	C	ASN D 243	38.207	60.210	143.825	1.00	46.63
	7257	O	ASN D 243	37.946	60.247	142.637	1.00	44.75
	7258	N	ARG D 244	38.645	59.116	144.437	1.00	50.41
	7259	CA	ARG D 244	38.849	57.869	143.714	1.00	55.73
35	7260	CB	ARG D 244	39.581	56.855	144.592	1.00	58.07
	7261	CG	ARG D 244	41.077	56.769	144.384	1.00	66.11
	7262	CD	ARG D 244	41.807	57.981	144.923	1.00	73.72
	7263	NE	ARG D 244	43.230	57.696	145.119	1.00	81.74
	7264	CZ	ARG D 244	43.708	56.796	145.980	1.00	83.33
40	7265	NH1	ARG D 244	42.877	56.083	146.737	1.00	83.12
	7266	NH2	ARG D 244	45.019	56.612	146.090	1.00	80.19
	7267	C	ARG D 244	37.530	57.250	143.250	1.00	60.32
	7268	O	ARG D 244	37.494	56.543	142.242	1.00	59.48

	7269	N	ARG D 245	36.451	57.504	143.992	1.00	64.78
	7270	CA	ARG D 245	35.142	56.949	143.644	1.00	68.16
	7271	CB	ARG D 245	34.039	57.496	144.566	1.00	65.72
	7272	CG	ARG D 245	34.225	57.207	146.067	1.00	60.86
5	7273	CD	ARG D 245	34.319	55.718	146.387	1.00	58.67
	7274	NE	ARG D 245	34.593	55.463	147.805	1.00	51.79
	7275	CZ	ARG D 245	33.721	55.656	148.801	1.00	52.67
	7276	NH1	ARG D 245	32.488	56.109	148.554	1.00	45.94
	7277	NH2	ARG D 245	34.089	55.398	150.054	1.00	45.11
10	7278	C	ARG D 245	34.794	57.256	142.190	1.00	71.26
	7279	O	ARG D 245	34.316	56.383	141.466	1.00	73.19
	7280	N	HIS D 246	35.031	58.491	141.761	1.00	73.65
	7281	CA	HIS D 246	34.745	58.860	140.378	1.00	79.01
	7282	CB	HIS D 246	33.237	58.792	140.101	1.00	78.89
15	7283	CG	HIS D 246	32.889	58.873	138.647	0.00	77.33
	7284	CD2	HIS D 246	32.214	58.017	137.843	0.00	76.89
	7285	ND1	HIS D 246	33.258	59.935	137.850	0.00	76.89
	7286	CE1	HIS D 246	32.827	59.730	136.619	0.00	76.50
	7287	NE2	HIS D 246	32.191	58.573	136.587	0.00	76.50
20	7288	C	HIS D 246	35.260	60.255	140.049	1.00	82.15
	7289	O	HIS D 246	36.122	60.361	139.148	1.00	84.44
	7290	OT	HIS D 246	34.795	61.221	140.697	1.00	84.17
	7291	OH2	WAT W 1	12.352	55.472	151.847	1.00	24.41
	7292	OH2	WAT W 2	15.293	54.604	111.003	1.00	21.51
25	7293	OH2	WAT W 3	27.317	84.305	156.593	1.00	21.55
	7294	OH2	WAT W 4	27.468	46.755	136.235	1.00	38.67
	7295	OH2	WAT W 5	24.047	56.899	150.017	1.00	19.58
	7296	OH2	WAT W 6	40.712	77.293	159.352	1.00	35.70
	7297	OH2	WAT W 7	25.651	81.348	162.658	1.00	19.98
30	7298	OH2	WAT W 8	29.652	80.856	155.647	1.00	19.57
	7299	OH2	WAT W 9	26.976	30.048	105.048	1.00	19.75
	7300	OH2	WAT W 10	23.088	35.617	104.810	1.00	25.33
	7301	OH2	WAT W 11	21.407	77.279	163.358	1.00	28.48
	7302	OH2	WAT W 12	16.562	63.433	156.365	1.00	18.54
35	7303	OH2	WAT W 13	13.154	67.674	105.333	1.00	44.98
	7304	OH2	WAT W 14	29.814	86.622	162.346	1.00	18.68
	7305	OH2	WAT W 15	27.244	36.086	111.611	1.00	20.08
	7306	OH2	WAT W 16	21.421	64.439	109.100	1.00	29.10
	7307	OH2	WAT W 17	15.953	40.959	124.848	1.00	65.65
40	7308	OH2	WAT W 18	36.160	30.885	107.084	1.00	49.15
	7309	OH2	WAT W 19	43.075	55.192	170.279	1.00	28.24
	7310	OH2	WAT W 20	4.788	35.046	152.724	1.00	23.90
	7311	OH2	WAT W 21	15.333	68.040	148.104	1.00	28.72

	7312	OH2	WAT	W	22	30.959	61.833	94.884	1.00	26.91
	7313	OH2	WAT	W	23	13.805	60.126	163.832	1.00	30.48
	7314	OH2	WAT	W	24	27.234	69.610	148.193	1.00	22.34
	7315	OH2	WAT	W	25	18.824	60.189	114.266	1.00	23.07
5	7316	OH2	WAT	W	26	41.077	49.283	99.183	1.00	37.57
	7317	OH2	WAT	W	27	10.572	28.703	137.018	1.00	37.26
	7318	OH2	WAT	W	28	16.340	75.164	175.623	1.00	27.57
	7319	OH2	WAT	W	29	23.460	60.770	117.115	1.00	26.41
	7320	OH2	WAT	W	30	40.206	58.426	156.934	1.00	32.69
10	7321	OH2	WAT	W	31	6.625	51.188	155.796	1.00	23.16
	7322	OH2	WAT	W	32	45.626	67.086	162.002	1.00	34.83
	7323	OH2	WAT	W	33	10.396	75.275	139.683	1.00	44.91
	7324	OH2	WAT	W	34	-0.601	31.861	146.272	1.00	24.79
	7325	OH2	WAT	W	35	17.494	70.622	152.608	1.00	24.54
15	7326	OH2	WAT	W	36	40.844	64.399	177.253	1.00	38.86
	7327	OH2	WAT	W	37	9.317	76.714	155.588	1.00	44.72
	7328	OH2	WAT	W	38	27.274	48.442	122.282	1.00	49.70
	7329	OH2	WAT	W	39	16.004	37.400	99.199	1.00	43.82
	7330	OH2	WAT	W	40	12.464	57.862	103.307	1.00	25.85
20	7331	OH2	WAT	W	41	16.000	50.457	119.288	1.00	41.83
	7332	OH2	WAT	W	42	11.536	62.676	115.517	1.00	21.38
	7333	OH2	WAT	W	43	29.945	32.976	146.925	1.00	40.38
	7334	OH2	WAT	W	44	34.140	42.113	149.283	1.00	42.33
	7335	OH2	WAT	W	45	7.925	76.405	126.399	1.00	39.14
25	7336	OH2	WAT	W	46	18.170	61.725	111.986	1.00	20.89
	7337	OH2	WAT	W	47	30.755	77.804	153.505	1.00	19.49
	7338	OH2	WAT	W	48	41.754	57.323	159.509	1.00	50.17
	7339	OH2	WAT	W	49	0.432	34.807	151.800	1.00	32.45
	7340	OH2	WAT	W	50	7.115	42.218	141.155	1.00	44.48
30	7341	OH2	WAT	W	51	41.819	59.321	114.776	1.00	45.33
	7342	OH2	WAT	W	52	42.222	64.241	166.321	1.00	48.53
	7343	OH2	WAT	W	53	-2.402	32.063	152.567	1.00	40.97
	7344	OH2	WAT	W	54	30.018	57.511	96.725	1.00	31.64
	7345	OH2	WAT	W	55	25.854	47.763	118.781	1.00	31.76
35	7346	OH2	WAT	W	56	29.404	29.191	146.912	1.00	39.21
	7347	OH2	WAT	W	57	7.137	64.606	107.354	1.00	35.06
	7348	OH2	WAT	W	58	30.727	50.059	87.237	1.00	54.96
	7349	OH2	WAT	W	59	19.413	28.876	101.654	1.00	35.31
	7350	OH2	WAT	W	60	25.838	88.427	157.351	1.00	26.19
40	7351	OH2	WAT	W	61	27.419	47.353	95.987	1.00	57.79
	7352	OH2	WAT	W	62	30.203	48.522	96.797	1.00	54.20
	7353	OH2	WAT	W	63	21.496	84.485	164.897	1.00	41.99
	7354	OH2	WAT	W	64	22.158	87.861	165.582	1.00	33.54



	7355	OH2	WAT	W	65	32.737	64.431	169.451	1.00	46.70
	7356	OH2	WAT	W	66	23.474	36.307	90.026	1.00	30.93
	7357	OH2	WAT	W	67	37.442	85.717	167.677	1.00	32.95
	7358	OH2	WAT	W	68	43.064	58.724	84.014	1.00	56.06
5	7359	OH2	WAT	W	69	37.636	65.647	93.288	1.00	51.34
	7360	OH2	WAT	W	70	14.664	53.056	122.611	1.00	30.55
	7361	OH2	WAT	W	71	27.474	70.999	145.857	1.00	35.94
	7362	OH2	WAT	W	72	39.270	57.654	108.939	1.00	37.38
	7363	OH2	WAT	W	73	16.244	57.666	96.290	1.00	44.21
10	7364	OH2	WAT	W	74	-3.798	83.958	124.924	1.00	37.61
	7365	OH2	WAT	W	75	16.259	33.643	100.272	1.00	51.46
	7366	OH2	WAT	W	76	6.618	61.191	165.181	1.00	38.97
	7367	OH2	WAT	W	77	28.046	70.339	130.551	1.00	42.50
	7368	OH2	WAT	W	78	29.190	69.902	171.263	1.00	56.72
15	7369	OH2	WAT	W	79	20.726	51.978	96.057	1.00	49.92
	7370	OH2	WAT	W	80	44.221	78.297	161.702	1.00	62.56
	7371	OH2	WAT	W	81	20.581	57.209	157.438	1.00	33.26
	7372	OH2	WAT	W	82	-5.940	53.812	101.396	1.00	57.11
	7373	OH2	WAT	W	83	39.911	58.910	106.658	1.00	47.81
20	7374	OH2	WAT	W	84	32.796	77.176	106.744	1.00	64.09
	7375	OH2	WAT	W	85	17.139	72.633	163.285	1.00	28.02
	7376	OH2	WAT	W	86	34.325	39.961	113.739	1.00	34.28
	7377	OH2	WAT	W	87	30.341	49.026	120.813	1.00	48.22
	7378	OH2	WAT	W	88	31.350	29.293	111.400	1.00	25.00
25	7379	OH2	WAT	W	89	25.746	49.413	82.127	1.00	80.91
	7380	OH2	WAT	W	90	31.461	59.204	170.711	1.00	34.92
	7381	OH2	WAT	W	91	38.148	49.077	171.219	1.00	48.66
	7382	OH2	WAT	W	92	31.372	68.755	145.926	1.00	49.47
	7383	OH2	WAT	W	93	13.562	59.502	143.993	1.00	32.29
30	7384	OH2	WAT	W	94	44.826	58.384	114.708	1.00	50.20
	7385	OH2	WAT	W	95	-2.561	42.769	110.565	1.00	55.80
	7386	OH2	WAT	W	96	-9.137	42.055	139.221	1.00	55.45
	7387	OH2	WAT	W	97	24.513	32.763	110.869	1.00	29.48
	7388	OH2	WAT	W	98	6.282	67.456	111.806	1.00	35.29
35	7389	OH2	WAT	W	99	45.544	73.075	151.194	1.00	64.91
	7390	OH2	WAT	W	100	1.241	38.634	145.992	1.00	30.64
	7391	OH2	WAT	W	101	37.842	82.237	155.326	1.00	37.54
	7392	OH2	WAT	W	102	9.223	65.502	142.805	1.00	40.50
	7393	OH2	WAT	W	103	38.369	50.230	174.074	1.00	45.42
40	7394	OH2	WAT	W	104	14.928	84.636	180.437	1.00	52.27
	7395	OH2	WAT	W	105	19.987	46.457	129.894	1.00	60.28
	7396	OH2	WAT	W	106	8.000	66.630	109.794	1.00	34.16
	7397	OH2	WAT	W	107	34.830	34.213	152.025	1.00	60.46

	7398	OH2	WAT	W	108	13.929	50.264	161.908	1.00	38.42
	7399	OH2	WAT	W	109	7.928	47.573	126.723	1.00	61.79
	7400	OH2	WAT	W	110	16.984	39.547	84.255	1.00	46.21
	7401	OH2	WAT	W	111	15.832	47.366	114.819	1.00	33.95
5	7402	OH2	WAT	W	112	13.984	73.451	167.234	1.00	54.71
	7403	OH2	WAT	W	113	9.368	43.081	92.878	1.00	24.54
	7404	OH2	WAT	W	114	-3.176	65.328	167.249	1.00	54.79
	7405	OH2	WAT	W	115	10.815	55.601	163.806	1.00	36.83
	7406	OH2	WAT	W	116	15.643	54.415	93.626	1.00	56.57
10	7407	OH2	WAT	W	117	18.184	73.663	165.116	1.00	34.52
	7408	OH2	WAT	W	118	5.305	83.283	114.524	1.00	25.41
	7409	OH2	WAT	W	119	32.518	33.657	139.051	1.00	49.90
	7410	OH2	WAT	W	120	17.065	74.471	161.007	1.00	49.07
	7411	OH2	WAT	W	121	33.595	77.512	125.281	1.00	50.88
15	7412	OH2	WAT	W	122	17.588	81.103	156.085	1.00	50.84
	7413	OH2	WAT	W	123	41.500	66.054	175.536	1.00	56.58
	7414	OH2	WAT	W	124	5.172	72.068	141.250	1.00	41.51
	7415	OH2	WAT	W	125	21.568	76.166	143.755	1.00	73.77
	7416	OH2	WAT	W	126	9.185	62.735	142.948	1.00	41.89
20	7417	OH2	WAT	W	127	34.832	65.837	107.513	1.00	45.85
	7418	OH2	WAT	W	128	7.851	35.881	155.165	1.00	39.11
	7419	OH2	WAT	W	129	22.684	74.042	102.458	1.00	46.57
	7420	OH2	WAT	W	130	27.459	69.125	104.582	1.00	38.96
	7421	OH2	WAT	W	131	-4.070	57.066	158.275	1.00	52.53
25	7422	OH2	WAT	W	132	28.752	47.213	86.649	1.00	58.61
	7423	OH2	WAT	W	133	24.922	79.092	178.645	1.00	45.28
	7424	OH2	WAT	W	134	33.981	87.885	155.674	1.00	30.59
	7425	OH2	WAT	W	135	14.099	51.868	139.548	1.00	46.13
	7426	OH2	WAT	W	136	37.470	57.626	139.398	1.00	56.59
30	7427	OH2	WAT	W	137	38.013	46.409	158.862	1.00	44.49
	7428	OH2	WAT	W	138	42.958	74.833	168.772	1.00	53.20
	7429	OH2	WAT	W	139	33.235	67.237	144.157	1.00	65.83
	7430	OH2	WAT	W	140	20.003	42.431	109.124	1.00	49.61
	7431	OH2	WAT	W	141	41.759	42.209	106.675	1.00	39.16
35	7432	OH2	WAT	W	142	8.901	53.309	162.622	1.00	56.01
	7433	OH2	WAT	W	143	16.104	50.816	159.620	1.00	23.82
	7434	OH2	WAT	W	144	21.060	66.173	103.443	1.00	39.92
	7435	OH2	WAT	W	145	38.774	52.907	155.516	1.00	51.22
	7436	OH2	WAT	W	146	9.091	62.725	124.194	1.00	54.32
40	7437	OH2	WAT	W	147	35.574	36.847	95.584	1.00	35.16
	7438	OH2	WAT	W	148	33.660	52.072	140.583	1.00	66.74
	7439	OH2	WAT	W	149	40.340	51.425	100.220	1.00	41.74
	7440	OH2	WAT	W	150	13.217	56.304	100.592	1.00	48.44

	7441	OH2 WAT W 151	15.809	35.169	93.881	1.00	36.82
	7442	OH2 WAT W 152	43.749	54.141	159.341	1.00	49.92
	7443	OH2 WAT W 153	8.381	53.500	160.048	1.00	38.45
	7444	OH2 WAT W 154	-7.450	38.246	113.088	1.00	57.23
5	7445	OH2 WAT W 155	39.605	51.795	96.149	1.00	42.35
	7446	OH2 WAT W 156	27.641	86.516	174.798	1.00	49.43
	7447	OH2 WAT W 157	19.659	43.633	123.947	1.00	48.13
	7448	OH2 WAT W 158	8.545	82.516	112.335	1.00	35.36
	7449	OH2 WAT W 159	29.587	78.673	116.351	1.00	38.45
10	7450	OH2 WAT W 160	28.282	34.353	116.120	1.00	54.63
	7451	OH2 WAT W 161	18.260	64.362	113.456	1.00	40.75
	7452	OH2 WAT W 162	37.593	37.899	91.930	1.00	42.03
	7453	OH2 WAT W 163	20.758	62.378	168.812	1.00	45.81
	7454	OH2 WAT W 164	42.801	70.932	168.778	1.00	49.19
15	7455	OH2 WAT W 165	31.332	43.694	156.858	1.00	42.46
	7456	OH2 WAT W 166	30.851	84.352	119.919	1.00	32.84
	7457	OH2 WAT W 167	22.448	62.746	148.516	1.00	26.48
	7458	OH2 WAT W 168	44.948	58.806	158.723	1.00	45.40
	7459	OH2 WAT W 169	39.166	64.459	108.187	1.00	55.69
20	7460	OH2 WAT W 170	24.393	53.890	119.635	1.00	36.14
	7461	OH2 WAT W 171	19.317	60.251	109.525	1.00	28.83
	7462	OH2 WAT W 172	35.270	45.665	89.814	1.00	60.03
	7463	OH2 WAT W 173	2.228	80.152	121.569	1.00	28.15
	7464	OH2 WAT W 174	14.529	76.811	142.401	1.00	76.14
25	7465	OH2 WAT W 175	39.713	51.533	158.570	1.00	43.77
	7466	OH2 WAT W 176	-0.689	50.846	156.437	1.00	43.91
	7467	OH2 WAT W 177	45.485	60.600	175.420	1.00	31.57
	7468	OH2 WAT W 178	43.533	46.174	104.781	1.00	60.39
	7469	OH2 WAT W 179	44.711	72.158	164.885	1.00	54.52
30	7470	OH2 WAT W 180	21.325	82.757	174.169	1.00	40.71
	7471	OH2 WAT W 181	31.490	55.222	123.312	1.00	48.97
	7472	OH2 WAT W 182	28.553	39.273	113.835	1.00	21.94
	7473	OH2 WAT W 183	37.410	79.950	154.127	1.00	41.15
	7474	OH2 WAT W 184	25.004	29.149	169.017	1.00	59.49
35	7475	OH2 WAT W 185	33.213	52.592	160.132	1.00	55.21
	7476	OH2 WAT W 186	41.785	52.878	81.404	1.00	53.58
	7477	OH2 WAT W 187	18.161	61.775	116.771	1.00	28.65
	7478	OH2 WAT W 188	13.094	58.426	141.544	1.00	37.23
	7479	OH2 WAT W 189	19.007	56.184	155.273	1.00	24.76
40	7480	OH2 WAT W 190	8.311	51.697	157.650	1.00	36.76
	7481	OH2 WAT W 191	21.997	52.779	161.525	1.00	51.68
	7482	OH2 WAT W 192	9.467	77.657	153.414	1.00	54.89
	7483	OH2 WAT W 193	25.425	63.541	125.121	1.00	37.99

	7484	OH2 WAT W 194	20.346	52.419	120.546	1.00	33.76
	7485	OH2 WAT W 195	12.818	58.419	123.108	1.00	31.44
	7486	OH2 WAT W 196	24.730	88.494	166.050	1.00	25.94
	7487	OH2 WAT W 197	4.548	57.308	102.624	1.00	45.28
5	7488	OH2 WAT W 198	31.389	68.648	170.957	1.00	42.18
	7489	OH2 WAT W 199	18.968	76.265	165.093	1.00	31.64
	7490	OH2 WAT W 200	21.469	54.980	118.706	1.00	31.60
	7491	OH2 WAT W 201	17.289	55.788	98.032	1.00	48.07
	7492	OH2 WAT W 202	7.713	41.343	112.424	1.00	41.31
10	7493	OH2 WAT W 203	15.407	67.707	145.749	1.00	57.01
	7494	OH2 WAT W 204	28.793	48.258	137.817	1.00	52.39
	7495	OH2 WAT W 205	23.350	81.638	161.367	1.00	29.54
	7496	OH2 WAT W 206	17.591	68.791	150.567	1.00	25.64
	7497	OH2 WAT W 207	20.349	40.959	122.780	1.00	55.20
15	7498	OH2 WAT W 208	16.530	63.240	174.067	1.00	66.40
	7499	OH2 WAT W 209	15.790	75.009	167.795	1.00	47.28
	7500	OH2 WAT W 210	31.837	29.177	147.623	1.00	39.53
	7501	OH2 WAT W 211	19.090	56.117	150.527	1.00	32.03
	7502	OH2 WAT W 212	39.389	85.919	169.049	1.00	44.32
20	7503	OH2 WAT W 213	36.384	87.330	157.003	1.00	40.13
	7504	OH2 WAT W 214	12.005	61.488	102.867	1.00	45.75
	7505	OH2 WAT W 215	35.131	52.930	153.302	1.00	41.26
	7506	OH2 WAT W 216	-13.852	61.202	152.038	1.00	36.69
	7507	OH2 WAT W 217	18.671	53.234	153.593	1.00	34.43
25	7508	OH2 WAT W 218	-3.123	63.317	146.203	1.00	54.30
	7509	OH2 WAT W 219	-0.395	79.345	117.846	1.00	35.70
	7510	OH2 WAT W 220	20.926	35.613	106.024	1.00	41.81
	7511	OH2 WAT W 221	9.411	62.210	165.135	1.00	37.37
	7512	OH2 WAT W 222	36.420	76.474	153.048	1.00	35.85
30	7513	OH2 WAT W 223	35.187	87.292	169.327	1.00	27.72
	7514	OH2 WAT W 224	21.292	41.098	100.462	1.00	47.58
	7515	OH2 WAT W 225	14.534	45.202	104.320	1.00	28.71
	7516	OH2 WAT W 226	8.591	65.733	103.272	1.00	57.01
	7517	OH2 WAT W 227	30.428	51.766	96.862	1.00	50.60
35	7518	OH2 WAT W 228	44.492	73.582	159.662	1.00	43.18
	7519	OH2 WAT W 229	32.532	65.642	171.323	1.00	47.34
	7520	OH2 WAT W 230	19.465	41.490	138.172	1.00	54.20
	7521	OH2 WAT W 231	13.642	56.805	126.904	1.00	40.69
	7522	OH2 WAT W 232	44.304	58.292	163.071	1.00	49.23
40	7523	OH2 WAT W 233	33.111	41.717	159.137	1.00	54.29
	7524	OH2 WAT W 234	19.277	79.626	183.577	1.00	34.10
	7525	OH2 WAT W 235	34.633	63.753	113.280	1.00	47.87
	7526	OH2 WAT W 236	22.154	58.890	155.143	1.00	34.96

	7527	OH2 WAT W 237	41.806	55.096	166.377	1.00	34.24
	7528	OH2 WAT W 238	21.432	37.843	88.704	1.00	44.13
	7529	OH2 WAT W 239	34.643	72.266	132.775	1.00	54.92
	7530	OH2 WAT W 240	35.338	85.572	172.058	1.00	53.95
5	7531	OH2 WAT W 241	16.256	49.306	116.927	1.00	31.04
	7532	OH2 WAT W 242	41.709	64.265	169.935	1.00	38.19
	7533	OH2 WAT W 243	28.757	83.671	179.021	1.00	53.65
	7534	OH2 WAT W 244	38.413	67.817	108.876	1.00	52.81
	7535	OH2 WAT W 245	20.663	64.332	111.428	1.00	38.62
10	7536	OH2 WAT W 246	43.979	55.862	105.039	1.00	50.24
	7537	OH2 WAT W 247	43.780	71.588	161.864	1.00	34.98
	7538	OH2 WAT W 248	11.436	89.641	129.977	1.00	42.00
	7539	OH2 WAT W 249	41.365	43.999	104.687	1.00	30.91
	7540	OH2 WAT W 250	15.533	65.748	164.990	1.00	39.00
15	7541	OH2 WAT W 251	42.846	65.656	89.632	1.00	43.71
	7542	OH2 WAT W 252	21.227	58.593	112.048	1.00	35.62
	7543	OH2 WAT W 253	5.127	90.024	111.033	1.00	52.52
	7544	OH2 WAT W 254	35.042	73.905	117.216	1.00	44.07
	7545	OH2 WAT W 255	18.017	23.723	142.245	1.00	67.41
20	7546	OH2 WAT W 256	-1.547	33.928	137.556	1.00	47.00
	7547	OH2 WAT W 257	10.061	75.671	157.442	1.00	55.48
	7548	OH2 WAT W 258	7.530	43.022	110.558	1.00	55.53
	7549	OH2 WAT W 259	26.307	46.356	121.321	1.00	52.54
	7550	OH2 WAT W 260	37.686	38.689	95.823	1.00	44.59
25	7551	OH2 WAT W 261	25.245	31.371	90.883	1.00	53.17
	7552	OH2 WAT W 262	-4.652	34.436	142.767	1.00	43.66
	7553	OH2 WAT W 263	40.945	75.530	172.545	1.00	55.53
	7554	OH2 WAT W 264	-0.740	50.671	134.055	1.00	53.15
	7555	OH2 WAT W 265	11.352	89.628	133.396	1.00	49.20
30	7556	OH2 WAT W 266	37.290	34.588	109.736	1.00	50.49
	7557	OH2 WAT W 267	40.825	37.013	101.903	1.00	49.39
	7558	OH2 WAT W 268	18.719	39.974	104.690	1.00	26.07
	7559	OH2 WAT W 269	0.643	78.513	120.772	1.00	40.99
	7560	OH2 WAT W 270	-4.940	85.263	126.927	1.00	31.26
35	7561	OH2 WAT W 271	13.901	63.373	129.175	1.00	60.43
	7562	OH2 WAT W 272	40.786	77.684	170.897	1.00	53.15
	7563	OH2 WAT W 273	37.863	51.299	89.365	1.00	43.90
	7564	OH2 WAT W 274	30.617	68.966	134.676	1.00	42.40
	7565	OH2 WAT W 275	11.659	72.354	106.387	1.00	43.46
40	7566	OH2 WAT W 276	45.443	62.469	166.796	1.00	59.20
	7567	OH2 WAT W 277	43.987	48.932	103.728	1.00	43.78
	7568	OH2 WAT W 278	42.769	60.533	95.807	1.00	59.32
	7569	OH2 WAT W 279	40.776	65.445	180.203	1.00	55.54

	7570	OH2	WAT	W	280	-10.848	62.130	148.427	1.00	55.28
	7571	OH2	WAT	W	281	19.914	83.970	134.430	1.00	59.38
	7572	OH2	WAT	W	282	21.483	38.567	111.403	1.00	36.86
	7573	OH2	WAT	W	283	38.967	62.592	110.346	1.00	60.29
5	7574	OH2	WAT	W	284	1.572	27.360	152.361	1.00	37.17
	7575	OH2	WAT	W	285	37.723	50.008	156.080	1.00	70.26
	7576	OH2	WAT	W	286	2.966	54.156	103.222	1.00	49.50
	7577	OH2	WAT	W	287	-1.589	50.288	102.705	1.00	73.77
	7578	OH2	WAT	W	288	37.516	34.582	95.648	1.00	47.25
10	7579	OH2	WAT	W	289	18.845	80.053	161.444	1.00	58.39
	7580	OH2	WAT	W	290	7.134	66.706	164.340	1.00	38.74
	7581	OH2	WAT	W	291	-5.751	62.419	111.073	1.00	38.80
	7582	OH2	WAT	W	292	28.331	79.237	149.230	1.00	45.26
	7583	OH2	WAT	W	293	28.736	72.020	170.198	1.00	50.37
15	7584	OH2	WAT	W	294	7.807	53.256	124.651	1.00	35.93
	7585	OH2	WAT	W	295	5.276	73.692	117.621	1.00	48.57
	7586	OH2	WAT	W	296	25.199	57.397	157.092	1.00	56.90
	7587	OH2	WAT	W	297	23.531	47.649	123.560	1.00	48.49
	7588	OH2	WAT	W	298	22.536	36.594	112.333	1.00	38.66
20	7589	OH2	WAT	W	299	21.236	80.762	157.102	1.00	43.11
	7590	OH2	WAT	W	300	43.516	82.149	164.770	1.00	51.55
	7591	OH2	WAT	W	301	24.994	36.436	113.441	1.00	33.28
	7592	OH2	WAT	W	302	35.020	50.272	154.159	1.00	45.25
	7593	OH2	WAT	W	303	19.366	38.121	119.490	1.00	44.24
25	7594	OH2	WAT	W	304	22.848	43.321	164.662	1.00	52.52
	7595	OH2	WAT	W	305	28.803	63.842	185.096	1.00	62.39
	7596	OH2	WAT	W	306	20.912	50.896	136.612	1.00	50.93
	7597	OH2	WAT	W	307	-0.130	77.384	157.579	1.00	59.19
	7598	OH2	WAT	W	308	-3.536	78.882	123.927	1.00	52.36
30	7599	OH2	WAT	W	309	1.063	83.592	115.474	1.00	37.76
	7600	OH2	WAT	W	310	38.405	33.383	98.424	1.00	38.93
	7601	OH2	WAT	W	311	7.475	83.652	139.796	1.00	51.86
	7602	OH2	WAT	W	312	17.857	62.182	169.577	1.00	59.11
	7603	OH2	WAT	W	313	32.002	27.544	113.378	1.00	46.06
35	7604	OH2	WAT	W	314	12.387	55.358	90.969	1.00	55.61
	7605	OH2	WAT	W	315	0.891	43.126	160.848	1.00	48.12
	7606	OH2	WAT	W	316	41.633	50.708	127.755	1.00	47.27
	7607	OH2	WAT	W	317	32.423	54.653	172.147	1.00	25.42
	7608	OH2	WAT	W	318	12.331	35.147	88.139	1.00	55.24
40	7609	OH2	WAT	W	319	15.441	65.067	144.764	1.00	33.20
	7610	OH2	WAT	W	320	40.548	54.085	157.210	1.00	43.00
	7611	OH2	WAT	W	321	22.089	52.705	98.234	1.00	61.73
	7612	OH2	WAT	W	322	7.239	64.978	154.179	1.00	37.09

	7613	OH2	WAT	W	323	0.550	86.841	121.144	1.00	22.51
	7614	OH2	WAT	W	324	24.184	50.980	99.752	1.00	47.16
	7615	OH2	WAT	W	325	23.665	59.158	109.888	1.00	45.49
	7616	OH2	WAT	W	326	19.813	52.728	98.891	1.00	46.97
5	7617	OH2	WAT	W	327	-2.839	32.085	138.129	1.00	39.78
	7618	OH2	WAT	W	328	9.499	62.749	103.240	1.00	46.62
	7619	OH2	WAT	W	329	7.415	41.030	114.734	1.00	40.46
	7620	OH2	WAT	W	330	-0.069	86.118	130.467	1.00	49.80
	7621	OH2	WAT	W	331	40.673	60.694	99.873	1.00	33.56
10	7622	OH2	WAT	W	332	14.416	50.697	121.483	1.00	64.77
	7623	OH2	WAT	W	333	24.011	78.487	155.905	1.00	38.04
	7624	OH2	WAT	W	334	20.533	77.071	160.985	1.00	58.11
	7625	OH2	WAT	W	335	23.195	83.022	158.527	1.00	44.92
	7626	OH2	WAT	W	336	16.270	78.813	129.819	1.00	54.00
15	7627	OH2	WAT	W	337	15.464	66.982	107.609	1.00	26.03
	7628	OH2	WAT	W	338	31.640	37.939	156.771	1.00	64.40
	7629	OH2	WAT	W	339	46.976	64.163	165.205	1.00	36.91
	7630	OH2	WAT	W	340	33.304	48.195	153.946	1.00	52.87
	7631	OH2	WAT	W	341	-1.048	39.586	149.790	1.00	44.96
20	7632	OH2	WAT	W	342	35.287	57.004	186.624	1.00	52.61
	7633	OH2	WAT	W	343	2.662	60.413	144.348	1.00	57.31
	7634	OH2	WAT	W	344	14.848	52.164	166.291	1.00	42.67
	7635	OH2	WAT	W	345	4.916	39.701	110.853	1.00	50.26
	7636	OH2	WAT	W	346	26.538	38.184	115.313	1.00	30.74
25	7637	OH2	WAT	W	347	34.541	89.227	153.452	1.00	50.57
	7638	OH2	WAT	W	348	16.788	48.259	160.825	1.00	33.71
	7639	OH2	WAT	W	349	35.250	49.549	156.822	1.00	55.52
	7640	OH2	WAT	W	350	-3.272	54.762	155.638	1.00	42.76
	7641	OH2	WAT	W	351	26.550	78.335	147.072	1.00	48.38
30	7642	OH2	WAT	W	352	32.287	29.392	98.163	1.00	26.70
	7643	OH2	WAT	W	353	34.002	66.690	112.543	1.00	45.32
	7644	OH2	WAT	W	354	0.508	65.282	103.717	1.00	52.50
	7645	OH2	WAT	W	355	4.524	36.515	131.330	1.00	56.33
	7646	OH2	WAT	W	356	45.262	59.545	161.086	1.00	41.72
35	7647	OH2	WAT	W	357	4.961	65.132	143.556	1.00	59.00
	7648	OH2	WAT	W	358	12.179	86.053	112.142	1.00	38.89
	7649	OH2	WAT	W	359	32.530	38.766	141.377	1.00	47.21
	7650	OH2	WAT	W	360	6.570	81.549	111.394	1.00	44.16
	7651	OH2	WAT	W	361	13.004	72.367	165.279	1.00	45.96
40	7652	OH2	WAT	W	362	31.973	68.206	100.661	1.00	67.06
	7653	OH2	WAT	W	363	44.263	51.590	120.936	1.00	54.89
	7654	OH2	WAT	W	364	30.071	47.302	147.740	1.00	47.85
	7655	OH2	WAT	W	365	20.166	55.086	98.322	1.00	37.15

	7656	OH2	WAT	W	366	15.595	43.155	106.386	1.00	66.70
	7657	OH2	WAT	W	367	-3.446	69.862	164.261	1.00	46.11
	7658	OH2	WAT	W	368	35.229	67.308	109.860	1.00	59.10
	7659	OH2	WAT	W	369	20.753	88.034	127.140	1.00	46.69
5	7660	OH2	WAT	W	370	9.041	55.783	142.925	1.00	48.36
	7661	OH2	WAT	W	371	26.451	83.995	180.936	1.00	60.29
	7662	OH2	WAT	W	372	33.378	81.968	123.649	1.00	57.47
	7663	OH2	WAT	W	373	7.117	59.500	167.632	1.00	54.66
	7664	OH2	WAT	W	374	-13.134	61.653	154.371	1.00	37.87
10	7665	OH2	WAT	W	375	39.406	42.629	92.387	1.00	48.35
	7666	OH2	WAT	W	376	-1.509	54.871	151.229	1.00	50.25
	7667	OH2	WAT	W	377	2.526	67.268	166.696	1.00	68.89
	7668	OH2	WAT	W	378	42.944	66.027	151.239	1.00	61.53
	7669	OH2	WAT	W	379	-5.381	84.022	118.746	1.00	46.28
15	7670	OH2	WAT	W	380	25.886	36.345	89.108	1.00	44.82
	7671	OH2	WAT	W	381	36.757	88.320	174.167	1.00	46.84
	7672	OH2	WAT	W	382	9.522	77.097	151.130	1.00	49.50
	7673	OH2	WAT	W	383	27.175	43.869	121.483	1.00	64.70
	7674	OH2	WAT	W	384	25.188	89.834	168.031	1.00	29.17
20	7675	OH2	WAT	W	385	-2.133	41.763	107.962	1.00	55.32
	7676	OH2	WAT	W	386	17.581	68.108	147.353	1.00	50.43
	7677	OH2	WAT	W	387	-2.716	54.084	153.333	1.00	47.42
	7678	OH2	WAT	W	388	1.214	58.353	145.206	1.00	54.87
	7679	OH2	WAT	W	389	32.478	44.660	97.842	1.00	36.41
25	7680	OH2	WAT	W	390	-0.526	39.840	108.033	1.00	60.43
	7681	OH2	WAT	W	391	49.539	60.328	164.723	1.00	48.42
	7682	OH2	WAT	W	392	-1.977	85.907	128.985	1.00	43.64
	7683	OH2	WAT	W	393	19.586	57.647	152.990	1.00	20.10
	7684	OH2	WAT	W	394	10.485	50.231	124.846	1.00	41.75
30	7685	OH2	WAT	W	395	44.275	56.470	80.377	1.00	45.96
	7686	OH2	WAT	W	396	-5.305	81.386	124.897	1.00	42.75
	7687	OH2	WAT	W	397	8.432	55.753	124.650	1.00	41.19
	7688	OH2	WAT	W	398	13.851	49.974	119.218	1.00	31.25
	7689	OH2	WAT	W	399	31.233	30.782	96.006	1.00	45.70
35	7690	OH2	WAT	W	400	19.392	60.601	89.688	1.00	52.10
	7691	OH2	WAT	W	401	21.499	64.661	106.290	1.00	56.95
	7692	OH2	WAT	W	402	38.194	38.717	107.570	1.00	38.44
	7693	OH2	WAT	W	403	19.114	46.019	85.421	1.00	37.30
	7694	OH2	WAT	W	404	40.014	53.000	88.531	1.00	44.55
40	7695	OH2	WAT	W	405	6.431	62.587	154.353	1.00	39.93
	7696	OH2	WAT	W	406	14.586	65.974	100.731	1.00	36.94
	7697	OH2	WAT	W	407	28.758	79.062	151.934	1.00	37.27
	7698	OH2	WAT	W	408	38.693	41.435	95.010	1.00	57.50



7699	OH2 WAT W 409	25.591	57.948	93.946	1.00	45.44
7700	OH2 WAT W 410	27.357	55.891	95.673	1.00	63.85
END						

Table IB

## Atomic Coordinates of UPPS in complex with FPP

CRYST1 58.108 44.558 115.535 90.00 98.69 90.00						
	ATOM	RESIDUE	X	Y	Z	Occ B
5	1 CB	GLU A 14	-6.102	26.564	37.502	1.00 65.83
	2 CG	GLU A 14	-7.057	26.920	36.373	1.00 66.40
	3 CD	GLU A 14	-6.477	26.604	34.993	1.00 67.15
	4 OE1	GLU A 14	-7.128	26.938	33.975	1.00 68.21
10	5 OE2	GLU A 14	-5.370	26.021	34.921	1.00 66.67
	6 C	GLU A 14	-4.263	24.924	37.894	1.00 63.83
	7 O	GLU A 14	-3.819	25.328	38.969	1.00 63.93
	8 N	GLU A 14	-6.625	24.367	38.522	1.00 67.24
	9 CA	GLU A 14	-5.741	25.079	37.555	1.00 65.39
15	10 N	VAL A 15	-3.500	24.350	36.966	1.00 48.09
	11 CA	VAL A 15	-2.072	24.131	37.182	1.00 46.83
	12 CB	VAL A 15	-1.842	23.108	38.340	1.00 46.56
	13 CG1	VAL A 15	-2.644	21.840	38.082	1.00 51.75
	14 CG2	VAL A 15	-0.363	22.773	38.479	1.00 50.29
20	15 C	VAL A 15	-1.330	23.654	35.931	1.00 43.02
	16 O	VAL A 15	-1.893	22.995	35.044	1.00 43.85
	17 N	PRO A 16	-0.048	24.004	35.838	1.00 43.32
	18 CD	PRO A 16	0.613	25.086	36.582	1.00 43.32
	19 CA	PRO A 16	0.758	23.600	34.690	1.00 45.94
25	20 CB	PRO A 16	1.936	24.573	34.734	1.00 46.50
	21 CG	PRO A 16	1.389	25.757	35.498	1.00 46.71
	22 C	PRO A 16	1.212	22.152	34.830	1.00 46.22
	23 O	PRO A 16	1.215	21.590	35.929	1.00 44.84
	24 N	THR A 17	1.607	21.556	33.713	1.00 47.29
30	25 CA	THR A 17	2.064	20.178	33.727	1.00 43.32
	26 CB	THR A 17	1.170	19.291	32.879	1.00 39.41
	27 OG1	THR A 17	-0.198	19.511	33.243	1.00 43.75
	28 CG2	THR A 17	1.539	17.826	33.084	1.00 37.92
	29 C	THR A 17	3.452	20.059	33.149	1.00 41.03
35	30 O	THR A 17	3.773	20.728	32.162	1.00 43.88
	31 N	GLN A 18	4.278	19.215	33.760	1.00 41.44
	32 CA	GLN A 18	5.614	19.000	33.231	1.00 41.88
	33 CB	GLN A 18	6.348	17.893	33.993	1.00 46.62
	34 CG	GLN A 18	6.760	18.209	35.417	1.00 52.25
40	35 CD	GLN A 18	7.791	17.221	35.947	1.00 57.97
	36 OE1	GLN A 18	8.915	17.147	35.448	1.00 58.34
	37 NE2	GLN A 18	7.408	16.454	36.958	1.00 52.89
	38 C	GLN A 18	5.345	18.518	31.811	1.00 39.78

	39	O	GLN	A	18	4.495	17.642	31.603	1.00	34.46
	40	N	VAL	A	19	6.041	19.089	30.836	1.00	41.79
	41	CA	VAL	A	19	5.838	18.682	29.452	1.00	43.01
	42	CB	VAL	A	19	5.263	19.845	28.599	1.00	43.44
5	43	CG1	VAL	A	19	6.153	21.066	28.705	1.00	47.93
	44	CG2	VAL	A	19	5.132	19.413	27.150	1.00	37.93
	45	C	VAL	A	19	7.143	18.184	28.837	1.00	41.23
	46	O	VAL	A	19	8.130	18.915	28.775	1.00	42.44
	47	N	PRO	A	20	7.162	16.922	28.373	1.00	40.76
10	48	CD	PRO	A	20	5.990	16.042	28.223	1.00	38.76
	49	CA	PRO	A	20	8.344	16.306	27.760	1.00	38.00
	50	CB	PRO	A	20	7.797	14.993	27.198	1.00	36.72
	51	CG	PRO	A	20	6.338	15.287	26.983	1.00	35.57
	52	C	PRO	A	20	9.015	17.164	26.694	1.00	35.22
15	53	O	PRO	A	20	8.363	17.638	25.771	1.00	32.45
	54	N	ALA	A	21	10.323	17.354	26.830	1.00	30.30
	55	CA	ALA	A	21	11.079	18.157	25.882	1.00	23.48
	56	CB	ALA	A	21	12.369	18.617	26.524	1.00	21.08
	57	C	ALA	A	21	11.374	17.384	24.595	1.00	22.21
20	58	O	ALA	A	21	11.337	17.942	23.499	1.00	24.75
	59	N	HIS	A	22	11.687	16.101	24.739	1.00	22.28
	60	CA	HIS	A	22	11.961	15.241	23.597	1.00	23.83
	61	CB	HIS	A	22	13.429	14.815	23.561	1.00	17.45
	62	CG	HIS	A	22	13.760	13.888	22.432	1.00	22.21
25	63	CD2	HIS	A	22	12.968	13.139	21.626	1.00	18.61
	64	ND1	HIS	A	22	15.054	13.650	22.020	1.00	22.86
	65	CE1	HIS	A	22	15.045	12.798	21.009	1.00	27.15
	66	NE2	HIS	A	22	13.791	12.471	20.750	1.00	23.08
	67	C	HIS	A	22	11.077	14.032	23.786	1.00	24.54
30	68	O	HIS	A	22	11.089	13.415	24.845	1.00	24.16
	69	N	ILE	A	23	10.298	13.704	22.763	1.00	25.14
	70	CA	ILE	A	23	9.398	12.572	22.846	1.00	23.91
	71	CB	ILE	A	23	7.925	12.994	22.659	1.00	16.92
	72	CG2	ILE	A	23	7.035	11.765	22.660	1.00	16.92
35	73	CG1	ILE	A	23	7.495	13.927	23.797	1.00	16.92
	74	CD1	ILE	A	23	6.026	14.354	23.750	1.00	16.92
	75	C	ILE	A	23	9.714	11.516	21.818	1.00	25.13
	76	O	ILE	A	23	10.001	11.827	20.668	1.00	27.80
	77	N	GLY	A	24	9.663	10.261	22.254	1.00	25.44
40	78	CA	GLY	A	24	9.915	9.147	21.367	1.00	27.69
	79	C	GLY	A	24	8.578	8.514	21.053	1.00	29.71
	80	O	GLY	A	24	7.783	8.259	21.956	1.00	29.35
	81	N	ILE	A	25	8.306	8.275	19.777	1.00	29.96

	82	CA	ILE	A	25	7.042	7.666	19.417	1.00	32.73
	83	CB	ILE	A	25	6.142	8.643	18.668	1.00	32.52
	84	CG2	ILE	A	25	4.757	8.043	18.501	1.00	38.35
	85	CG1	ILE	A	25	6.051	9.948	19.446	1.00	29.69
5	86	CD1	ILE	A	25	5.008	10.891	18.930	1.00	34.05
	87	C	ILE	A	25	7.209	6.436	18.555	1.00	34.24
	88	O	ILE	A	25	7.801	6.497	17.478	1.00	40.45
	89	N	ILE	A	26	6.695	5.315	19.052	1.00	32.06
	90	CA	ILE	A	26	6.727	4.045	18.331	1.00	33.80
10	91	CB	ILE	A	26	7.215	2.884	19.234	1.00	32.81
	92	CG2	ILE	A	26	7.180	1.582	18.467	1.00	24.54
	93	CG1	ILE	A	26	8.635	3.159	19.726	1.00	30.96
	94	CD1	ILE	A	26	9.173	2.099	20.658	1.00	34.97
	95	C	ILE	A	26	5.269	3.804	17.933	1.00	36.67
15	96	O	ILE	A	26	4.468	3.302	18.734	1.00	33.26
	97	N	MET	A	27	4.921	4.177	16.702	1.00	39.29
	98	CA	MET	A	27	3.547	4.036	16.247	1.00	40.87
	99	CB	MET	A	27	3.221	5.071	15.159	1.00	36.66
	100	CG	MET	A	27	4.216	5.228	14.023	1.00	33.29
20	101	SD	MET	A	27	4.359	6.996	13.573	1.00	28.20
	102	CE	MET	A	27	6.102	7.183	13.528	1.00	29.62
	103	C	MET	A	27	3.140	2.653	15.801	1.00	41.49
	104	O	MET	A	27	3.772	2.041	14.937	1.00	44.33
	105	N	ASP	A	28	2.070	2.175	16.431	1.00	38.82
25	106	CA	ASP	A	28	1.496	0.863	16.171	1.00	37.15
	107	CB	ASP	A	28	1.780	-0.083	17.340	1.00	36.09
	108	CG	ASP	A	28	3.026	-0.902	17.131	1.00	37.61
	109	OD1	ASP	A	28	4.123	-0.315	17.056	1.00	40.92
	110	OD2	ASP	A	28	2.904	-2.139	17.031	1.00	43.44
30	111	C	ASP	A	28	-0.006	0.990	15.992	1.00	37.00
	112	O	ASP	A	28	-0.608	1.968	16.437	1.00	40.30
	113	N	GLY	A	29	-0.603	-0.001	15.339	1.00	32.98
	114	CA	GLY	A	29	-2.037	0.013	15.128	1.00	31.71
	115	C	GLY	A	29	-2.440	0.281	13.694	1.00	34.52
35	116	O	GLY	A	29	-3.585	0.056	13.323	1.00	35.45
	117	N	ASN	A	30	-1.503	0.762	12.886	1.00	35.21
	118	CA	ASN	A	30	-1.776	1.068	11.492	1.00	34.55
	119	CB	ASN	A	30	-0.463	1.227	10.733	1.00	21.98
	120	CG	ASN	A	30	0.173	2.589	10.951	1.00	23.62
40	121	OD1	ASN	A	30	1.272	2.853	10.470	1.00	20.30
	122	ND2	ASN	A	30	-0.523	3.465	11.670	1.00	20.74
	123	C	ASN	A	30	-2.646	0.022	10.819	1.00	38.93
	124	O	ASN	A	30	-3.787	0.301	10.463	1.00	42.50

	125	N	GLY	A	31	-2.111	-1.183	10.654	1.00	38.13
	126	CA	GLY	A	31	-2.863	-2.253	10.014	1.00	37.44
	127	C	GLY	A	31	-4.101	-2.713	10.768	1.00	37.86
	128	O	GLY	A	31	-5.128	-3.027	10.172	1.00	33.07
5	129	N	ARG	A	32	-4.001	-2.769	12.089	1.00	41.86
	130	CA	ARG	A	32	-5.119	-3.184	12.921	1.00	43.79
	131	CB	ARG	A	32	-4.672	-3.236	14.384	1.00	50.98
	132	CG	ARG	A	32	-5.607	-3.971	15.326	1.00	67.82
	133	CD	ARG	A	32	-5.003	-4.019	16.720	1.00	72.94
10	134	NE	ARG	A	32	-5.992	-4.324	17.750	1.00	79.64
	135	CZ	ARG	A	32	-5.790	-4.149	19.054	1.00	90.52
	136	NH1	ARG	A	32	-4.629	-3.672	19.490	1.00	100.13
	137	NH2	ARG	A	32	-6.750	-4.440	19.923	1.00	94.94
	138	C	ARG	A	32	-6.220	-2.150	12.721	1.00	41.07
15	139	O	ARG	A	32	-7.386	-2.497	12.564	1.00	39.65
	140	N	TRP	A	33	-5.823	-0.880	12.716	1.00	39.29
	141	CA	TRP	A	33	-6.724	0.256	12.519	1.00	37.27
	142	CB	TRP	A	33	-5.924	1.559	12.530	1.00	28.51
	143	CG	TRP	A	33	-6.725	2.789	12.216	1.00	29.95
20	144	CD2	TRP	A	33	-6.861	3.421	10.939	1.00	34.19
	145	CE2	TRP	A	33	-7.700	4.540	11.115	1.00	29.68
	146	CE3	TRP	A	33	-6.357	3.147	9.662	1.00	47.07
	147	CD1	TRP	A	33	-7.467	3.528	13.087	1.00	35.81
	148	NE1	TRP	A	33	-8.055	4.583	12.436	1.00	31.40
25	149	CZ2	TRP	A	33	-8.048	5.390	10.059	1.00	27.96
	150	CZ3	TRP	A	33	-6.705	3.993	8.612	1.00	47.40
	151	CH2	TRP	A	33	-7.543	5.100	8.820	1.00	33.44
	152	C	TRP	A	33	-7.427	0.136	11.174	1.00	35.31
	153	O	TRP	A	33	-8.641	0.289	11.071	1.00	35.16
30	154	N	ALA	A	34	-6.639	-0.119	10.139	1.00	30.64
	155	CA	ALA	A	34	-7.164	-0.263	8.792	1.00	26.94
	156	CB	ALA	A	34	-6.012	-0.370	7.806	1.00	21.71
	157	C	ALA	A	34	-8.055	-1.499	8.689	1.00	29.54
	158	O	ALA	A	34	-9.206	-1.421	8.253	1.00	30.57
35	159	N	LYS	A	35	-7.509	-2.637	9.104	1.00	30.23
	160	CA	LYS	A	35	-8.218	-3.903	9.049	1.00	32.86
	161	CB	LYS	A	35	-7.350	-5.005	9.663	1.00	42.27
	162	CG	LYS	A	35	-7.354	-6.323	8.896	1.00	58.11
	163	CD	LYS	A	35	-6.766	-7.438	9.746	1.00	74.59
40	164	CE	LYS	A	35	-7.559	-7.597	11.042	1.00	85.25
	165	NZ	LYS	A	35	-6.948	-8.562	11.994	1.00	84.42
	166	C	LYS	A	35	-9.572	-3.845	9.754	1.00	38.17
	167	O	LYS	A	35	-10.486	-4.593	9.412	1.00	41.62

	168	N	LYS	A	36	-9.715	-2.956	10.730	1.00	41.65
	169	CA	LYS	A	36	-10.980	-2.859	11.445	1.00	43.49
	170	CB	LYS	A	36	-10.767	-2.303	12.859	1.00	52.09
	171	CG	LYS	A	36	-10.543	-0.792	12.929	1.00	61.96
5	172	CD	LYS	A	36	-10.483	-0.276	14.383	1.00	65.82
	173	CE	LYS	A	36	-10.290	1.253	14.449	1.00	62.88
	174	NZ	LYS	A	36	-10.338	1.809	15.840	1.00	66.92
	175	C	LYS	A	36	-11.975	-1.986	10.688	1.00	44.16
	176	O	LYS	A	36	-13.180	-2.102	10.885	1.00	46.34
10	177	N	ARG	A	37	-11.473	-1.119	9.816	1.00	44.81
	178	CA	ARG	A	37	-12.340	-0.237	9.049	1.00	46.91
	179	CB	ARG	A	37	-11.709	1.145	8.899	1.00	54.16
	180	CG	ARG	A	37	-11.521	1.863	10.211	1.00	51.20
	181	CD	ARG	A	37	-10.928	3.241	10.027	1.00	52.57
15	182	NE	ARG	A	37	-10.378	3.727	11.289	1.00	61.49
	183	CZ	ARG	A	37	-11.093	3.938	12.390	1.00	65.32
	184	NH1	ARG	A	37	-12.399	3.714	12.381	1.00	68.41
	185	NH2	ARG	A	37	-10.499	4.347	13.508	1.00	59.01
	186	C	ARG	A	37	-12.666	-0.780	7.672	1.00	46.38
20	187	O	ARG	A	37	-13.074	-0.031	6.795	1.00	45.99
	188	N	MET	A	38	-12.479	-2.078	7.472	1.00	46.89
	189	CA	MET	A	38	-12.789	-2.699	6.187	1.00	49.02
	190	CB	MET	A	38	-14.225	-2.363	5.758	1.00	46.95
	191	CG	MET	A	38	-15.302	-2.537	6.821	1.00	54.51
25	192	SD	MET	A	38	-15.594	-4.248	7.302	1.00	62.23
	193	CE	MET	A	38	-16.454	-4.891	5.835	1.00	68.23
	194	C	MET	A	38	-11.856	-2.287	5.045	1.00	49.28
	195	O	MET	A	38	-12.048	-2.727	3.911	1.00	50.06
	196	N	GLN	A	39	-10.860	-1.449	5.311	1.00	49.00
30	197	CA	GLN	A	39	-9.976	-1.035	4.229	1.00	48.43
	198	CB	GLN	A	39	-9.816	0.487	4.233	1.00	40.73
	199	CG	GLN	A	39	-9.794	1.139	5.598	1.00	51.03
	200	CD	GLN	A	39	-9.923	2.651	5.498	1.00	54.07
	201	OE1	GLN	A	39	-9.101	3.313	4.862	1.00	57.42
35	202	NE2	GLN	A	39	-10.962	3.203	6.120	1.00	38.98
	203	C	GLN	A	39	-8.617	-1.715	4.203	1.00	50.38
	204	O	GLN	A	39	-8.168	-2.262	5.202	1.00	52.17
	205	N	PRO	A	40	-7.946	-1.694	3.041	1.00	51.48
	206	CD	PRO	A	40	-8.342	-0.995	1.804	1.00	50.84
40	207	CA	PRO	A	40	-6.631	-2.313	2.876	1.00	49.78
	208	CB	PRO	A	40	-6.124	-1.694	1.576	1.00	50.09
	209	CG	PRO	A	40	-7.360	-1.543	0.784	1.00	50.00
	210	C	PRO	A	40	-5.687	-2.057	4.040	1.00	46.59

	211	O	PRO	A	40	-5.391	-0.918	4.374	1.00	44.73
	212	N	ARG	A	41	-5.222	-3.129	4.656	1.00	44.90
	213	CA	ARG	A	41	-4.293	-3.028	5.765	1.00	46.18
	214	CB	ARG	A	41	-3.560	-4.366	5.912	1.00	48.57
5	215	CG	ARG	A	41	-2.470	-4.443	6.982	1.00	54.03
	216	CD	ARG	A	41	-1.621	-5.703	6.774	1.00	54.03
	217	NE	ARG	A	41	-1.919	-6.838	7.664	1.00	58.63
	218	CZ	ARG	A	41	-3.134	-7.268	8.024	1.00	55.36
	219	NH1	ARG	A	41	-4.237	-6.661	7.596	1.00	56.78
10	220	NH2	ARG	A	41	-3.248	-8.344	8.799	1.00	41.95
	221	C	ARG	A	41	-3.294	-1.907	5.474	1.00	49.28
	222	O	ARG	A	41	-2.985	-1.085	6.338	1.00	51.60
	223	N	VAL	A	42	-2.819	-1.867	4.235	1.00	46.21
	224	CA	VAL	A	42	-1.823	-0.889	3.802	1.00	45.66
15	225	CB	VAL	A	42	-1.361	-1.228	2.344	1.00	36.84
	226	CG1	VAL	A	42	-2.084	-0.351	1.340	1.00	30.96
	227	CG2	VAL	A	42	0.155	-1.107	2.221	1.00	31.91
	228	C	VAL	A	42	-2.214	0.604	3.915	1.00	49.01
	229	O	VAL	A	42	-1.341	1.467	4.028	1.00	53.47
20	230	N	PHE	A	43	-3.508	0.915	3.887	1.00	46.72
	231	CA	PHE	A	43	-3.942	2.311	4.002	1.00	44.27
	232	CB	PHE	A	43	-5.458	2.448	3.827	1.00	37.66
	233	CG	PHE	A	43	-5.920	2.446	2.397	1.00	36.94
	234	CD1	PHE	A	43	-5.009	2.523	1.345	1.00	36.78
25	235	CD2	PHE	A	43	-7.283	2.383	2.102	1.00	39.68
	236	CE1	PHE	A	43	-5.450	2.534	0.020	1.00	29.77
	237	CE2	PHE	A	43	-7.731	2.395	0.785	1.00	31.31
	238	CZ	PHE	A	43	-6.813	2.470	-0.258	1.00	29.07
	239	C	PHE	A	43	-3.583	2.844	5.375	1.00	46.39
30	240	O	PHE	A	43	-3.142	3.987	5.512	1.00	46.33
	241	N	GLY	A	44	-3.798	2.001	6.385	1.00	46.54
	242	CA	GLY	A	44	-3.512	2.362	7.763	1.00	43.50
	243	C	GLY	A	44	-2.251	3.185	7.894	1.00	40.10
	244	O	GLY	A	44	-2.189	4.130	8.681	1.00	40.32
35	245	N	HIS	A	45	-1.242	2.823	7.114	1.00	33.52
	246	CA	HIS	A	45	0.015	3.539	7.133	1.00	30.60
	247	CB	HIS	A	45	1.029	2.821	6.252	1.00	16.92
	248	CG	HIS	A	45	1.469	1.501	6.803	1.00	28.29
	249	CD2	HIS	A	45	2.701	0.954	6.934	1.00	34.82
40	250	ND1	HIS	A	45	0.582	0.560	7.277	1.00	34.82
	251	CE1	HIS	A	45	1.247	-0.511	7.675	1.00	39.36
	252	NE2	HIS	A	45	2.536	-0.297	7.477	1.00	40.10
	253	C	HIS	A	45	-0.169	4.986	6.686	1.00	34.04

	254	O	HIS	A	45	0.362	5.893	7.321	1.00	33.04
	255	N	LYS	A	46	-0.918	5.226	5.613	1.00	37.67
	256	CA	LYS	A	46	-1.112	6.606	5.190	1.00	36.56
	257	CB	LYS	A	46	-2.029	6.714	3.981	1.00	27.77
5	258	CG	LYS	A	46	-2.167	8.154	3.490	1.00	36.67
	259	CD	LYS	A	46	-2.906	8.248	2.160	1.00	47.11
	260	CE	LYS	A	46	-2.187	7.465	1.060	1.00	45.30
	261	NZ	LYS	A	46	-2.935	7.463	-0.231	1.00	54.67
	262	C	LYS	A	46	-1.737	7.348	6.350	1.00	35.24
10	263	O	LYS	A	46	-1.280	8.429	6.723	1.00	34.48
	264	N	ALA	A	47	-2.781	6.757	6.924	1.00	34.22
	265	CA	ALA	A	47	-3.462	7.358	8.069	1.00	33.65
	266	CB	ALA	A	47	-4.588	6.451	8.550	1.00	22.25
	267	C	ALA	A	47	-2.457	7.601	9.201	1.00	33.26
15	268	O	ALA	A	47	-2.505	8.632	9.876	1.00	35.94
	269	N	GLY	A	48	-1.558	6.643	9.413	1.00	31.73
	270	CA	GLY	A	48	-0.562	6.814	10.443	1.00	31.22
	271	C	GLY	A	48	0.056	8.162	10.156	1.00	28.17
	272	O	GLY	A	48	0.063	9.050	11.005	1.00	30.21
20	273	N	MET	A	49	0.546	8.321	8.933	1.00	26.41
	274	CA	MET	A	49	1.168	9.565	8.510	1.00	26.13
	275	CB	MET	A	49	1.525	9.501	7.019	1.00	26.11
	276	CG	MET	A	49	1.999	10.831	6.415	1.00	31.14
	277	SD	MET	A	49	2.596	10.723	4.688	1.00	30.86
25	278	CE	MET	A	49	1.149	10.009	3.871	1.00	27.72
	279	C	MET	A	49	0.267	10.764	8.780	1.00	26.86
	280	O	MET	A	49	0.740	11.812	9.209	1.00	25.74
	281	N	GLU	A	50	-1.028	10.621	8.532	1.00	26.86
	282	CA	GLU	A	50	-1.943	11.725	8.780	1.00	29.13
30	283	CB	GLU	A	50	-3.364	11.333	8.397	1.00	35.38
	284	CG	GLU	A	50	-3.465	10.916	6.948	1.00	42.20
	285	CD	GLU	A	50	-4.615	11.578	6.221	1.00	55.85
	286	OE1	GLU	A	50	-4.707	12.826	6.279	1.00	54.70
	287	OE2	GLU	A	50	-5.414	10.848	5.585	1.00	62.59
35	288	C	GLU	A	50	-1.885	12.137	10.246	1.00	33.72
	289	O	GLU	A	50	-1.701	13.311	10.566	1.00	40.50
	290	N	ALA	A	51	-2.031	11.172	11.143	1.00	30.97
	291	CA	ALA	A	51	-1.972	11.485	12.560	1.00	29.01
	292	CB	ALA	A	51	-2.288	10.257	13.384	1.00	33.60
40	293	C	ALA	A	51	-0.587	12.009	12.910	1.00	28.16
	294	O	ALA	A	51	-0.448	12.799	13.835	1.00	28.15
	295	N	LEU	A	52	0.439	11.576	12.182	1.00	26.73
	296	CA	LEU	A	52	1.785	12.051	12.475	1.00	26.65



	297	CB	LEU	A	52	2.809	11.478	11.499	1.00	16.92
	298	CG	LEU	A	52	4.267	11.370	11.979	1.00	16.92
	299	CD1	LEU	A	52	5.184	11.281	10.768	1.00	16.92
	300	CD2	LEU	A	52	4.661	12.570	12.823	1.00	22.52
5	301	C	LEU	A	52	1.765	13.561	12.338	1.00	32.69
	302	O	LEU	A	52	2.309	14.273	13.180	1.00	34.28
	303	N	GLN	A	53	1.124	14.041	11.272	1.00	32.34
	304	CA	GLN	A	53	1.016	15.475	11.005	1.00	28.24
	305	CB	GLN	A	53	0.241	15.729	9.714	1.00	22.43
10	306	CG	GLN	A	53	0.219	17.194	9.297	1.00	16.92
	307	CD	GLN	A	53	1.467	17.602	8.535	1.00	16.92
	308	OE1	GLN	A	53	2.512	16.956	8.631	1.00	26.60
	309	NE2	GLN	A	53	1.364	18.685	7.779	1.00	16.92
	310	C	GLN	A	53	0.302	16.180	12.150	1.00	31.47
15	311	O	GLN	A	53	0.740	17.227	12.618	1.00	30.88
	312	N	THR	A	54	-0.809	15.598	12.583	1.00	32.71
	313	CA	THR	A	54	-1.599	16.137	13.679	1.00	29.40
	314	CB	THR	A	54	-2.824	15.282	13.932	1.00	22.85
	315	OG1	THR	A	54	-3.692	15.346	12.796	1.00	33.45
20	316	CG2	THR	A	54	-3.545	15.751	15.186	1.00	16.92
	317	C	THR	A	54	-0.819	16.176	14.977	1.00	32.23
	318	O	THR	A	54	-0.781	17.197	15.652	1.00	35.38
	319	N	VAL	A	55	-0.219	15.049	15.337	1.00	33.35
	320	CA	VAL	A	55	0.552	14.958	16.568	1.00	32.18
25	321	CB	VAL	A	55	1.029	13.501	16.835	1.00	26.17
	322	CG1	VAL	A	55	1.962	13.460	18.026	1.00	16.92
	323	CG2	VAL	A	55	-0.164	12.606	17.105	1.00	28.32
	324	C	VAL	A	55	1.760	15.875	16.514	1.00	32.33
	325	O	VAL	A	55	1.981	16.666	17.429	1.00	31.60
30	326	N	THR	A	56	2.531	15.773	15.435	1.00	31.81
	327	CA	THR	A	56	3.732	16.582	15.266	1.00	36.75
	328	CB	THR	A	56	4.422	16.248	13.924	1.00	33.23
	329	OG1	THR	A	56	5.715	16.861	13.877	1.00	35.26
	330	CG2	THR	A	56	3.599	16.758	12.764	1.00	48.73
35	331	C	THR	A	56	3.416	18.082	15.341	1.00	40.46
	332	O	THR	A	56	4.227	18.881	15.801	1.00	43.12
	333	N	LYS	A	57	2.222	18.450	14.897	1.00	42.26
	334	CA	LYS	A	57	1.774	19.838	14.907	1.00	43.45
	335	CB	LYS	A	57	0.629	19.988	13.907	1.00	47.22
40	336	CG	LYS	A	57	0.464	21.352	13.292	1.00	47.96
	337	CD	LYS	A	57	-0.497	21.262	12.116	1.00	49.91
	338	CE	LYS	A	57	-1.823	20.642	12.534	1.00	55.23
	339	NZ	LYS	A	57	-2.759	20.430	11.394	1.00	63.19

	340	C	LYS	A	57	1.301	20.167	16.324	1.00	44.75
	341	O	LYS	A	57	1.783	21.104	16.955	1.00	48.17
	342	N	ALA	A	58	0.359	19.377	16.819	1.00	44.02
	343	CA	ALA	A	58	-0.174	19.557	18.158	1.00	45.02
5	344	CB	ALA	A	58	-1.048	18.379	18.520	1.00	31.05
	345	C	ALA	A	58	0.957	19.682	19.165	1.00	45.60
	346	O	ALA	A	58	0.940	20.550	20.028	1.00	47.49
	347	N	ALA	A	59	1.941	18.800	19.046	1.00	43.55
	348	CA	ALA	A	59	3.085	18.785	19.948	1.00	44.39
10	349	CB	ALA	A	59	3.934	17.555	19.682	1.00	36.73
	350	C	ALA	A	59	3.931	20.035	19.802	1.00	48.03
	351	O	ALA	A	59	4.663	20.409	20.714	1.00	49.73
	352	N	ASN	A	60	3.830	20.680	18.646	1.00	50.14
	353	CA	ASN	A	60	4.599	21.891	18.380	1.00	50.72
15	354	CB	ASN	A	60	4.661	22.151	16.870	1.00	56.81
	355	CG	ASN	A	60	5.519	23.346	16.516	1.00	59.09
	356	OD1	ASN	A	60	6.699	23.405	16.855	1.00	50.39
	357	ND2	ASN	A	60	4.927	24.306	15.820	1.00	68.87
	358	C	ASN	A	60	3.998	23.099	19.095	1.00	48.92
20	359	O	ASN	A	60	4.729	23.925	19.648	1.00	49.57
	360	N	LYS	A	61	2.668	23.189	19.091	1.00	44.16
	361	CA	LYS	A	61	1.978	24.296	19.739	1.00	42.23
	362	CB	LYS	A	61	0.494	24.296	19.378	1.00	38.81
	363	CG	LYS	A	61	-0.376	23.520	20.360	1.00	49.61
25	364	CD	LYS	A	61	-1.847	23.893	20.228	1.00	61.71
	365	CE	LYS	A	61	-2.674	23.282	21.355	1.00	76.26
	366	NZ	LYS	A	61	-4.111	23.687	21.306	1.00	77.30
	367	C	LYS	A	61	2.105	24.171	21.247	1.00	41.26
	368	O	LYS	A	61	1.872	25.120	21.987	1.00	38.34
30	369	N	LEU	A	62	2.470	22.982	21.697	1.00	43.33
	370	CA	LEU	A	62	2.598	22.724	23.117	1.00	40.43
	371	CB	LEU	A	62	2.047	21.331	23.436	1.00	41.05
	372	CG	LEU	A	62	1.512	21.076	24.843	1.00	43.45
	373	CD1	LEU	A	62	0.465	22.122	25.216	1.00	49.97
35	374	CD2	LEU	A	62	0.909	19.691	24.888	1.00	41.95
	375	C	LEU	A	62	4.043	22.852	23.572	1.00	37.78
	376	O	LEU	A	62	4.361	22.576	24.721	1.00	36.77
	377	N	GLY	A	63	4.919	23.254	22.662	1.00	34.00
	378	CA	GLY	A	63	6.310	23.445	23.026	1.00	34.47
40	379	C	GLY	A	63	7.250	22.257	23.130	1.00	34.70
	380	O	GLY	A	63	8.370	22.399	23.623	1.00	37.15
	381	N	VAL	A	64	6.830	21.078	22.703	1.00	32.50
	382	CA	VAL	A	64	7.745	19.951	22.764	1.00	33.85

	383	CB	VAL	A	64	7.075	18.672	22.254	1.00	38.31
	384	CG1	VAL	A	64	8.104	17.563	22.102	1.00	45.70
	385	CG2	VAL	A	64	5.981	18.254	23.216	1.00	30.49
	386	C	VAL	A	64	8.923	20.305	21.861	1.00	32.11
5	387	O	VAL	A	64	8.738	20.626	20.693	1.00	35.71
	388	N	LYS	A	65	10.133	20.264	22.398	1.00	30.11
	389	CA	LYS	A	65	11.301	20.604	21.598	1.00	32.19
	390	CB	LYS	A	65	12.555	20.633	22.464	1.00	34.45
	391	CG	LYS	A	65	13.133	22.024	22.668	1.00	28.19
10	392	CD	LYS	A	65	12.183	22.927	23.451	1.00	32.70
	393	CE	LYS	A	65	12.850	24.251	23.841	1.00	50.92
	394	NZ	LYS	A	65	14.038	24.082	24.743	1.00	60.18
	395	C	LYS	A	65	11.542	19.683	20.411	1.00	32.24
	396	O	LYS	A	65	11.799	20.154	19.307	1.00	32.31
15	397	N	VAL	A	66	11.466	18.374	20.634	1.00	29.19
	398	CA	VAL	A	66	11.695	17.399	19.561	1.00	27.66
	399	CB	VAL	A	66	13.232	17.130	19.391	1.00	30.38
	400	CG1	VAL	A	66	13.926	17.314	20.720	1.00	29.01
	401	CG2	VAL	A	66	13.498	15.717	18.840	1.00	16.92
20	402	C	VAL	A	66	10.970	16.069	19.763	1.00	22.57
	403	O	VAL	A	66	10.605	15.725	20.879	1.00	18.50
	404	N	ILE	A	67	10.730	15.346	18.670	1.00	23.89
	405	CA	ILE	A	67	10.099	14.028	18.744	1.00	31.24
	406	CB	ILE	A	67	8.541	14.075	18.622	1.00	30.49
25	407	CG2	ILE	A	67	7.963	14.971	19.709	1.00	32.00
	408	CG1	ILE	A	67	8.113	14.561	17.242	1.00	35.49
	409	CD1	ILE	A	67	6.610	14.613	17.079	1.00	44.48
	410	C	ILE	A	67	10.671	13.104	17.674	1.00	32.32
	411	O	ILE	A	67	10.849	13.495	16.512	1.00	36.35
30	412	N	THR	A	68	10.988	11.885	18.100	1.00	27.06
	413	CA	THR	A	68	11.554	10.866	17.229	1.00	22.58
	414	CB	THR	A	68	12.836	10.287	17.823	1.00	20.26
	415	OG1	THR	A	68	13.811	11.331	17.956	1.00	31.06
	416	CG2	THR	A	68	13.373	9.182	16.937	1.00	16.92
35	417	C	THR	A	68	10.540	9.750	17.040	1.00	26.08
	418	O	THR	A	68	10.226	9.008	17.969	1.00	28.24
	419	N	VAL	A	69	10.028	9.657	15.818	1.00	25.72
	420	CA	VAL	A	69	9.022	8.677	15.450	1.00	22.44
	421	CB	VAL	A	69	8.025	9.297	14.488	1.00	20.89
40	422	CG1	VAL	A	69	7.234	10.378	15.180	1.00	16.92
	423	CG2	VAL	A	69	8.770	9.892	13.313	1.00	16.92
	424	C	VAL	A	69	9.667	7.490	14.770	1.00	23.00
	425	O	VAL	A	69	10.401	7.652	13.794	1.00	23.85

	426	N	TYR	A	70	9.399	6.299	15.295	1.00	25.89
	427	CA	TYR	A	70	9.943	5.066	14.727	1.00	26.71
	428	CB	TYR	A	70	9.802	3.916	15.728	1.00	22.08
	429	CG	TYR	A	70	10.817	2.805	15.552	1.00	16.92
5	430	CD1	TYR	A	70	11.756	2.842	14.518	1.00	16.92
	431	CE1	TYR	A	70	12.708	1.834	14.374	1.00	16.92
	432	CD2	TYR	A	70	10.856	1.723	16.440	1.00	18.76
	433	CE2	TYR	A	70	11.802	0.710	16.306	1.00	20.19
	434	CZ	TYR	A	70	12.723	0.774	15.272	1.00	23.85
10	435	OH	TYR	A	70	13.660	-0.218	15.136	1.00	28.88
	436	C	TYR	A	70	9.150	4.752	13.454	1.00	27.42
	437	O	TYR	A	70	8.125	4.053	13.508	1.00	29.24
	438	N	ALA	A	71	9.640	5.272	12.324	1.00	26.20
	439	CA	ALA	A	71	9.004	5.115	11.013	1.00	27.77
15	440	CB	ALA	A	71	9.336	6.326	10.149	1.00	21.40
	441	C	ALA	A	71	9.302	3.821	10.232	1.00	33.28
	442	O	ALA	A	71	8.441	3.314	9.513	1.00	35.06
	443	N	PHE	A	72	10.514	3.292	10.344	1.00	34.13
	444	CA	PHE	A	72	10.837	2.055	9.640	1.00	35.25
20	445	CB	PHE	A	72	11.105	2.336	8.152	1.00	28.54
	446	CG	PHE	A	72	11.098	1.096	7.289	1.00	32.61
	447	CD1	PHE	A	72	9.897	0.518	6.880	1.00	33.56
	448	CD2	PHE	A	72	12.290	0.478	6.917	1.00	35.80
	449	CE1	PHE	A	72	9.885	-0.661	6.113	1.00	28.42
25	450	CE2	PHE	A	72	12.283	-0.698	6.154	1.00	32.48
	451	CZ	PHE	A	72	11.077	-1.265	5.753	1.00	31.11
	452	C	PHE	A	72	12.053	1.386	10.275	1.00	40.63
	453	O	PHE	A	72	13.172	1.865	10.135	1.00	43.32
	454	N	SER	A	73	11.832	0.280	10.980	1.00	47.02
30	455	CA	SER	A	73	12.932	-0.435	11.627	1.00	49.68
	456	CB	SER	A	73	12.409	-1.381	12.708	1.00	43.74
	457	OG	SER	A	73	12.032	-2.624	12.145	1.00	33.26
	458	C	SER	A	73	13.703	-1.250	10.601	1.00	52.36
	459	O	SER	A	73	13.227	-1.477	9.487	1.00	53.00
35	460	N	THR	A	74	14.893	-1.697	10.985	1.00	57.20
	461	CA	THR	A	74	15.726	-2.488	10.092	1.00	62.04
	462	CB	THR	A	74	17.131	-2.742	10.714	1.00	67.14
	463	OG1	THR	A	74	17.593	-1.557	11.374	1.00	74.37
	464	CG2	THR	A	74	18.136	-3.103	9.632	1.00	71.77
40	465	C	THR	A	74	15.027	-3.826	9.856	1.00	62.95
	466	O	THR	A	74	15.157	-4.441	8.798	1.00	62.39
	467	N	GLU	A	75	14.256	-4.252	10.850	1.00	63.63
	468	CA	GLU	A	75	13.553	-5.525	10.786	1.00	66.15

	469	CB	GLU	A	75	13.387	-6.084	12.203	1.00	75.90
	470	CG	GLU	A	75	12.911	-7.521	12.255	1.00	93.53
	471	CD	GLU	A	75	12.685	-8.000	13.669	1.00	103.81
	472	OE1	GLU	A	75	11.907	-7.347	14.399	1.00	110.70
5	473	OE2	GLU	A	75	13.283	-9.030	14.048	1.00	111.36
	474	C	GLU	A	75	12.193	-5.457	10.096	1.00	66.40
	475	O	GLU	A	75	11.395	-6.390	10.193	1.00	68.91
	476	N	ASN	A	76	11.925	-4.362	9.393	1.00	64.57
	477	CA	ASN	A	76	10.646	-4.222	8.702	1.00	59.63
10	478	CB	ASN	A	76	10.136	-2.778	8.788	1.00	53.70
	479	CG	ASN	A	76	9.370	-2.506	10.066	1.00	46.89
	480	OD1	ASN	A	76	8.523	-3.299	10.470	1.00	50.66
	481	ND2	ASN	A	76	9.652	-1.377	10.700	1.00	40.20
	482	C	ASN	A	76	10.685	-4.656	7.240	1.00	56.27
15	483	O	ASN	A	76	9.636	-4.897	6.642	1.00	55.41
	484	N	TRP	A	77	11.882	-4.763	6.666	1.00	53.67
	485	CA	TRP	A	77	12.007	-5.160	5.266	1.00	51.94
	486	CB	TRP	A	77	13.469	-5.096	4.805	1.00	48.90
	487	CG	TRP	A	77	14.125	-3.744	4.934	1.00	51.60
20	488	CD2	TRP	A	77	14.156	-2.698	3.948	1.00	51.70
	489	CE2	TRP	A	77	14.900	-1.627	4.497	1.00	52.11
	490	CE3	TRP	A	77	13.628	-2.561	2.655	1.00	43.86
	491	CD1	TRP	A	77	14.826	-3.274	6.007	1.00	52.12
	492	NE1	TRP	A	77	15.295	-2.005	5.752	1.00	53.74
25	493	CZ2	TRP	A	77	15.130	-0.436	3.799	1.00	43.91
	494	CZ3	TRP	A	77	13.859	-1.369	1.960	1.00	37.41
	495	CH2	TRP	A	77	14.605	-0.326	2.537	1.00	35.61
	496	C	TRP	A	77	11.466	-6.574	5.063	1.00	50.29
	497	O	TRP	A	77	11.212	-7.006	3.935	1.00	54.30
30	498	N	THR	A	78	11.286	-7.280	6.172	1.00	46.30
	499	CA	THR	A	78	10.778	-8.646	6.171	1.00	40.87
	500	CB	THR	A	78	10.756	-9.200	7.602	1.00	40.94
	501	OG1	THR	A	78	12.097	-9.255	8.103	1.00	41.23
	502	CG2	THR	A	78	10.125	-10.585	7.642	1.00	43.72
35	503	C	THR	A	78	9.370	-8.747	5.597	1.00	39.63
	504	O	THR	A	78	8.927	-9.828	5.208	1.00	43.77
	505	N	ARG	A	79	8.671	-7.616	5.540	1.00	33.93
	506	CA	ARG	A	79	7.294	-7.568	5.044	1.00	29.09
	507	CB	ARG	A	79	6.661	-6.236	5.455	1.00	22.71
40	508	CG	ARG	A	79	6.579	-6.105	6.955	1.00	24.31
	509	CD	ARG	A	79	6.030	-4.783	7.396	1.00	23.41
	510	NE	ARG	A	79	5.578	-4.870	8.778	1.00	19.61
	511	CZ	ARG	A	79	4.964	-3.891	9.431	1.00	25.88

	512	NH1	ARG	A	79	4.728	-2.734	8.824	1.00	35.60
	513	NH2	ARG	A	79	4.576	-4.073	10.687	1.00	23.97
	514	C	ARG	A	79	7.122	-7.797	3.543	1.00	31.63
	515	O	ARG	A	79	8.073	-7.675	2.766	1.00	31.85
5	516	N	PRO	A	80	5.897	-8.153	3.119	1.00	30.10
	517	CD	PRO	A	80	4.644	-8.334	3.874	1.00	30.04
	518	CA	PRO	A	80	5.689	-8.381	1.689	1.00	31.57
	519	CB	PRO	A	80	4.202	-8.760	1.605	1.00	29.71
	520	CG	PRO	A	80	3.598	-8.109	2.810	1.00	29.28
10	521	C	PRO	A	80	6.050	-7.134	0.882	1.00	38.32
	522	O	PRO	A	80	5.480	-6.060	1.088	1.00	42.42
	523	N	ASP	A	81	7.015	-7.292	-0.022	1.00	41.93
	524	CA	ASP	A	81	7.497	-6.209	-0.876	1.00	45.58
	525	CB	ASP	A	81	7.875	-6.757	-2.257	1.00	63.07
15	526	CG	ASP	A	81	8.838	-7.933	-2.187	1.00	67.38
	527	OD1	ASP	A	81	9.879	-7.825	-1.503	1.00	73.52
	528	OD2	ASP	A	81	8.555	-8.966	-2.830	1.00	72.51
	529	C	ASP	A	81	6.483	-5.078	-1.044	1.00	44.34
	530	O	ASP	A	81	6.771	-3.923	-0.733	1.00	45.14
20	531	N	GLN	A	82	5.294	-5.416	-1.533	1.00	43.19
	532	CA	GLN	A	82	4.256	-4.420	-1.742	1.00	46.00
	533	CB	GLN	A	82	2.942	-5.109	-2.094	1.00	45.03
	534	CG	GLN	A	82	2.790	-5.364	-3.578	1.00	34.60
	535	CD	GLN	A	82	2.538	-4.088	-4.368	1.00	16.92
25	536	OE1	GLN	A	82	1.466	-3.485	-4.274	1.00	26.54
	537	NE2	GLN	A	82	3.529	-3.667	-5.147	1.00	16.92
	538	C	GLN	A	82	4.050	-3.463	-0.573	1.00	47.51
	539	O	GLN	A	82	4.062	-2.248	-0.762	1.00	51.03
	540	N	GLU	A	83	3.858	-4.001	0.629	1.00	44.67
30	541	CA	GLU	A	83	3.656	-3.158	1.807	1.00	37.68
	542	CB	GLU	A	83	3.515	-4.008	3.073	1.00	35.83
	543	CG	GLU	A	83	3.023	-3.238	4.301	1.00	39.43
	544	CD	GLU	A	83	2.869	-4.125	5.534	1.00	43.90
	545	OE1	GLU	A	83	2.112	-3.747	6.462	1.00	48.19
35	546	OE2	GLU	A	83	3.515	-5.197	5.579	1.00	48.89
	547	C	GLU	A	83	4.842	-2.227	1.964	1.00	32.89
	548	O	GLU	A	83	4.672	-1.054	2.262	1.00	32.08
	549	N	VAL	A	84	6.045	-2.759	1.769	1.00	30.13
	550	CA	VAL	A	84	7.249	-1.948	1.876	1.00	31.93
40	551	CB	VAL	A	84	8.531	-2.810	1.794	1.00	35.84
	552	CG1	VAL	A	84	9.765	-1.930	1.967	1.00	39.26
	553	CG2	VAL	A	84	8.505	-3.881	2.873	1.00	34.99
	554	C	VAL	A	84	7.217	-0.958	0.718	1.00	33.63

	555	O	VAL	A	84	7.455	0.240	0.895	1.00	34.73
	556	N	LYS	A	85	6.914	-1.471	-0.471	1.00	33.74
	557	CA	LYS	A	85	6.804	-0.646	-1.669	1.00	35.59
	558	CB	LYS	A	85	6.140	-1.478	-2.783	1.00	48.55
5	559	CG	LYS	A	85	5.367	-0.707	-3.855	1.00	59.03
	560	CD	LYS	A	85	6.264	-0.085	-4.912	1.00	67.33
	561	CE	LYS	A	85	5.426	0.664	-5.948	1.00	72.93
	562	NZ	LYS	A	85	6.266	1.391	-6.950	1.00	68.29
	563	C	LYS	A	85	5.956	0.576	-1.290	1.00	33.73
10	564	O	LYS	A	85	6.393	1.716	-1.434	1.00	32.87
	565	N	PHE	A	86	4.760	0.305	-0.771	1.00	34.91
	566	CA	PHE	A	86	3.796	1.318	-0.334	1.00	38.00
	567	CB	PHE	A	86	2.579	0.617	0.286	1.00	29.90
	568	CG	PHE	A	86	1.520	1.553	0.814	1.00	28.19
15	569	CD1	PHE	A	86	0.306	1.694	0.150	1.00	28.34
	570	CD2	PHE	A	86	1.703	2.237	2.014	1.00	30.14
	571	CE1	PHE	A	86	-0.714	2.495	0.678	1.00	16.92
	572	CE2	PHE	A	86	0.692	3.039	2.547	1.00	31.79
	573	CZ	PHE	A	86	-0.519	3.166	1.879	1.00	23.42
20	574	C	PHE	A	86	4.372	2.317	0.671	1.00	41.33
	575	O	PHE	A	86	4.384	3.522	0.413	1.00	44.39
	576	N	ILE	A	87	4.828	1.817	1.820	1.00	42.94
	577	CA	ILE	A	87	5.390	2.670	2.870	1.00	44.91
	578	CB	ILE	A	87	5.999	1.842	4.021	1.00	33.27
25	579	CG2	ILE	A	87	6.499	2.760	5.114	1.00	35.47
	580	CG1	ILE	A	87	4.951	0.912	4.614	1.00	33.55
	581	CD1	ILE	A	87	5.500	0.015	5.692	1.00	34.35
	582	C	ILE	A	87	6.485	3.585	2.341	1.00	49.45
	583	O	ILE	A	87	6.391	4.805	2.460	1.00	51.81
30	584	N	MET	A	88	7.519	2.990	1.756	1.00	49.47
	585	CA	MET	A	88	8.635	3.762	1.226	1.00	49.30
	586	CB	MET	A	88	9.641	2.842	0.525	1.00	50.22
	587	CG	MET	A	88	10.269	1.771	1.418	1.00	45.64
	588	SD	MET	A	88	11.035	2.374	2.938	1.00	36.68
35	589	CE	MET	A	88	12.225	3.505	2.300	1.00	32.68
	590	C	MET	A	88	8.226	4.897	0.281	1.00	47.36
	591	O	MET	A	88	9.031	5.777	-0.022	1.00	47.71
	592	N	ASN	A	89	6.988	4.898	-0.194	1.00	47.87
	593	CA	ASN	A	89	6.582	5.981	-1.074	1.00	53.55
40	594	CB	ASN	A	89	5.710	5.476	-2.219	1.00	59.69
	595	CG	ASN	A	89	5.490	6.540	-3.274	1.00	60.29
	596	OD1	ASN	A	89	6.432	6.962	-3.949	1.00	58.66
	597	ND2	ASN	A	89	4.249	6.994	-3.411	1.00	59.82

	598	C	ASN	A	89	5.828	7.053	-0.300	1.00	54.69
	599	O	ASN	A	89	5.351	8.034	-0.875	1.00	55.77
	600	N	LEU	A	90	5.718	6.851	1.010	1.00	53.91
	601	CA	LEU	A	90	5.039	7.803	1.877	1.00	50.26
5	602	CB	LEU	A	90	4.694	7.152	3.218	1.00	44.32
	603	CG	LEU	A	90	3.552	6.134	3.213	1.00	38.54
	604	CD1	LEU	A	90	3.422	5.504	4.582	1.00	43.04
	605	CD2	LEU	A	90	2.258	6.821	2.830	1.00	42.59
	606	C	LEU	A	90	5.909	9.039	2.091	1.00	47.14
10	607	O	LEU	A	90	5.391	10.136	2.305	1.00	44.55
	608	N	PRO	A	91	7.247	8.875	2.061	1.00	46.27
	609	CD	PRO	A	91	7.996	7.616	2.220	1.00	44.80
	610	CA	PRO	A	91	8.140	10.024	2.247	1.00	46.47
	611	CB	PRO	A	91	9.521	9.376	2.300	1.00	43.34
15	612	CG	PRO	A	91	9.234	8.073	2.951	1.00	45.54
	613	C	PRO	A	91	8.009	11.030	1.094	1.00	47.41
	614	O	PRO	A	91	8.412	12.186	1.208	1.00	46.38
	615	N	VAL	A	92	7.442	10.578	-0.020	1.00	47.94
	616	CA	VAL	A	92	7.249	11.439	-1.180	1.00	45.52
20	617	CB	VAL	A	92	7.204	10.622	-2.467	1.00	34.17
	618	CG1	VAL	A	92	7.081	11.547	-3.642	1.00	38.02
	619	CG2	VAL	A	92	8.456	9.775	-2.583	1.00	38.64
	620	C	VAL	A	92	5.940	12.205	-1.026	1.00	45.50
	621	O	VAL	A	92	5.919	13.431	-1.117	1.00	44.68
25	622	N	GLU	A	93	4.851	11.476	-0.791	1.00	42.90
	623	CA	GLU	A	93	3.557	12.103	-0.582	1.00	42.53
	624	CB	GLU	A	93	2.522	11.082	-0.124	1.00	49.87
	625	CG	GLU	A	93	2.449	9.818	-0.951	1.00	57.60
	626	CD	GLU	A	93	1.189	9.021	-0.657	1.00	61.78
30	627	OE1	GLU	A	93	1.046	7.896	-1.187	1.00	71.50
	628	OE2	GLU	A	93	0.337	9.531	0.105	1.00	52.19
	629	C	GLU	A	93	3.753	13.110	0.539	1.00	43.12
	630	O	GLU	A	93	3.322	14.255	0.452	1.00	45.85
	631	N	PHE	A	94	4.414	12.664	1.601	1.00	45.41
35	632	CA	PHE	A	94	4.678	13.514	2.752	1.00	46.26
	633	CB	PHE	A	94	5.575	12.787	3.756	1.00	42.53
	634	CG	PHE	A	94	5.711	13.507	5.067	1.00	32.85
	635	CD1	PHE	A	94	4.633	13.568	5.956	1.00	28.47
	636	CD2	PHE	A	94	6.894	14.167	5.396	1.00	28.12
40	637	CE1	PHE	A	94	4.726	14.279	7.153	1.00	19.92
	638	CE2	PHE	A	94	6.999	14.882	6.590	1.00	31.07
	639	CZ	PHE	A	94	5.909	14.936	7.468	1.00	25.79
	640	C	PHE	A	94	5.346	14.817	2.326	1.00	45.67



	641	O	PHE	A	94	4.858	15.901	2.636	1.00	41.22
	642	N	TYR	A	95	6.462	14.706	1.613	1.00	44.67
	643	CA	TYR	A	95	7.185	15.884	1.154	1.00	42.71
	644	CB	TYR	A	95	8.467	15.487	0.430	1.00	44.48
5	645	CG	TYR	A	95	9.245	16.675	-0.099	1.00	45.34
	646	CD1	TYR	A	95	9.725	17.655	0.764	1.00	46.34
	647	CE1	TYR	A	95	10.449	18.740	0.292	1.00	50.00
	648	CD2	TYR	A	95	9.509	16.814	-1.458	1.00	46.57
	649	CE2	TYR	A	95	10.230	17.895	-1.938	1.00	49.96
10	650	CZ	TYR	A	95	10.700	18.853	-1.058	1.00	53.17
	651	OH	TYR	A	95	11.434	19.918	-1.521	1.00	55.77
	652	C	TYR	A	95	6.352	16.738	0.215	1.00	41.47
	653	O	TYR	A	95	6.237	17.951	0.399	1.00	41.86
	654	N	ASP	A	96	5.782	16.105	-0.804	1.00	38.09
15	655	CA	ASP	A	96	4.975	16.838	-1.761	1.00	34.86
	656	CB	ASP	A	96	4.278	15.907	-2.751	1.00	28.63
	657	CG	ASP	A	96	5.178	15.499	-3.898	1.00	32.06
	658	OD1	ASP	A	96	6.190	16.203	-4.142	1.00	29.64
	659	OD2	ASP	A	96	4.857	14.482	-4.561	1.00	33.25
20	660	C	ASP	A	96	3.924	17.694	-1.100	1.00	31.39
	661	O	ASP	A	96	3.933	18.908	-1.268	1.00	31.77
	662	N	ASN	A	97	3.025	17.087	-0.335	1.00	26.14
	663	CA	ASN	A	97	1.976	17.889	0.269	1.00	29.32
	664	CB	ASN	A	97	0.650	17.565	-0.433	1.00	34.58
25	665	CG	ASN	A	97	0.375	16.077	-0.515	1.00	33.64
	666	OD1	ASN	A	97	-0.464	15.628	-1.310	1.00	31.70
	667	ND2	ASN	A	97	1.067	15.299	0.319	1.00	25.32
	668	C	ASN	A	97	1.790	17.924	1.791	1.00	33.75
	669	O	ASN	A	97	0.826	18.521	2.275	1.00	31.16
30	670	N	TYR	A	98	2.699	17.319	2.552	1.00	37.18
	671	CA	TYR	A	98	2.586	17.361	4.012	1.00	35.12
	672	CB	TYR	A	98	2.683	15.966	4.605	1.00	33.51
	673	CG	TYR	A	98	1.360	15.282	4.649	1.00	29.03
	674	CD1	TYR	A	98	0.990	14.378	3.656	1.00	24.71
35	675	CE1	TYR	A	98	-0.266	13.797	3.651	1.00	19.15
	676	CD2	TYR	A	98	0.445	15.589	5.645	1.00	24.62
	677	CE2	TYR	A	98	-0.814	15.022	5.655	1.00	22.79
	678	CZ	TYR	A	98	-1.168	14.125	4.652	1.00	25.75
	679	OH	TYR	A	98	-2.433	13.574	4.644	1.00	31.99
40	680	C	TYR	A	98	3.645	18.253	4.649	1.00	36.88
	681	O	TYR	A	98	3.412	18.883	5.691	1.00	38.14
	682	N	VAL	A	99	4.811	18.293	4.012	1.00	34.30
	683	CA	VAL	A	99	5.932	19.105	4.465	1.00	27.39

	684	CB	VAL A	99	7.193	18.760	3.658	1.00	20.34
	685	CG1	VAL A	99	8.284	19.772	3.929	1.00	16.92
	686	CG2	VAL A	99	7.661	17.358	4.021	1.00	19.75
	687	C	VAL A	99	5.646	20.614	4.371	1.00	31.44
5	688	O	VAL A	99	6.009	21.371	5.272	1.00	35.10
	689	N	PRO A	100	4.991	21.072	3.285	1.00	34.59
	690	CD	PRO A	100	4.444	20.363	2.115	1.00	35.82
	691	CA	PRO A	100	4.706	22.502	3.183	1.00	33.54
	692	CB	PRO A	100	3.679	22.561	2.064	1.00	31.42
10	693	CG	PRO A	100	4.144	21.503	1.162	1.00	35.80
	694	C	PRO A	100	4.147	23.037	4.490	1.00	34.59
	695	O	PRO A	100	4.646	24.024	5.027	1.00	36.94
	696	N	GLU A	101	3.117	22.369	5.002	1.00	33.67
	697	CA	GLU A	101	2.481	22.785	6.245	1.00	31.97
15	698	CB	GLU A	101	1.248	21.937	6.533	1.00	16.92
	699	CG	GLU A	101	0.725	22.160	7.935	1.00	16.92
	700	CD	GLU A	101	-0.679	21.648	8.139	1.00	26.55
	701	OE1	GLU A	101	-0.967	20.504	7.711	1.00	21.07
	702	OE2	GLU A	101	-1.484	22.396	8.743	1.00	22.12
20	703	C	GLU A	101	3.394	22.744	7.459	1.00	33.18
	704	O	GLU A	101	3.421	23.682	8.258	1.00	32.52
	705	N	LEU A	102	4.121	21.648	7.624	1.00	33.81
	706	CA	LEU A	102	5.019	21.560	8.756	1.00	31.47
	707	CB	LEU A	102	5.820	20.262	8.694	1.00	30.43
25	708	CG	LEU A	102	4.974	18.997	8.837	1.00	34.74
	709	CD1	LEU A	102	5.866	17.776	8.764	1.00	25.10
	710	CD2	LEU A	102	4.232	19.029	10.162	1.00	36.87
	711	C	LEU A	102	5.942	22.769	8.685	1.00	30.29
	712	O	LEU A	102	6.206	23.429	9.694	1.00	33.60
30	713	N	HIS A	103	6.398	23.067	7.471	1.00	28.12
	714	CA	HIS A	103	7.298	24.186	7.214	1.00	30.58
	715	CB	HIS A	103	7.735	24.153	5.760	1.00	32.00
	716	CG	HIS A	103	8.864	25.083	5.451	1.00	35.36
	717	CD2	HIS A	103	8.953	26.123	4.590	1.00	34.89
35	718	ND1	HIS A	103	10.104	24.967	6.042	1.00	38.53
	719	CE1	HIS A	103	10.909	25.894	5.555	1.00	36.15
	720	NE2	HIS A	103	10.235	26.608	4.672	1.00	34.36
	721	C	HIS A	103	6.677	25.552	7.523	1.00	31.60
	722	O	HIS A	103	7.365	26.488	7.931	1.00	26.65
40	723	N	ALA A	104	5.378	25.672	7.297	1.00	30.94
	724	CA	ALA A	104	4.694	26.912	7.584	1.00	28.23
	725	CB	ALA A	104	3.284	26.869	7.056	1.00	23.85
	726	C	ALA A	104	4.677	27.033	9.091	1.00	32.92

	727	O	ALA A 104	4.762	28.128	9.631	1.00	40.90
	728	N	ASN A 105	4.580	25.897	9.773	1.00	32.79
	729	CA	ASN A 105	4.543	25.899	11.233	1.00	29.90
	730	CB	ASN A 105	3.645	24.762	11.739	1.00	42.45
5	731	CG	ASN A 105	2.169	25.048	11.509	1.00	48.96
	732	OD1	ASN A 105	1.617	25.989	12.076	1.00	60.59
	733	ND2	ASN A 105	1.529	24.245	10.667	1.00	37.91
	734	C	ASN A 105	5.915	25.846	11.909	1.00	24.31
	735	O	ASN A 105	6.030	25.474	13.075	1.00	24.21
10	736	N	ASN A 106	6.950	26.228	11.167	1.00	21.42
	737	CA	ASN A 106	8.314	26.278	11.687	1.00	21.95
	738	CB	ASN A 106	8.390	27.294	12.834	1.00	16.92
	739	CG	ASN A 106	9.818	27.682	13.180	1.00	18.90
	740	OD1	ASN A 106	10.091	28.173	14.275	1.00	20.83
15	741	ND2	ASN A 106	10.736	27.473	12.238	1.00	16.92
	742	C	ASN A 106	8.854	24.937	12.177	1.00	26.82
	743	O	ASN A 106	9.655	24.892	13.111	1.00	28.64
	744	N	VAL A 107	8.430	23.842	11.561	1.00	28.06
	745	CA	VAL A 107	8.914	22.538	11.988	1.00	25.22
20	746	CB	VAL A 107	7.825	21.456	11.791	1.00	24.13
	747	CG1	VAL A 107	8.322	20.100	12.286	1.00	37.12
	748	CG2	VAL A 107	6.560	21.865	12.528	1.00	24.46
	749	C	VAL A 107	10.152	22.172	11.176	1.00	28.07
	750	O	VAL A 107	10.168	22.351	9.962	1.00	33.25
25	751	N	LYS A 108	11.199	21.698	11.847	1.00	25.06
	752	CA	LYS A 108	12.422	21.280	11.157	1.00	24.60
	753	CB	LYS A 108	13.665	21.628	11.975	1.00	19.20
	754	CG	LYS A 108	14.972	21.164	11.350	1.00	17.42
	755	CD	LYS A 108	16.158	21.849	12.020	1.00	18.52
30	756	CE	LYS A 108	17.488	21.171	11.715	1.00	23.17
	757	NZ	LYS A 108	17.816	21.133	10.267	1.00	26.96
	758	C	LYS A 108	12.325	19.771	10.976	1.00	28.32
	759	O	LYS A 108	11.738	19.079	11.808	1.00	32.57
	760	N	ILE A 109	12.882	19.252	9.892	1.00	29.02
35	761	CA	ILE A 109	12.797	17.819	9.668	1.00	29.85
	762	CB	ILE A 109	11.940	17.492	8.406	1.00	29.54
	763	CG2	ILE A 109	11.773	15.980	8.268	1.00	24.76
	764	CG1	ILE A 109	10.557	18.139	8.519	1.00	26.25
	765	CD1	ILE A 109	9.602	17.740	7.412	1.00	26.43
40	766	C	ILE A 109	14.171	17.176	9.530	1.00	31.25
	767	O	ILE A 109	15.019	17.653	8.775	1.00	31.58
	768	N	GLN A 110	14.383	16.099	10.283	1.00	34.94
	769	CA	GLN A 110	15.636	15.360	10.254	1.00	35.94

	770	CB	GLN	A	110	16.491	15.699	11.472	1.00	43.90
	771	CG	GLN	A	110	16.579	17.182	11.769	1.00	52.49
	772	CD	GLN	A	110	17.578	17.513	12.860	1.00	53.12
	773	OE1	GLN	A	110	17.710	18.673	13.266	1.00	42.83
5	774	NE2	GLN	A	110	18.298	16.496	13.338	1.00	66.31
	775	C	GLN	A	110	15.264	13.892	10.293	1.00	35.02
	776	O	GLN	A	110	14.195	13.534	10.792	1.00	36.09
	777	N	MET	A	111	16.135	13.044	9.762	1.00	34.95
	778	CA	MET	A	111	15.879	11.613	9.758	1.00	38.29
10	779	CB	MET	A	111	15.299	11.184	8.401	1.00	54.75
	780	CG	MET	A	111	16.107	11.572	7.159	1.00	63.44
	781	SD	MET	A	111	17.262	10.296	6.580	1.00	75.55
	782	CE	MET	A	111	16.222	8.800	6.651	1.00	63.96
	783	C	MET	A	111	17.137	10.816	10.093	1.00	39.52
15	784	O	MET	A	111	18.190	11.030	9.501	1.00	42.08
	785	N	ILE	A	112	17.018	9.903	11.057	1.00	39.74
	786	CA	ILE	A	112	18.140	9.069	11.494	1.00	38.26
	787	CB	ILE	A	112	18.291	9.077	13.030	1.00	37.80
	788	CG2	ILE	A	112	18.536	10.490	13.526	1.00	34.53
20	789	CG1	ILE	A	112	17.039	8.470	13.667	1.00	42.15
	790	CD1	ILE	A	112	17.143	8.260	15.149	1.00	40.41
	791	C	ILE	A	112	17.978	7.612	11.078	1.00	33.52
	792	O	ILE	A	112	16.862	7.104	10.969	1.00	28.71
	793	N	GLY	A	113	19.104	6.943	10.860	1.00	30.89
25	794	CA	GLY	A	113	19.061	5.547	10.485	1.00	37.18
	795	C	GLY	A	113	19.963	5.229	9.322	1.00	39.38
	796	O	GLY	A	113	20.621	6.113	8.785	1.00	38.55
	797	N	GLU	A	114	19.994	3.954	8.944	1.00	42.25
	798	CA	GLU	A	114	20.802	3.489	7.826	1.00	50.83
30	799	CB	GLU	A	114	20.946	1.961	7.878	1.00	64.49
	800	CG	GLU	A	114	21.957	1.446	8.913	1.00	73.99
	801	CD	GLU	A	114	21.327	0.579	9.988	1.00	75.69
	802	OE1	GLU	A	114	20.709	1.131	10.927	1.00	75.15
	803	OE2	GLU	A	114	21.449	-0.661	9.888	1.00	71.34
35	804	C	GLU	A	114	20.102	3.923	6.542	1.00	55.84
	805	O	GLU	A	114	19.401	3.148	5.895	1.00	57.72
	806	N	THR	A	115	20.311	5.183	6.189	1.00	57.14
	807	CA	THR	A	115	19.697	5.786	5.017	1.00	58.68
	808	CB	THR	A	115	19.866	7.297	5.065	1.00	53.84
40	809	OG1	THR	A	115	21.235	7.618	4.805	1.00	53.59
	810	CG2	THR	A	115	19.488	7.830	6.443	1.00	49.34
	811	C	THR	A	115	20.256	5.310	3.684	1.00	63.08
	812	O	THR	A	115	19.840	5.791	2.635	1.00	63.55

	813	N	ASP A 116	21.186	4.363	3.713	1.00	67.68
	814	CA	ASP A 116	21.799	3.880	2.480	1.00	72.55
	815	CB	ASP A 116	23.270	3.539	2.737	1.00	76.81
	816	CG	ASP A 116	24.099	4.767	3.082	1.00	82.99
5	817	OD1	ASP A 116	23.821	5.405	4.121	1.00	84.93
	818	OD2	ASP A 116	25.025	5.098	2.310	1.00	75.26
	819	C	ASP A 116	21.117	2.713	1.772	1.00	74.26
	820	O	ASP A 116	21.426	2.430	0.614	1.00	76.40
	821	N	ARG A 117	20.196	2.034	2.448	1.00	75.22
10	822	CA	ARG A 117	19.494	0.909	1.828	1.00	76.00
	823	CB	ARG A 117	19.350	-0.249	2.824	1.00	91.55
	824	CG	ARG A 117	20.511	-0.377	3.803	1.00	106.10
	825	CD	ARG A 117	20.344	-1.581	4.725	1.00	116.76
	826	NE	ARG A 117	21.056	-1.408	5.992	1.00	125.02
15	827	CZ	ARG A 117	22.348	-1.107	6.100	1.00	129.50
	828	NH1	ARG A 117	23.090	-0.941	5.012	1.00	133.15
	829	NH2	ARG A 117	22.899	-0.968	7.300	1.00	131.90
	830	C	ARG A 117	18.109	1.378	1.378	1.00	73.15
	831	O	ARG A 117	17.267	0.581	0.952	1.00	75.52
20	832	N	LEU A 118	17.892	2.686	1.472	1.00	65.43
	833	CA	LEU A 118	16.622	3.288	1.103	1.00	59.80
	834	CB	LEU A 118	16.446	4.623	1.819	1.00	53.32
	835	CG	LEU A 118	16.371	4.648	3.341	1.00	51.22
	836	CD1	LEU A 118	16.223	6.094	3.814	1.00	43.14
25	837	CD2	LEU A 118	15.189	3.800	3.807	1.00	48.18
	838	C	LEU A 118	16.463	3.541	-0.382	1.00	55.75
	839	O	LEU A 118	17.432	3.758	-1.099	1.00	56.56
	840	N	PRO A 119	15.220	3.507	-0.863	1.00	50.27
	841	CD	PRO A 119	14.050	2.957	-0.157	1.00	47.23
30	842	CA	PRO A 119	14.916	3.750	-2.272	1.00	48.03
	843	CB	PRO A 119	13.411	3.533	-2.330	1.00	44.88
	844	CG	PRO A 119	13.193	2.469	-1.286	1.00	43.34
	845	C	PRO A 119	15.305	5.199	-2.577	1.00	50.30
	846	O	PRO A 119	15.220	6.060	-1.706	1.00	51.90
35	847	N	LYS A 120	15.722	5.475	-3.805	1.00	52.17
	848	CA	LYS A 120	16.137	6.826	-4.166	1.00	56.36
	849	CB	LYS A 120	16.618	6.865	-5.617	1.00	63.53
	850	CG	LYS A 120	17.297	8.175	-6.000	1.00	63.00
	851	CD	LYS A 120	17.350	8.374	-7.509	1.00	73.77
40	852	CE	LYS A 120	15.955	8.616	-8.070	1.00	77.05
	853	NZ	LYS A 120	15.992	8.975	-9.510	1.00	69.29
	854	C	LYS A 120	15.056	7.888	-3.982	1.00	55.74
	855	O	LYS A 120	15.253	8.864	-3.258	1.00	56.30

	856	N	GLN	A	121	13.920	7.704	-4.649	1.00	55.41
	857	CA	GLN	A	121	12.840	8.675	-4.559	1.00	54.91
	858	CB	GLN	A	121	11.614	8.206	-5.359	1.00	67.90
	859	CG	GLN	A	121	10.674	7.252	-4.630	1.00	74.11
5	860	CD	GLN	A	121	11.197	5.837	-4.544	1.00	76.82
	861	OE1	GLN	A	121	10.562	4.967	-3.945	1.00	72.18
	862	NE2	GLN	A	121	12.355	5.593	-5.147	1.00	76.38
	863	C	GLN	A	121	12.466	8.916	-3.104	1.00	52.21
	864	O	GLN	A	121	12.071	10.018	-2.728	1.00	53.09
10	865	N	THR	A	122	12.604	7.878	-2.286	1.00	49.30
	866	CA	THR	A	122	12.290	7.973	-0.862	1.00	43.48
	867	CB	THR	A	122	12.344	6.585	-0.179	1.00	42.07
	868	OG1	THR	A	122	11.548	5.650	-0.918	1.00	47.12
	869	CG2	THR	A	122	11.827	6.677	1.251	1.00	43.57
15	870	C	THR	A	122	13.329	8.865	-0.189	1.00	35.33
	871	O	THR	A	122	13.001	9.836	0.504	1.00	27.53
	872	N	PHE	A	123	14.590	8.512	-0.406	1.00	33.58
	873	CA	PHE	A	123	15.706	9.239	0.166	1.00	35.10
	874	CB	PHE	A	123	17.022	8.656	-0.330	1.00	37.63
20	875	CG	PHE	A	123	18.222	9.257	0.318	1.00	44.54
	876	CD1	PHE	A	123	18.427	9.116	1.688	1.00	53.52
	877	CD2	PHE	A	123	19.145	9.972	-0.432	1.00	46.30
	878	CE1	PHE	A	123	19.539	9.679	2.304	1.00	61.21
	879	CE2	PHE	A	123	20.262	10.541	0.173	1.00	47.50
25	880	CZ	PHE	A	123	20.459	10.394	1.544	1.00	55.61
	881	C	PHE	A	123	15.632	10.698	-0.223	1.00	37.43
	882	O	PHE	A	123	15.521	11.575	0.636	1.00	39.83
	883	N	GLU	A	124	15.693	10.950	-1.525	1.00	37.07
	884	CA	GLU	A	124	15.637	12.305	-2.038	1.00	35.49
30	885	CB	GLU	A	124	15.495	12.274	-3.552	1.00	33.74
	886	CG	GLU	A	124	16.775	11.871	-4.251	1.00	34.11
	887	CD	GLU	A	124	16.563	11.549	-5.712	1.00	43.15
	888	OE1	GLU	A	124	17.570	11.327	-6.420	1.00	48.58
	889	OE2	GLU	A	124	15.390	11.511	-6.150	1.00	60.13
35	890	C	GLU	A	124	14.499	13.096	-1.419	1.00	35.66
	891	O	GLU	A	124	14.661	14.274	-1.112	1.00	36.51
	892	N	ALA	A	125	13.356	12.450	-1.219	1.00	34.75
	893	CA	ALA	A	125	12.207	13.124	-0.629	1.00	37.21
	894	CB	ALA	A	125	11.065	12.146	-0.453	1.00	34.20
40	895	C	ALA	A	125	12.576	13.730	0.715	1.00	40.90
	896	O	ALA	A	125	12.393	14.926	0.946	1.00	44.51
	897	N	LEU	A	126	13.104	12.894	1.598	1.00	39.91
	898	CA	LEU	A	126	13.490	13.331	2.929	1.00	38.45

	899	CB	LEU A 126	13.847	12.114	3.773	1.00	36.01
	900	CG	LEU A 126	12.648	11.198	4.027	1.00	28.88
	901	CD1	LEU A 126	13.135	9.787	4.318	1.00	32.10
	902	CD2	LEU A 126	11.803	11.764	5.167	1.00	22.64
5	903	C	LEU A 126	14.650	14.306	2.900	1.00	39.09
	904	O	LEU A 126	14.644	15.313	3.595	1.00	41.65
	905	N	THR A 127	15.652	13.998	2.097	1.00	36.98
	906	CA	THR A 127	16.810	14.864	1.971	1.00	42.37
	907	CB	THR A 127	17.677	14.406	0.801	1.00	49.56
10	908	OG1	THR A 127	18.086	13.050	1.023	1.00	47.49
	909	CG2	THR A 127	18.893	15.294	0.657	1.00	48.08
	910	C	THR A 127	16.352	16.299	1.726	1.00	46.79
	911	O	THR A 127	16.787	17.232	2.405	1.00	50.37
	912	N	LYS A 128	15.463	16.456	0.749	1.00	49.56
15	913	CA	LYS A 128	14.914	17.754	0.387	1.00	46.71
	914	CB	LYS A 128	14.019	17.616	-0.848	1.00	47.68
	915	CG	LYS A 128	14.777	17.671	-2.171	1.00	55.98
	916	CD	LYS A 128	14.193	16.722	-3.211	1.00	60.97
	917	CE	LYS A 128	12.713	16.978	-3.451	1.00	65.54
20	918	NZ	LYS A 128	12.070	15.978	-4.364	1.00	64.13
	919	C	LYS A 128	14.126	18.376	1.531	1.00	45.28
	920	O	LYS A 128	14.382	19.513	1.918	1.00	41.48
	921	N	ALA A 129	13.168	17.635	2.073	1.00	45.11
	922	CA	ALA A 129	12.359	18.145	3.177	1.00	46.45
25	923	CB	ALA A 129	11.411	17.068	3.665	1.00	49.46
	924	C	ALA A 129	13.229	18.634	4.332	1.00	44.27
	925	O	ALA A 129	12.800	19.463	5.132	1.00	41.06
	926	N	GLU A 130	14.445	18.099	4.418	1.00	44.20
	927	CA	GLU A 130	15.391	18.487	5.455	1.00	46.78
30	928	CB	GLU A 130	16.494	17.442	5.599	1.00	44.22
	929	CG	GLU A 130	16.006	16.064	6.000	1.00	49.59
	930	CD	GLU A 130	17.142	15.111	6.324	1.00	49.64
	931	OE1	GLU A 130	17.967	14.821	5.427	1.00	49.46
	932	OE2	GLU A 130	17.209	14.652	7.484	1.00	53.99
35	933	C	GLU A 130	16.004	19.782	4.989	1.00	48.99
	934	O	GLU A 130	16.207	20.715	5.764	1.00	48.82
	935	N	GLU A 131	16.300	19.810	3.697	1.00	47.76
	936	CA	GLU A 131	16.879	20.969	3.046	1.00	41.07
	937	CB	GLU A 131	17.122	20.653	1.573	1.00	33.82
40	938	CG	GLU A 131	18.573	20.638	1.213	1.00	48.83
	939	CD	GLU A 131	19.281	21.865	1.754	1.00	53.69
	940	OE1	GLU A 131	18.859	22.996	1.413	1.00	54.79
	941	OE2	GLU A 131	20.251	21.699	2.529	1.00	67.98

	942	C	GLU A 131	15.954	22.179	3.170	1.00	39.85
	943	O	GLU A 131	16.388	23.289	3.481	1.00	39.50
	944	N	LEU A 132	14.671	21.957	2.926	1.00	40.81
	945	CA	LEU A 132	13.686	23.023	3.008	1.00	40.93
5	946	CB	LEU A 132	12.303	22.480	2.631	1.00	42.02
	947	CG	LEU A 132	11.104	23.429	2.735	1.00	37.20
	948	CD1	LEU A 132	11.372	24.670	1.914	1.00	40.73
	949	CD2	LEU A 132	9.840	22.736	2.246	1.00	22.65
	950	C	LEU A 132	13.630	23.631	4.401	1.00	39.99
10	951	O	LEU A 132	13.697	24.845	4.565	1.00	37.40
	952	N	THR A 133	13.533	22.767	5.404	1.00	43.53
	953	CA	THR A 133	13.416	23.187	6.797	1.00	43.29
	954	CB	THR A 133	12.535	22.179	7.565	1.00	30.42
	955	OG1	THR A 133	12.944	20.842	7.242	1.00	32.09
15	956	CG2	THR A 133	11.076	22.353	7.178	1.00	29.55
	957	C	THR A 133	14.686	23.450	7.618	1.00	40.62
	958	O	THR A 133	14.588	23.716	8.817	1.00	37.19
	959	N	LYS A 134	15.858	23.393	6.985	1.00	34.90
	960	CA	LYS A 134	17.126	23.639	7.683	1.00	36.42
20	961	CB	LYS A 134	18.223	24.079	6.713	1.00	20.34
	962	CG	LYS A 134	18.756	23.011	5.786	1.00	39.12
	963	CD	LYS A 134	19.867	23.565	4.875	1.00	44.98
	964	CE	LYS A 134	19.364	24.690	3.969	1.00	44.22
	965	NZ	LYS A 134	20.388	25.145	2.986	1.00	45.46
25	966	C	LYS A 134	17.033	24.715	8.751	1.00	44.36
	967	O	LYS A 134	17.078	24.432	9.945	1.00	48.76
	968	N	ASN A 135	16.905	25.958	8.303	1.00	49.25
	969	CA	ASN A 135	16.853	27.099	9.202	1.00	49.89
	970	CB	ASN A 135	17.041	28.398	8.413	1.00	51.24
30	971	CG	ASN A 135	18.124	28.291	7.360	1.00	56.46
	972	OD1	ASN A 135	19.136	27.616	7.555	1.00	47.82
	973	ND2	ASN A 135	17.923	28.970	6.237	1.00	67.17
	974	C	ASN A 135	15.610	27.229	10.072	1.00	51.52
	975	O	ASN A 135	15.421	28.261	10.715	1.00	52.67
35	976	N	ASN A 136	14.754	26.213	10.099	1.00	51.08
	977	CA	ASN A 136	13.567	26.307	10.942	1.00	50.58
	978	CB	ASN A 136	12.529	25.261	10.544	1.00	44.34
	979	CG	ASN A 136	11.579	25.769	9.477	1.00	37.46
	980	OD1	ASN A 136	10.561	25.144	9.194	1.00	26.38
40	981	ND2	ASN A 136	11.907	26.910	8.880	1.00	42.23
	982	C	ASN A 136	13.949	26.157	12.410	1.00	51.60
	983	O	ASN A 136	14.959	25.537	12.739	1.00	53.87
	984	N	THR A 137	13.142	26.724	13.297	1.00	50.58



	985	CA	THR A 137	13.458	26.671	14.711	1.00	46.19
	986	CB	THR A 137	13.846	28.054	15.207	1.00	44.64
	987	OG1	THR A 137	12.770	28.959	14.951	1.00	35.45
	988	CG2	THR A 137	15.082	28.542	14.499	1.00	28.58
5	989	C	THR A 137	12.347	26.155	15.610	1.00	44.33
	990	O	THR A 137	12.276	26.531	16.784	1.00	47.55
	991	N	GLY A 138	11.479	25.303	15.080	1.00	40.76
	992	CA	GLY A 138	10.400	24.775	15.899	1.00	38.50
	993	C	GLY A 138	10.707	23.363	16.349	1.00	37.87
10	994	O	GLY A 138	11.874	22.969	16.433	1.00	35.95
	995	N	LEU A 139	9.662	22.602	16.649	1.00	37.09
	996	CA	LEU A 139	9.832	21.214	17.063	1.00	37.28
	997	CB	LEU A 139	8.460	20.535	17.193	1.00	41.93
	998	CG	LEU A 139	8.337	19.053	17.575	1.00	43.42
15	999	CD1	LEU A 139	6.873	18.749	17.833	1.00	36.62
	1000	CD2	LEU A 139	8.880	18.145	16.480	1.00	40.37
	1001	C	LEU A 139	10.635	20.544	15.959	1.00	35.36
	1002	O	LEU A 139	10.531	20.940	14.798	1.00	34.33
	1003	N	ILE A 140	11.440	19.548	16.306	1.00	33.22
20	1004	CA	ILE A 140	12.207	18.854	15.286	1.00	32.63
	1005	CB	ILE A 140	13.655	18.645	15.699	1.00	23.68
	1006	CG2	ILE A 140	14.432	18.033	14.548	1.00	18.34
	1007	CG1	ILE A 140	14.269	19.975	16.108	1.00	19.23
	1008	CD1	ILE A 140	15.655	19.844	16.651	1.00	16.92
25	1009	C	ILE A 140	11.578	17.496	15.065	1.00	33.01
	1010	O	ILE A 140	11.579	16.652	15.955	1.00	37.44
	1011	N	LEU A 141	11.021	17.290	13.879	1.00	29.19
	1012	CA	LEU A 141	10.397	16.017	13.566	1.00	27.02
	1013	CB	LEU A 141	9.327	16.205	12.499	1.00	16.92
30	1014	CG	LEU A 141	8.207	15.173	12.551	1.00	17.32
	1015	CD1	LEU A 141	7.058	15.618	11.662	1.00	16.92
	1016	CD2	LEU A 141	8.748	13.827	12.129	1.00	16.92
	1017	C	LEU A 141	11.495	15.076	13.087	1.00	28.94
	1018	O	LEU A 141	11.910	15.103	11.927	1.00	25.64
35	1019	N	ASN A 142	11.962	14.249	14.014	1.00	31.00
	1020	CA	ASN A 142	13.032	13.309	13.753	1.00	33.31
	1021	CB	ASN A 142	13.838	13.150	15.035	1.00	23.76
	1022	CG	ASN A 142	15.281	12.806	14.778	1.00	30.31
	1023	OD1	ASN A 142	15.962	13.478	14.009	1.00	44.03
40	1024	ND2	ASN A 142	15.763	11.762	15.432	1.00	27.58
	1025	C	ASN A 142	12.493	11.960	13.285	1.00	38.34
	1026	O	ASN A 142	11.766	11.290	14.018	1.00	41.87
	1027	N	PHE A 143	12.849	11.563	12.065	1.00	38.96

	1028	CA	PHE A 143	12.385	10.291	11.509	1.00	38.15
	1029	CB	PHE A 143	12.110	10.411	10.004	1.00	29.21
	1030	CG	PHE A 143	10.791	11.031	9.678	1.00	26.76
	1031	CD1	PHE A 143	10.718	12.332	9.191	1.00	28.11
5	1032	CD2	PHE A 143	9.613	10.327	9.885	1.00	23.22
	1033	CE1	PHE A 143	9.488	12.929	8.915	1.00	33.48
	1034	CE2	PHE A 143	8.375	10.914	9.615	1.00	17.47
	1035	CZ	PHE A 143	8.313	12.219	9.129	1.00	19.85
	1036	C	PHE A 143	13.321	9.114	11.705	1.00	40.69
10	1037	O	PHE A 143	14.480	9.163	11.310	1.00	42.36
	1038	N	ALA A 144	12.808	8.048	12.306	1.00	40.34
	1039	CA	ALA A 144	13.601	6.840	12.495	1.00	34.53
	1040	CB	ALA A 144	13.225	6.156	13.813	1.00	32.61
	1041	C	ALA A 144	13.289	5.923	11.296	1.00	30.81
15	1042	O	ALA A 144	12.313	5.162	11.316	1.00	22.94
	1043	N	LEU A 145	14.110	6.017	10.249	1.00	30.25
	1044	CA	LEU A 145	13.922	5.219	9.040	1.00	32.00
	1045	CB	LEU A 145	13.781	6.140	7.839	1.00	29.70
	1046	CG	LEU A 145	12.459	6.894	7.980	1.00	33.67
20	1047	CD1	LEU A 145	12.561	8.263	7.345	1.00	32.67
	1048	CD2	LEU A 145	11.341	6.054	7.382	1.00	17.99
	1049	C	LEU A 145	15.061	4.245	8.834	1.00	32.87
	1050	O	LEU A 145	16.225	4.632	8.831	1.00	34.08
	1051	N	ASN A 146	14.702	2.979	8.642	1.00	36.56
25	1052	CA	ASN A 146	15.663	1.895	8.491	1.00	38.10
	1053	CB	ASN A 146	16.417	1.996	7.163	1.00	32.16
	1054	CG	ASN A 146	17.237	0.749	6.872	1.00	36.02
	1055	OD1	ASN A 146	16.755	-0.371	7.039	1.00	38.28
	1056	ND2	ASN A 146	18.476	0.934	6.431	1.00	37.10
30	1057	C	ASN A 146	16.629	1.984	9.672	1.00	39.84
	1058	O	ASN A 146	17.826	1.723	9.546	1.00	40.22
	1059	N	TYR A 147	16.073	2.356	10.824	1.00	37.99
	1060	CA	TYR A 147	16.816	2.513	12.069	1.00	38.54
	1061	CB	TYR A 147	16.317	3.747	12.827	1.00	36.21
35	1062	CG	TYR A 147	16.811	3.827	14.258	1.00	32.62
	1063	CD1	TYR A 147	18.019	4.449	14.570	1.00	29.51
	1064	CE1	TYR A 147	18.503	4.467	15.882	1.00	33.34
	1065	CD2	TYR A 147	16.094	3.227	15.298	1.00	32.87
	1066	CE2	TYR A 147	16.570	3.237	16.611	1.00	33.52
40	1067	CZ	TYR A 147	17.773	3.858	16.896	1.00	36.75
	1068	OH	TYR A 147	18.247	3.867	18.191	1.00	40.69
	1069	C	TYR A 147	16.682	1.304	12.981	1.00	38.81
	1070	O	TYR A 147	15.587	0.783	13.191	1.00	39.53

	1071	N	GLY A 148	17.809	0.883	13.540	1.00	34.56
	1072	CA	GLY A 148	17.815	-0.244	14.448	1.00	35.29
	1073	C	GLY A 148	18.628	0.068	15.692	1.00	36.55
	1074	O	GLY A 148	19.794	0.440	15.601	1.00	34.11
5	1075	N	GLY A 149	18.013	-0.085	16.858	1.00	35.88
	1076	CA	GLY A 149	18.703	0.187	18.106	1.00	35.86
	1077	C	GLY A 149	20.111	-0.372	18.193	1.00	33.73
	1078	O	GLY A 149	21.093	0.372	18.130	1.00	34.86
	1079	N	ARG A 150	20.221	-1.685	18.345	1.00	29.19
10	1080	CA	ARG A 150	21.528	-2.315	18.450	1.00	28.55
	1081	CB	ARG A 150	21.378	-3.830	18.591	1.00	21.40
	1082	CG	ARG A 150	20.591	-4.283	19.817	1.00	21.80
	1083	CD	ARG A 150	20.657	-5.792	19.979	1.00	16.92
	1084	NE	ARG A 150	19.782	-6.260	21.046	1.00	16.92
15	1085	CZ	ARG A 150	19.684	-7.531	21.433	1.00	19.59
	1086	NH1	ARG A 150	20.414	-8.471	20.839	1.00	23.32
	1087	NH2	ARG A 150	18.847	-7.872	22.409	1.00	21.38
	1088	C	ARG A 150	22.378	-1.989	17.227	1.00	30.06
	1089	O	ARG A 150	23.603	-1.875	17.310	1.00	26.00
20	1090	N	ALA A 151	21.719	-1.838	16.088	1.00	35.94
	1091	CA	ALA A 151	22.422	-1.517	14.859	1.00	37.38
	1092	CB	ALA A 151	21.438	-1.469	13.698	1.00	52.48
	1093	C	ALA A 151	23.156	-0.179	14.990	1.00	35.17
	1094	O	ALA A 151	24.338	-0.080	14.656	1.00	31.19
25	1095	N	GLU A 152	22.451	0.844	15.474	1.00	32.94
	1096	CA	GLU A 152	23.033	2.171	15.650	1.00	35.48
	1097	CB	GLU A 152	21.992	3.143	16.207	1.00	30.00
	1098	CG	GLU A 152	22.577	4.440	16.751	1.00	19.49
	1099	CD	GLU A 152	21.535	5.292	17.460	1.00	22.76
30	1100	OE1	GLU A 152	20.658	4.718	18.145	1.00	21.18
	1101	OE2	GLU A 152	21.595	6.539	17.351	1.00	25.44
	1102	C	GLU A 152	24.241	2.148	16.576	1.00	38.76
	1103	O	GLU A 152	25.270	2.743	16.259	1.00	39.19
	1104	N	ILE A 153	24.116	1.473	17.718	1.00	39.55
35	1105	CA	ILE A 153	25.219	1.396	18.677	1.00	38.31
	1106	CB	ILE A 153	24.817	0.652	19.964	1.00	32.60
	1107	CG2	ILE A 153	25.968	0.664	20.942	1.00	35.83
	1108	CG1	ILE A 153	23.601	1.316	20.601	1.00	37.55
	1109	CD1	ILE A 153	23.133	0.639	21.862	1.00	34.30
40	1110	C	ILE A 153	26.424	0.676	18.086	1.00	40.62
	1111	O	ILE A 153	27.565	1.043	18.352	1.00	37.23
	1112	N	THR A 154	26.157	-0.353	17.286	1.00	45.36
	1113	CA	THR A 154	27.209	-1.140	16.647	1.00	47.53

	1114	CB	THR A 154	26.615	-2.327	15.885	1.00	36.71
	1115	OG1	THR A 154	25.681	-3.005	16.726	1.00	34.10
	1116	CG2	THR A 154	27.703	-3.297	15.490	1.00	31.30
	1117	C	THR A 154	28.000	-0.277	15.672	1.00	51.16
5	1118	O	THR A 154	29.222	-0.385	15.574	1.00	50.52
	1119	N	GLN A 155	27.285	0.577	14.950	1.00	55.38
	1120	CA	GLN A 155	27.893	1.479	13.985	1.00	57.33
	1121	CB	GLN A 155	26.798	2.173	13.167	1.00	67.23
	1122	CG	GLN A 155	27.241	3.405	12.392	1.00	83.16
10	1123	CD	GLN A 155	26.953	4.706	13.134	1.00	90.67
	1124	OE1	GLN A 155	27.244	5.796	12.635	1.00	95.55
	1125	NE2	GLN A 155	26.375	4.597	14.328	1.00	94.98
	1126	C	GLN A 155	28.743	2.501	14.726	1.00	56.79
	1127	O	GLN A 155	29.854	2.818	14.306	1.00	57.35
15	1128	N	ALA A 156	28.219	3.008	15.837	1.00	54.82
	1129	CA	ALA A 156	28.937	3.990	16.631	1.00	52.43
	1130	CB	ALA A 156	28.023	4.569	17.694	1.00	53.56
	1131	C	ALA A 156	30.129	3.314	17.281	1.00	52.01
	1132	O	ALA A 156	31.203	3.898	17.398	1.00	50.83
20	1133	N	LEU A 157	29.935	2.069	17.696	1.00	53.20
	1134	CA	LEU A 157	30.989	1.304	18.347	1.00	54.15
	1135	CB	LEU A 157	30.382	0.056	18.996	1.00	59.88
	1136	CG	LEU A 157	31.257	-0.820	19.894	1.00	68.36
	1137	CD1	LEU A 157	30.382	-1.459	20.970	1.00	66.20
25	1138	CD2	LEU A 157	31.992	-1.869	19.058	1.00	73.25
	1139	C	LEU A 157	32.082	0.921	17.349	1.00	53.24
	1140	O	LEU A 157	33.220	0.654	17.728	1.00	53.64
	1141	N	LYS A 158	31.725	0.912	16.071	1.00	48.90
	1142	CA	LYS A 158	32.656	0.571	15.003	1.00	43.03
30	1143	CB	LYS A 158	31.868	0.042	13.799	1.00	51.76
	1144	CG	LYS A 158	32.699	-0.542	12.667	1.00	50.73
	1145	CD	LYS A 158	31.946	-1.683	11.978	1.00	59.64
	1146	CE	LYS A 158	30.530	-1.275	11.550	1.00	62.25
	1147	NZ	LYS A 158	29.722	-2.409	10.995	1.00	58.23
35	1148	C	LYS A 158	33.470	1.807	14.621	1.00	38.44
	1149	O	LYS A 158	34.691	1.745	14.521	1.00	36.00
	1150	N	LEU A 159	32.782	2.928	14.415	1.00	39.17
	1151	CA	LEU A 159	33.427	4.193	14.067	1.00	39.21
	1152	CB	LEU A 159	32.393	5.317	14.005	1.00	46.03
40	1153	CG	LEU A 159	31.495	5.432	12.778	1.00	49.65
	1154	CD1	LEU A 159	30.339	6.380	13.064	1.00	52.44
	1155	CD2	LEU A 159	32.322	5.929	11.611	1.00	50.53
	1156	C	LEU A 159	34.487	4.570	15.097	1.00	38.04

	1157	O	LEU A 159	35.552	5.070	14.745	1.00	32.72
	1158	N	ILE A 160	34.180	4.346	16.372	1.00	39.18
	1159	CA	ILE A 160	35.110	4.661	17.451	1.00	39.26
	1160	CB	ILE A 160	34.451	4.464	18.828	1.00	29.65
5	1161	CG2	ILE A 160	35.467	4.701	19.939	1.00	21.54
	1162	CG1	ILE A 160	33.274	5.424	18.981	1.00	33.17
	1163	CD1	ILE A 160	32.497	5.216	20.252	1.00	27.59
	1164	C	ILE A 160	36.346	3.768	17.358	1.00	42.75
	1165	O	ILE A 160	37.472	4.253	17.404	1.00	41.60
10	1166	N	SER A 161	36.138	2.463	17.224	1.00	47.98
	1167	CA	SER A 161	37.261	1.539	17.113	1.00	52.98
	1168	CB	SER A 161	36.779	0.087	17.167	1.00	51.83
	1169	OG	SER A 161	36.293	-0.244	18.457	1.00	47.45
	1170	C	SER A 161	37.998	1.778	15.805	1.00	54.93
15	1171	O	SER A 161	38.787	0.945	15.366	1.00	59.36
	1172	N	GLN A 162	37.722	2.915	15.177	1.00	54.75
	1173	CA	GLN A 162	38.367	3.277	13.927	1.00	57.55
	1174	CB	GLN A 162	37.323	3.550	12.849	1.00	57.42
	1175	CG	GLN A 162	37.917	3.877	11.489	1.00	59.30
20	1176	CD	GLN A 162	38.609	2.687	10.859	1.00	61.11
	1177	OE1	GLN A 162	39.542	2.125	11.427	1.00	65.88
	1178	NE2	GLN A 162	38.152	2.296	9.676	1.00	72.94
	1179	C	GLN A 162	39.194	4.530	14.176	1.00	60.23
	1180	O	GLN A 162	40.353	4.614	13.776	1.00	61.01
25	1181	N	ASP A 163	38.587	5.507	14.839	1.00	61.53
	1182	CA	ASP A 163	39.277	6.745	15.166	1.00	59.20
	1183	CB	ASP A 163	38.298	7.743	15.792	1.00	59.79
	1184	CG	ASP A 163	37.203	8.170	14.834	1.00	63.02
	1185	OD1	ASP A 163	36.632	7.292	14.158	1.00	72.81
30	1186	OD2	ASP A 163	36.904	9.380	14.762	1.00	61.86
	1187	C	ASP A 163	40.388	6.400	16.159	1.00	57.70
	1188	O	ASP A 163	41.429	7.051	16.193	1.00	55.82
	1189	N	VAL A 164	40.151	5.367	16.963	1.00	57.73
	1190	CA	VAL A 164	41.119	4.914	17.953	1.00	59.37
35	1191	CB	VAL A 164	40.519	3.862	18.891	1.00	55.59
	1192	CG1	VAL A 164	41.604	3.296	19.801	1.00	47.40
	1193	CG2	VAL A 164	39.416	4.479	19.714	1.00	51.18
	1194	C	VAL A 164	42.286	4.270	17.242	1.00	62.08
	1195	O	VAL A 164	43.447	4.509	17.573	1.00	65.19
40	1196	N	LEU A 165	41.963	3.430	16.268	1.00	63.92
	1197	CA	LEU A 165	42.978	2.744	15.490	1.00	62.86
	1198	CB	LEU A 165	42.311	1.737	14.555	1.00	45.47
	1199	CG	LEU A 165	43.218	0.747	13.834	1.00	40.70

	1200	CD1	LEU	A	165	42.521	-0.595	13.698	1.00	39.99
	1201	CD2	LEU	A	165	43.592	1.318	12.485	1.00	39.90
	1202	C	LEU	A	165	43.750	3.796	14.704	1.00	63.35
	1203	O	LEU	A	165	44.981	3.788	14.683	1.00	63.16
5	1204	N	ASP	A	166	43.020	4.713	14.076	1.00	64.85
	1205	CA	ASP	A	166	43.634	5.793	13.312	1.00	65.80
	1206	CB	ASP	A	166	42.581	6.521	12.477	1.00	71.82
	1207	CG	ASP	A	166	42.153	5.728	11.263	1.00	70.86
	1208	OD1	ASP	A	166	41.740	4.561	11.428	1.00	65.25
10	1209	OD2	ASP	A	166	42.227	6.272	10.141	1.00	80.37
	1210	C	ASP	A	166	44.298	6.781	14.265	1.00	66.21
	1211	O	ASP	A	166	44.567	7.927	13.903	1.00	65.89
	1212	N	ALA	A	167	44.552	6.323	15.488	1.00	66.17
	1213	CA	ALA	A	167	45.185	7.138	16.519	1.00	66.51
15	1214	CB	ALA	A	167	46.691	7.204	16.277	1.00	63.12
	1215	C	ALA	A	167	44.602	8.547	16.600	1.00	67.20
	1216	O	ALA	A	167	45.170	9.499	16.067	1.00	64.87
	1217	N	LYS	A	168	43.457	8.666	17.264	1.00	69.56
	1218	CA	LYS	A	168	42.800	9.954	17.444	1.00	70.73
20	1219	CB	LYS	A	168	41.515	10.034	16.629	1.00	55.74
	1220	CG	LYS	A	168	41.739	10.195	15.158	1.00	43.98
	1221	CD	LYS	A	168	40.450	10.600	14.486	1.00	50.77
	1222	CE	LYS	A	168	40.682	10.922	13.021	1.00	54.71
	1223	NZ	LYS	A	168	41.325	9.779	12.312	1.00	56.54
25	1224	C	LYS	A	168	42.466	10.129	18.909	1.00	74.61
	1225	O	LYS	A	168	42.990	11.020	19.580	1.00	79.29
	1226	N	ILE	A	169	41.583	9.272	19.401	1.00	75.01
	1227	CA	ILE	A	169	41.196	9.325	20.795	1.00	77.20
	1228	CB	ILE	A	169	39.651	9.321	20.960	1.00	70.32
30	1229	CG2	ILE	A	169	39.053	10.497	20.203	1.00	64.44
	1230	CG1	ILE	A	169	39.049	8.011	20.444	1.00	67.21
	1231	CD1	ILE	A	169	39.169	7.812	18.957	1.00	62.39
	1232	C	ILE	A	169	41.805	8.112	21.478	1.00	81.65
	1233	O	ILE	A	169	41.777	7.008	20.933	1.00	82.71
35	1234	N	ASN	A	170	42.384	8.328	22.656	1.00	84.48
	1235	CA	ASN	A	170	43.003	7.240	23.402	1.00	86.01
	1236	CB	ASN	A	170	43.440	7.699	24.803	1.00	99.20
	1237	CG	ASN	A	170	44.062	9.090	24.809	1.00	105.24
	1238	OD1	ASN	A	170	44.731	9.491	23.855	1.00	109.37
40	1239	ND2	ASN	A	170	43.856	9.826	25.900	1.00	104.96
	1240	C	ASN	A	170	41.951	6.162	23.551	1.00	84.21
	1241	O	ASN	A	170	40.761	6.458	23.611	1.00	83.04
	1242	N	PRO	A	171	42.364	4.892	23.600	1.00	84.49

	1243	CD	PRO A 171	43.716	4.318	23.698	1.00	86.08
	1244	CA	PRO A 171	41.335	3.862	23.753	1.00	84.63
	1245	CB	PRO A 171	42.141	2.567	23.713	1.00	86.37
	1246	CG	PRO A 171	43.442	2.977	24.344	1.00	86.68
5	1247	C	PRO A 171	40.643	4.094	25.097	1.00	82.79
	1248	O	PRO A 171	39.598	3.513	25.392	1.00	82.76
	1249	N	GLY A 172	41.246	4.969	25.898	1.00	80.64
	1250	CA	GLY A 172	40.703	5.297	27.201	1.00	81.32
	1251	C	GLY A 172	39.764	6.488	27.163	1.00	81.29
10	1252	O	GLY A 172	39.094	6.783	28.151	1.00	83.71
	1253	N	ASP A 173	39.721	7.182	26.030	1.00	79.07
	1254	CA	ASP A 173	38.842	8.336	25.870	1.00	75.74
	1255	CB	ASP A 173	39.260	9.159	24.651	1.00	85.90
	1256	CG	ASP A 173	40.356	10.146	24.968	1.00	90.56
15	1257	OD1	ASP A 173	41.327	9.754	25.645	1.00	93.25
	1258	OD2	ASP A 173	40.248	11.313	24.536	1.00	92.57
	1259	C	ASP A 173	37.393	7.884	25.711	1.00	70.25
	1260	O	ASP A 173	36.464	8.691	25.777	1.00	68.50
	1261	N	ILE A 174	37.207	6.587	25.495	1.00	65.51
20	1262	CA	ILE A 174	35.876	6.023	25.340	1.00	60.45
	1263	CB	ILE A 174	35.956	4.517	25.071	1.00	48.40
	1264	CG2	ILE A 174	34.564	3.936	24.911	1.00	46.12
	1265	CG1	ILE A 174	36.789	4.274	23.815	1.00	44.86
	1266	CD1	ILE A 174	37.028	2.817	23.515	1.00	31.07
25	1267	C	ILE A 174	35.086	6.256	26.621	1.00	58.37
	1268	O	ILE A 174	35.421	5.712	27.668	1.00	58.27
	1269	N	THR A 175	34.042	7.071	26.535	1.00	55.65
	1270	CA	THR A 175	33.210	7.371	27.691	1.00	53.67
	1271	CB	THR A 175	33.526	8.765	28.240	1.00	57.15
30	1272	OG1	THR A 175	33.103	9.758	27.300	1.00	55.78
	1273	CG2	THR A 175	35.012	8.915	28.453	1.00	49.80
	1274	C	THR A 175	31.751	7.336	27.264	1.00	52.38
	1275	O	THR A 175	31.454	7.143	26.089	1.00	52.43
	1276	N	GLU A 176	30.835	7.512	28.208	1.00	51.31
35	1277	CA	GLU A 176	29.423	7.518	27.858	1.00	48.46
	1278	CB	GLU A 176	28.555	7.471	29.114	1.00	37.51
	1279	CG	GLU A 176	28.426	6.080	29.688	1.00	45.01
	1280	CD	GLU A 176	27.472	6.010	30.858	1.00	45.89
	1281	OE1	GLU A 176	26.435	6.716	30.834	1.00	42.92
40	1282	OE2	GLU A 176	27.757	5.231	31.792	1.00	34.90
	1283	C	GLU A 176	29.130	8.777	27.056	1.00	49.50
	1284	O	GLU A 176	28.255	8.793	26.192	1.00	49.76
	1285	N	GLU A 177	29.879	9.833	27.349	1.00	48.42

	1286	CA	GLU A 177	29.721	11.092	26.645	1.00	48.94
	1287	CB	GLU A 177	30.646	12.153	27.253	1.00	63.07
	1288	CG	GLU A 177	30.554	13.528	26.589	1.00	72.68
	1289	CD	GLU A 177	31.888	14.267	26.554	1.00	76.09
5	1290	OE1	GLU A 177	31.912	15.439	26.114	1.00	77.97
	1291	OE2	GLU A 177	32.914	13.675	26.957	1.00	76.21
	1292	C	GLU A 177	30.095	10.867	25.179	1.00	47.13
	1293	O	GLU A 177	29.340	11.210	24.269	1.00	43.82
	1294	N	LEU A 178	31.266	10.274	24.964	1.00	46.13
10	1295	CA	LEU A 178	31.774	10.012	23.620	1.00	41.18
	1296	CB	LEU A 178	33.167	9.373	23.704	1.00	31.24
	1297	CG	LEU A 178	33.980	9.227	22.411	1.00	29.48
	1298	CD1	LEU A 178	35.389	8.792	22.756	1.00	32.21
	1299	CD2	LEU A 178	33.344	8.213	21.481	1.00	38.13
15	1300	C	LEU A 178	30.839	9.128	22.800	1.00	41.26
	1301	O	LEU A 178	30.355	9.551	21.752	1.00	44.23
	1302	N	ILE A 179	30.596	7.905	23.271	1.00	37.47
	1303	CA	ILE A 179	29.716	6.967	22.573	1.00	33.95
	1304	CB	ILE A 179	29.324	5.780	23.479	1.00	25.86
20	1305	CG2	ILE A 179	28.262	4.950	22.807	1.00	27.50
	1306	CG1	ILE A 179	30.545	4.905	23.762	1.00	24.58
	1307	CD1	ILE A 179	30.292	3.777	24.748	1.00	16.92
	1308	C	ILE A 179	28.443	7.673	22.127	1.00	36.09
	1309	O	ILE A 179	27.885	7.374	21.069	1.00	36.52
25	1310	N	GLY A 180	27.997	8.622	22.944	1.00	37.19
	1311	CA	GLY A 180	26.792	9.370	22.639	1.00	34.45
	1312	C	GLY A 180	26.935	10.318	21.466	1.00	33.00
	1313	O	GLY A 180	25.951	10.639	20.794	1.00	32.59
	1314	N	ASN A 181	28.157	10.777	21.222	1.00	35.65
30	1315	CA	ASN A 181	28.411	11.687	20.114	1.00	34.95
	1316	CB	ASN A 181	29.701	12.475	20.339	1.00	30.99
	1317	CG	ASN A 181	29.654	13.321	21.578	1.00	27.11
	1318	OD1	ASN A 181	28.679	14.027	21.818	1.00	30.62
	1319	ND2	ASN A 181	30.715	13.268	22.372	1.00	34.99
35	1320	C	ASN A 181	28.528	10.929	18.804	1.00	32.99
	1321	O	ASN A 181	28.625	11.546	17.751	1.00	27.15
	1322	N	TYR A 182	28.523	9.599	18.868	1.00	31.98
	1323	CA	TYR A 182	28.645	8.778	17.670	1.00	30.09
	1324	CB	TYR A 182	29.708	7.712	17.869	1.00	29.07
40	1325	CG	TYR A 182	31.121	8.224	17.726	1.00	30.62
	1326	CD1	TYR A 182	31.630	9.198	18.589	1.00	31.56
	1327	CE1	TYR A 182	32.954	9.652	18.467	1.00	31.15
	1328	CD2	TYR A 182	31.965	7.715	16.735	1.00	32.17



	1329	CE2	TYR	A	182	33.287	8.156	16.606	1.00	29.49
	1330	CZ	TYR	A	182	33.774	9.123	17.473	1.00	30.88
	1331	OH	TYR	A	182	35.079	9.548	17.337	1.00	38.87
	1332	C	TYR	A	182	27.353	8.116	17.247	1.00	30.63
5	1333	O	TYR	A	182	27.316	7.417	16.238	1.00	27.81
	1334	N	LEU	A	183	26.296	8.331	18.023	1.00	33.68
	1335	CA	LEU	A	183	24.987	7.764	17.712	1.00	39.37
	1336	CB	LEU	A	183	24.169	7.618	18.995	1.00	39.69
	1337	CG	LEU	A	183	24.813	6.778	20.096	1.00	35.29
10	1338	CD1	LEU	A	183	23.932	6.801	21.332	1.00	30.83
	1339	CD2	LEU	A	183	25.016	5.361	19.602	1.00	36.26
	1340	C	LEU	A	183	24.250	8.671	16.715	1.00	40.34
	1341	O	LEU	A	183	24.537	9.865	16.626	1.00	39.87
	1342	N	PHE	A	184	23.302	8.110	15.969	1.00	38.84
15	1343	CA	PHE	A	184	22.556	8.890	14.984	1.00	37.83
	1344	CB	PHE	A	184	21.432	8.058	14.354	1.00	31.19
	1345	CG	PHE	A	184	21.894	6.766	13.729	1.00	28.22
	1346	CD1	PHE	A	184	23.182	6.633	13.229	1.00	30.85
	1347	CD2	PHE	A	184	21.019	5.687	13.616	1.00	33.99
20	1348	CE1	PHE	A	184	23.587	5.443	12.627	1.00	24.17
	1349	CE2	PHE	A	184	21.417	4.493	13.013	1.00	21.76
	1350	CZ	PHE	A	184	22.699	4.372	12.519	1.00	18.36
	1351	C	PHE	A	184	21.952	10.145	15.604	1.00	36.97
	1352	O	PHE	A	184	21.698	11.130	14.912	1.00	32.04
25	1353	N	THR	A	185	21.719	10.104	16.909	1.00	38.47
	1354	CA	THR	A	185	21.145	11.244	17.609	1.00	42.41
	1355	CB	THR	A	185	20.396	10.787	18.846	1.00	34.61
	1356	OG1	THR	A	185	21.213	9.862	19.570	1.00	41.28
	1357	CG2	THR	A	185	19.104	10.116	18.454	1.00	34.33
30	1358	C	THR	A	185	22.200	12.254	18.036	1.00	44.70
	1359	O	THR	A	185	21.946	13.086	18.905	1.00	41.53
	1360	N	GLN	A	186	23.374	12.179	17.413	1.00	48.74
	1361	CA	GLN	A	186	24.494	13.072	17.711	1.00	49.59
	1362	CB	GLN	A	186	25.775	12.501	17.132	1.00	45.10
35	1363	CG	GLN	A	186	25.837	12.676	15.628	1.00	43.93
	1364	CD	GLN	A	186	27.074	12.068	15.013	1.00	47.95
	1365	OE1	GLN	A	186	27.201	10.848	14.920	1.00	50.02
	1366	NE2	GLN	A	186	28.000	12.918	14.593	1.00	38.99
	1367	C	GLN	A	186	24.279	14.451	17.097	1.00	51.53
40	1368	O	GLN	A	186	25.031	15.389	17.370	1.00	55.42
	1369	N	HIS	A	187	23.262	14.555	16.249	1.00	50.40
	1370	CA	HIS	A	187	22.934	15.800	15.568	1.00	49.57
	1371	CB	HIS	A	187	22.157	15.474	14.295	1.00	42.89

	1372	CG	HIS A 187	22.856	14.473	13.427	1.00	49.91
	1373	CD2	HIS A 187	22.458	13.268	12.951	1.00	49.67
	1374	ND1	HIS A 187	24.159	14.638	13.006	1.00	43.80
	1375	CE1	HIS A 187	24.536	13.578	12.311	1.00	48.87
5	1376	NE2	HIS A 187	23.523	12.731	12.263	1.00	46.70
	1377	C	HIS A 187	22.145	16.735	16.469	1.00	52.33
	1378	O	HIS A 187	22.402	17.936	16.513	1.00	53.97
	1379	N	LEU A 188	21.187	16.182	17.196	1.00	54.52
	1380	CA	LEU A 188	20.391	16.982	18.109	1.00	51.83
10	1381	CB	LEU A 188	19.256	16.127	18.682	1.00	44.55
	1382	CG	LEU A 188	18.288	15.528	17.650	1.00	47.65
	1383	CD1	LEU A 188	17.311	14.577	18.332	1.00	49.93
	1384	CD2	LEU A 188	17.539	16.645	16.937	1.00	56.89
	1385	C	LEU A 188	21.309	17.487	19.229	1.00	52.44
15	1386	O	LEU A 188	22.248	16.802	19.628	1.00	53.35
	1387	N	PRO A 189	21.056	18.700	19.738	1.00	51.33
	1388	CD	PRO A 189	19.887	19.538	19.434	1.00	51.94
	1389	CA	PRO A 189	21.858	19.302	20.815	1.00	49.93
	1390	CB	PRO A 189	21.115	20.601	21.115	1.00	51.02
20	1391	CG	PRO A 189	19.701	20.275	20.733	1.00	52.36
	1392	C	PRO A 189	21.978	18.411	22.045	1.00	46.59
	1393	O	PRO A 189	21.001	17.807	22.476	1.00	45.97
	1394	N	LYS A 190	23.169	18.351	22.625	1.00	42.50
	1395	CA	LYS A 190	23.390	17.495	23.782	1.00	39.80
25	1396	CB	LYS A 190	24.672	17.885	24.526	1.00	36.33
	1397	CG	LYS A 190	25.964	17.462	23.825	1.00	38.65
	1398	CD	LYS A 190	27.169	17.626	24.750	1.00	42.37
	1399	CE	LYS A 190	28.493	17.455	24.007	1.00	50.39
	1400	NZ	LYS A 190	28.687	16.085	23.447	1.00	58.82
30	1401	C	LYS A 190	22.256	17.370	24.789	1.00	39.26
	1402	O	LYS A 190	21.827	16.256	25.075	1.00	39.95
	1403	N	ASP A 191	21.751	18.475	25.328	1.00	40.10
	1404	CA	ASP A 191	20.687	18.345	26.323	1.00	39.42
	1405	CB	ASP A 191	20.538	19.644	27.147	1.00	39.52
35	1406	CG	ASP A 191	20.012	20.819	26.328	1.00	44.32
	1407	OD1	ASP A 191	20.747	21.289	25.429	1.00	39.96
	1408	OD2	ASP A 191	18.866	21.275	26.589	1.00	42.53
	1409	C	ASP A 191	19.323	17.893	25.777	1.00	39.16
	1410	O	ASP A 191	18.378	17.670	26.544	1.00	41.35
40	1411	N	LEU A 192	19.223	17.730	24.460	1.00	37.21
	1412	CA	LEU A 192	17.962	17.297	23.850	1.00	34.43
	1413	CB	LEU A 192	17.484	18.337	22.815	1.00	26.76
	1414	CG	LEU A 192	16.902	19.649	23.372	1.00	23.82

	1415	CD1	LEU A 192	16.704	20.638	22.253	1.00	16.92
	1416	CD2	LEU A 192	15.570	19.379	24.088	1.00	16.92
	1417	C	LEU A 192	18.039	15.911	23.203	1.00	34.24
	1418	O	LEU A 192	17.031	15.380	22.746	1.00	38.50
5	1419	N	ARG A 193	19.235	15.328	23.193	1.00	30.50
	1420	CA	ARG A 193	19.469	14.016	22.598	1.00	29.14
	1421	CB	ARG A 193	20.949	13.650	22.679	1.00	23.71
	1422	CG	ARG A 193	21.825	14.473	21.795	1.00	24.21
	1423	CD	ARG A 193	23.274	14.087	21.962	1.00	20.84
10	1424	NE	ARG A 193	24.139	14.813	21.033	1.00	31.16
	1425	CZ	ARG A 193	25.463	14.694	20.994	1.00	37.18
	1426	NH1	ARG A 193	26.087	13.874	21.837	1.00	39.87
	1427	NH2	ARG A 193	26.163	15.390	20.107	1.00	37.17
	1428	C	ARG A 193	18.670	12.853	23.166	1.00	28.97
15	1429	O	ARG A 193	18.305	11.949	22.427	1.00	29.31
	1430	N	ASP A 194	18.399	12.846	24.463	1.00	24.43
	1431	CA	ASP A 194	17.665	11.723	25.024	1.00	26.20
	1432	CB	ASP A 194	18.295	11.282	26.354	1.00	21.25
	1433	CG	ASP A 194	19.764	10.856	26.208	1.00	25.14
20	1434	OD1	ASP A 194	20.134	10.315	25.138	1.00	16.92
	1435	OD2	ASP A 194	20.543	11.047	27.175	1.00	30.59
	1436	C	ASP A 194	16.187	12.025	25.228	1.00	24.70
	1437	O	ASP A 194	15.826	13.067	25.776	1.00	31.23
	1438	N	PRO A 195	15.309	11.110	24.784	1.00	19.04
25	1439	CD	PRO A 195	15.601	9.811	24.159	1.00	16.92
	1440	CA	PRO A 195	13.865	11.293	24.929	1.00	22.28
	1441	CB	PRO A 195	13.290	10.066	24.231	1.00	21.56
	1442	CG	PRO A 195	14.334	9.050	24.426	1.00	18.86
	1443	C	PRO A 195	13.490	11.347	26.391	1.00	24.96
30	1444	O	PRO A 195	14.092	10.660	27.206	1.00	30.51
	1445	N	ASP A 196	12.510	12.172	26.728	1.00	22.33
	1446	CA	ASP A 196	12.081	12.284	28.112	1.00	21.67
	1447	CB	ASP A 196	11.799	13.737	28.464	1.00	21.17
	1448	CG	ASP A 196	13.024	14.589	28.347	1.00	35.32
35	1449	OD1	ASP A 196	13.290	15.099	27.239	1.00	31.80
	1450	OD2	ASP A 196	13.739	14.725	29.361	1.00	44.56
	1451	C	ASP A 196	10.849	11.437	28.336	1.00	22.00
	1452	O	ASP A 196	10.383	11.258	29.461	1.00	22.34
	1453	N	LEU A 197	10.331	10.910	27.239	1.00	24.46
40	1454	CA	LEU A 197	9.164	10.063	27.283	1.00	22.14
	1455	CB	LEU A 197	7.896	10.900	27.460	1.00	16.92
	1456	CG	LEU A 197	6.573	10.182	27.174	1.00	16.92
	1457	CD1	LEU A 197	6.452	8.939	28.004	1.00	18.26

	1458	CD2	LEU A 197	5.424	11.093	27.470	1.00	23.97
	1459	C	LEU A 197	9.100	9.292	25.987	1.00	24.32
	1460	O	LEU A 197	9.396	9.825	24.925	1.00	31.10
	1461	N	ILE A 198	8.752	8.018	26.082	1.00	25.23
5	1462	CA	ILE A 198	8.617	7.198	24.899	1.00	23.49
	1463	CB	ILE A 198	9.663	6.079	24.843	1.00	16.92
	1464	CG2	ILE A 198	9.389	5.176	23.651	1.00	16.92
	1465	CG1	ILE A 198	11.057	6.698	24.719	1.00	19.52
	1466	CD1	ILE A 198	12.156	5.717	24.368	1.00	16.92
10	1467	C	ILE A 198	7.214	6.621	24.894	1.00	26.00
	1468	O	ILE A 198	6.835	5.840	25.767	1.00	23.12
	1469	N	ILE A 199	6.448	7.056	23.901	1.00	30.16
	1470	CA	ILE A 199	5.070	6.649	23.719	1.00	31.89
	1471	CB	ILE A 199	4.275	7.798	23.061	1.00	31.40
15	1472	CG2	ILE A 199	2.850	7.347	22.743	1.00	35.99
	1473	CG1	ILE A 199	4.300	9.019	23.991	1.00	30.96
	1474	CD1	ILE A 199	3.589	10.238	23.458	1.00	25.50
	1475	C	ILE A 199	4.976	5.393	22.859	1.00	30.27
	1476	O	ILE A 199	5.705	5.249	21.881	1.00	30.43
20	1477	N	ARG A 200	4.087	4.483	23.246	1.00	29.84
	1478	CA	ARG A 200	3.868	3.240	22.513	1.00	34.70
	1479	CB	ARG A 200	4.567	2.070	23.214	1.00	38.24
	1480	CG	ARG A 200	4.553	0.763	22.420	1.00	38.39
	1481	CD	ARG A 200	5.267	0.900	21.074	1.00	41.65
25	1482	NE	ARG A 200	5.195	-0.302	20.234	1.00	34.53
	1483	CZ	ARG A 200	5.923	-1.409	20.400	1.00	18.77
	1484	NH1	ARG A 200	6.807	-1.510	21.385	1.00	16.92
	1485	NH2	ARG A 200	5.771	-2.423	19.566	1.00	18.24
	1486	C	ARG A 200	2.361	3.011	22.461	1.00	35.76
30	1487	O	ARG A 200	1.688	3.032	23.490	1.00	33.19
	1488	N	THR A 201	1.834	2.801	21.261	1.00	38.28
	1489	CA	THR A 201	0.399	2.610	21.078	1.00	37.05
	1490	CB	THR A 201	-0.118	3.496	19.931	1.00	16.92
	1491	OG1	THR A 201	0.697	3.301	18.769	1.00	29.17
35	1492	CG2	THR A 201	-0.060	4.947	20.321	1.00	19.67
	1493	C	THR A 201	-0.005	1.174	20.781	1.00	39.68
	1494	O	THR A 201	0.844	0.295	20.648	1.00	41.56
	1495	N	SER A 202	-1.314	0.950	20.689	1.00	41.87
	1496	CA	SER A 202	-1.874	-0.363	20.376	1.00	39.34
40	1497	CB	SER A 202	-1.198	-0.919	19.122	1.00	19.15
	1498	OG	SER A 202	-1.663	-2.227	18.836	1.00	39.12
	1499	C	SER A 202	-1.828	-1.421	21.479	1.00	40.05
	1500	O	SER A 202	-2.303	-2.540	21.280	1.00	47.17

	1501	N	GLY A 203	-1.264	-1.080	22.634	1.00	38.45
	1502	CA	GLY A 203	-1.183	-2.038	23.729	1.00	37.08
	1503	C	GLY A 203	0.126	-2.815	23.773	1.00	35.70
	1504	O	GLY A 203	0.305	-3.717	24.591	1.00	37.31
5	1505	N	GLU A 204	1.048	-2.459	22.888	1.00	29.52
	1506	CA	GLU A 204	2.336	-3.121	22.824	1.00	28.07
	1507	CB	GLU A 204	3.010	-2.835	21.484	1.00	26.30
	1508	CG	GLU A 204	2.478	-3.664	20.328	1.00	48.79
	1509	CD	GLU A 204	2.437	-5.147	20.655	1.00	50.97
10	1510	OE1	GLU A 204	1.371	-5.628	21.104	1.00	42.50
	1511	OE2	GLU A 204	3.470	-5.829	20.481	1.00	50.61
	1512	C	GLU A 204	3.249	-2.673	23.942	1.00	29.34
	1513	O	GLU A 204	3.611	-1.507	24.014	1.00	34.97
	1514	N	LEU A 205	3.626	-3.604	24.811	1.00	24.91
15	1515	CA	LEU A 205	4.523	-3.307	25.925	1.00	25.98
	1516	CB	LEU A 205	3.943	-3.875	27.217	1.00	25.92
	1517	CG	LEU A 205	2.570	-3.293	27.561	1.00	23.50
	1518	CD1	LEU A 205	1.943	-4.043	28.704	1.00	16.92
	1519	CD2	LEU A 205	2.724	-1.837	27.917	1.00	30.67
20	1520	C	LEU A 205	5.905	-3.894	25.661	1.00	28.56
	1521	O	LEU A 205	6.494	-4.539	26.515	1.00	29.61
	1522	N	ARG A 206	6.418	-3.675	24.462	1.00	33.33
	1523	CA	ARG A 206	7.725	-4.191	24.108	1.00	37.25
	1524	CB	ARG A 206	7.681	-4.932	22.766	1.00	42.74
25	1525	CG	ARG A 206	6.327	-5.519	22.392	1.00	40.30
	1526	CD	ARG A 206	6.381	-6.273	21.057	1.00	44.32
	1527	NE	ARG A 206	6.932	-5.469	19.960	1.00	65.13
	1528	CZ	ARG A 206	6.926	-5.836	18.677	1.00	69.76
	1529	NH1	ARG A 206	6.392	-6.999	18.325	1.00	76.09
30	1530	NH2	ARG A 206	7.452	-5.045	17.741	1.00	74.71
	1531	C	ARG A 206	8.631	-2.991	23.963	1.00	42.39
	1532	O	ARG A 206	8.197	-1.852	24.144	1.00	42.90
	1533	N	LEU A 207	9.888	-3.247	23.625	1.00	44.87
	1534	CA	LEU A 207	10.834	-2.167	23.432	1.00	48.66
35	1535	CB	LEU A 207	12.136	-2.472	24.173	1.00	63.61
	1536	CG	LEU A 207	11.996	-2.330	25.693	1.00	70.49
	1537	CD1	LEU A 207	13.290	-2.729	26.376	1.00	76.92
	1538	CD2	LEU A 207	11.633	-0.885	26.044	1.00	75.21
	1539	C	LEU A 207	11.068	-1.969	21.939	1.00	47.29
40	1540	O	LEU A 207	11.315	-0.849	21.484	1.00	47.01
	1541	N	SER A 208	10.971	-3.060	21.183	1.00	42.15
	1542	CA	SER A 208	11.139	-3.019	19.732	1.00	32.73
	1543	CB	SER A 208	10.005	-2.214	19.099	1.00	33.90

	1544	OG	SER A 208	8.755	-2.556	19.666	1.00	24.12
	1545	C	SER A 208	12.470	-2.441	19.263	1.00	28.39
	1546	O	SER A 208	12.540	-1.821	18.198	1.00	29.45
	1547	N	ASN A 209	13.516	-2.629	20.064	1.00	26.85
5	1548	CA	ASN A 209	14.861	-2.162	19.719	1.00	27.50
	1549	CB	ASN A 209	15.404	-3.045	18.573	1.00	16.92
	1550	CG	ASN A 209	16.864	-2.763	18.222	1.00	22.61
	1551	OD1	ASN A 209	17.693	-2.495	19.087	1.00	26.46
	1552	ND2	ASN A 209	17.182	-2.857	16.939	1.00	20.95
10	1553	C	ASN A 209	14.909	-0.675	19.348	1.00	32.21
	1554	O	ASN A 209	15.759	-0.241	18.573	1.00	34.11
	1555	N	PHE A 210	14.006	0.108	19.929	1.00	34.72
	1556	CA	PHE A 210	13.947	1.539	19.638	1.00	30.65
	1557	CB	PHE A 210	12.484	2.000	19.582	1.00	21.62
15	1558	CG	PHE A 210	12.309	3.442	19.182	1.00	28.42
	1559	CD1	PHE A 210	12.788	3.902	17.960	1.00	32.07
	1560	CD2	PHE A 210	11.650	4.334	20.021	1.00	24.66
	1561	CE1	PHE A 210	12.614	5.221	17.580	1.00	22.48
	1562	CE2	PHE A 210	11.471	5.653	19.652	1.00	24.33
20	1563	CZ	PHE A 210	11.955	6.099	18.427	1.00	18.91
	1564	C	PHE A 210	14.708	2.350	20.677	1.00	30.28
	1565	O	PHE A 210	14.456	2.224	21.873	1.00	26.90
	1566	N	LEU A 211	15.636	3.179	20.202	1.00	31.38
	1567	CA	LEU A 211	16.460	4.030	21.060	1.00	30.02
25	1568	CB	LEU A 211	15.703	5.307	21.425	1.00	19.94
	1569	CG	LEU A 211	15.642	6.415	20.381	1.00	17.90
	1570	CD1	LEU A 211	15.015	7.668	21.000	1.00	17.79
	1571	CD2	LEU A 211	17.051	6.710	19.886	1.00	28.12
	1572	C	LEU A 211	16.940	3.356	22.344	1.00	33.52
30	1573	O	LEU A 211	16.784	3.899	23.445	1.00	35.70
	1574	N	PRO A 212	17.559	2.175	22.220	1.00	34.82
	1575	CD	PRO A 212	18.096	1.603	20.977	1.00	34.05
	1576	CA	PRO A 212	18.058	1.440	23.384	1.00	31.21
	1577	CB	PRO A 212	18.807	0.283	22.748	1.00	30.61
35	1578	CG	PRO A 212	19.305	0.881	21.473	1.00	33.84
	1579	C	PRO A 212	18.941	2.279	24.317	1.00	28.88
	1580	O	PRO A 212	18.734	2.286	25.529	1.00	28.95
	1581	N	TRP A 213	19.911	2.991	23.747	1.00	32.89
	1582	CA	TRP A 213	20.821	3.829	24.525	1.00	34.16
40	1583	CB	TRP A 213	22.076	4.133	23.699	1.00	36.50
	1584	CG	TRP A 213	23.063	5.051	24.377	1.00	40.25
	1585	CD2	TRP A 213	24.322	4.679	24.939	1.00	41.82
	1586	CE2	TRP A 213	24.917	5.856	25.451	1.00	42.56

	1587	CE3	TRP	A	213	25.011	3.463	25.060	1.00	36.15
	1588	CD1	TRP	A	213	22.944	6.404	24.569	1.00	34.48
	1589	NE1	TRP	A	213	24.054	6.892	25.212	1.00	35.36
	1590	CZ2	TRP	A	213	26.170	5.851	26.074	1.00	41.79
5	1591	CZ3	TRP	A	213	26.257	3.459	25.680	1.00	44.66
	1592	CH2	TRP	A	213	26.823	4.647	26.178	1.00	41.35
	1593	C	TRP	A	213	20.210	5.143	25.045	1.00	31.31
	1594	O	TRP	A	213	20.111	5.350	26.253	1.00	28.47
	1595	N	GLN	A	214	19.814	6.031	24.139	1.00	29.42
10	1596	CA	GLN	A	214	19.235	7.315	24.526	1.00	27.98
	1597	CB	GLN	A	214	18.794	8.086	23.276	1.00	29.16
	1598	CG	GLN	A	214	19.871	8.309	22.216	1.00	30.26
	1599	CD	GLN	A	214	20.002	7.167	21.211	1.00	35.27
	1600	OE1	GLN	A	214	20.512	7.361	20.106	1.00	35.10
15	1601	NE2	GLN	A	214	19.554	5.976	21.591	1.00	36.97
	1602	C	GLN	A	214	18.041	7.180	25.484	1.00	26.22
	1603	O	GLN	A	214	17.857	7.990	26.395	1.00	26.19
	1604	N	GLY	A	215	17.229	6.153	25.271	1.00	24.50
	1605	CA	GLY	A	215	16.068	5.956	26.115	1.00	20.34
20	1606	C	GLY	A	215	16.359	5.288	27.444	1.00	20.33
	1607	O	GLY	A	215	15.431	4.974	28.179	1.00	19.80
	1608	N	ALA	A	216	17.637	5.085	27.761	1.00	16.97
	1609	CA	ALA	A	216	18.049	4.435	29.008	1.00	17.93
	1610	CB	ALA	A	216	19.509	4.772	29.324	1.00	17.20
25	1611	C	ALA	A	216	17.160	4.770	30.207	1.00	20.59
	1612	O	ALA	A	216	16.717	3.863	30.912	1.00	23.60
	1613	N	TYR	A	217	16.887	6.055	30.442	1.00	24.42
	1614	CA	TYR	A	217	16.033	6.443	31.574	1.00	18.63
	1615	CB	TYR	A	217	16.766	7.389	32.533	1.00	16.92
30	1616	CG	TYR	A	217	18.180	7.000	32.935	1.00	16.92
	1617	CD1	TYR	A	217	19.248	7.152	32.043	1.00	16.92
	1618	CE1	TYR	A	217	20.558	6.868	32.436	1.00	16.92
	1619	CD2	TYR	A	217	18.462	6.543	34.233	1.00	16.92
	1620	CE2	TYR	A	217	19.768	6.256	34.632	1.00	16.92
35	1621	CZ	TYR	A	217	20.808	6.423	33.730	1.00	16.92
	1622	OH	TYR	A	217	22.103	6.168	34.115	1.00	16.92
	1623	C	TYR	A	217	14.730	7.134	31.154	1.00	16.92
	1624	O	TYR	A	217	14.170	7.927	31.910	1.00	16.92
	1625	N	SER	A	218	14.235	6.835	29.961	1.00	16.92
40	1626	CA	SER	A	218	13.011	7.469	29.502	1.00	16.92
	1627	CB	SER	A	218	12.851	7.259	27.999	1.00	23.90
	1628	OG	SER	A	218	14.058	7.569	27.330	1.00	36.44
	1629	C	SER	A	218	11.762	6.965	30.210	1.00	16.92

	1630	O	SER A 218	11.671	5.798	30.605	1.00	16.92
	1631	N	GLU A 219	10.801	7.861	30.386	1.00	16.92
	1632	CA	GLU A 219	9.537	7.487	30.992	1.00	24.28
	1633	CB	GLU A 219	8.704	8.727	31.298	1.00	24.60
5	1634	CG	GLU A 219	9.205	9.564	32.459	1.00	31.57
	1635	CD	GLU A 219	8.660	9.084	33.790	1.00	37.84
	1636	OE1	GLU A 219	7.419	9.099	33.964	1.00	42.71
	1637	OE2	GLU A 219	9.468	8.694	34.658	1.00	36.71
	1638	C	GLU A 219	8.881	6.704	29.875	1.00	30.17
10	1639	O	GLU A 219	9.309	6.791	28.729	1.00	36.16
	1640	N	LEU A 220	7.856	5.930	30.188	1.00	29.51
	1641	CA	LEU A 220	7.183	5.174	29.149	1.00	24.66
	1642	CB	LEU A 220	7.582	3.705	29.192	1.00	22.54
	1643	CG	LEU A 220	9.082	3.426	29.170	1.00	17.48
15	1644	CD1	LEU A 220	9.297	1.940	29.324	1.00	23.19
	1645	CD2	LEU A 220	9.707	3.943	27.887	1.00	16.92
	1646	C	LEU A 220	5.704	5.302	29.378	1.00	25.51
	1647	O	LEU A 220	5.217	5.134	30.495	1.00	27.73
	1648	N	TYR A 221	4.995	5.633	28.311	1.00	23.31
20	1649	CA	TYR A 221	3.550	5.782	28.360	1.00	21.83
	1650	CB	TYR A 221	3.151	7.214	27.981	1.00	17.51
	1651	CG	TYR A 221	1.666	7.401	27.809	1.00	20.23
	1652	CD1	TYR A 221	0.807	7.349	28.904	1.00	25.68
	1653	CE1	TYR A 221	-0.581	7.476	28.746	1.00	30.87
25	1654	CD2	TYR A 221	1.113	7.588	26.544	1.00	26.61
	1655	CE2	TYR A 221	-0.273	7.713	26.372	1.00	32.18
	1656	CZ	TYR A 221	-1.112	7.655	27.479	1.00	35.05
	1657	OH	TYR A 221	-2.475	7.762	27.315	1.00	38.11
	1658	C	TYR A 221	2.981	4.782	27.353	1.00	22.41
30	1659	O	TYR A 221	3.383	4.763	26.191	1.00	23.28
	1660	N	PHE A 222	2.066	3.932	27.799	1.00	24.60
	1661	CA	PHE A 222	1.485	2.956	26.893	1.00	25.33
	1662	CB	PHE A 222	1.839	1.527	27.337	1.00	22.58
	1663	CG	PHE A 222	3.319	1.222	27.299	1.00	25.69
35	1664	CD1	PHE A 222	4.110	1.390	28.429	1.00	26.52
	1665	CD2	PHE A 222	3.918	0.772	26.127	1.00	30.15
	1666	CE1	PHE A 222	5.473	1.112	28.393	1.00	25.08
	1667	CE2	PHE A 222	5.281	0.492	26.084	1.00	36.11
	1668	CZ	PHE A 222	6.058	0.662	27.220	1.00	30.23
40	1669	C	PHE A 222	-0.024	3.140	26.818	1.00	25.48
	1670	O	PHE A 222	-0.702	3.235	27.838	1.00	24.81
	1671	N	THR A 223	-0.543	3.207	25.599	1.00	27.43
	1672	CA	THR A 223	-1.964	3.393	25.393	1.00	29.24



	1673	CB	THR A 223	-2.255	4.769	24.785	1.00	30.96
	1674	OG1	THR A 223	-3.666	4.928	24.634	1.00	38.54
	1675	CG2	THR A 223	-1.592	4.908	23.423	1.00	18.62
	1676	C	THR A 223	-2.473	2.338	24.449	1.00	31.84
5	1677	O	THR A 223	-1.721	1.809	23.645	1.00	30.89
	1678	N	ASP A 224	-3.757	2.030	24.544	1.00	36.42
	1679	CA	ASP A 224	-4.357	1.032	23.671	1.00	40.14
	1680	CB	ASP A 224	-5.613	0.456	24.324	1.00	41.56
	1681	CG	ASP A 224	-5.297	-0.570	25.387	1.00	46.72
10	1682	OD1	ASP A 224	-6.215	-0.916	26.160	1.00	43.47
	1683	OD2	ASP A 224	-4.137	-1.037	25.441	1.00	54.57
	1684	C	ASP A 224	-4.709	1.610	22.301	1.00	40.48
	1685	O	ASP A 224	-4.489	0.968	21.271	1.00	42.72
	1686	N	THR A 225	-5.250	2.824	22.293	1.00	37.47
15	1687	CA	THR A 225	-5.639	3.470	21.047	1.00	37.52
	1688	CB	THR A 225	-5.820	5.007	21.223	1.00	32.35
	1689	OG1	THR A 225	-4.654	5.558	21.843	1.00	45.94
	1690	CG2	THR A 225	-7.056	5.316	22.074	1.00	27.82
	1691	C	THR A 225	-4.625	3.211	19.937	1.00	36.64
20	1692	O	THR A 225	-3.412	3.257	20.168	1.00	32.74
	1693	N	LEU A 226	-5.143	2.912	18.744	1.00	40.20
	1694	CA	LEU A 226	-4.319	2.649	17.572	1.00	37.95
	1695	CB	LEU A 226	-5.147	2.000	16.465	1.00	27.85
	1696	CG	LEU A 226	-5.704	0.614	16.768	1.00	16.92
25	1697	CD1	LEU A 226	-4.646	-0.162	17.523	1.00	20.23
	1698	CD2	LEU A 226	-6.971	0.719	17.595	1.00	16.92
	1699	C	LEU A 226	-3.732	3.955	17.074	1.00	34.39
	1700	O	LEU A 226	-4.371	4.999	17.151	1.00	33.65
	1701	N	TRP A 227	-2.518	3.886	16.545	1.00	27.74
30	1702	CA	TRP A 227	-1.833	5.075	16.084	1.00	26.44
	1703	CB	TRP A 227	-0.542	4.705	15.378	1.00	16.92
	1704	CG	TRP A 227	0.144	5.911	14.859	1.00	16.92
	1705	CD2	TRP A 227	0.690	6.983	15.634	1.00	24.25
	1706	CE2	TRP A 227	1.252	7.907	14.728	1.00	21.82
35	1707	CE3	TRP A 227	0.766	7.251	17.007	1.00	27.14
	1708	CD1	TRP A 227	0.383	6.220	13.554	1.00	16.92
	1709	NE1	TRP A 227	1.047	7.417	13.465	1.00	18.37
	1710	CZ2	TRP A 227	1.884	9.079	15.150	1.00	17.65
	1711	CZ3	TRP A 227	1.394	8.413	17.424	1.00	22.73
40	1712	CH2	TRP A 227	1.944	9.313	16.496	1.00	19.73
	1713	C	TRP A 227	-2.610	6.050	15.211	1.00	29.41
	1714	O	TRP A 227	-2.675	7.237	15.529	1.00	29.54
	1715	N	PRO A 228	-3.185	5.581	14.085	1.00	34.10

	1716	CD	PRO A 228	-3.065	4.256	13.450	1.00	32.12
	1717	CA	PRO A 228	-3.938	6.495	13.220	1.00	33.56
	1718	CB	PRO A 228	-4.498	5.573	12.154	1.00	30.46
	1719	CG	PRO A 228	-3.411	4.568	12.010	1.00	31.06
5	1720	C	PRO A 228	-5.024	7.232	13.975	1.00	36.50
	1721	O	PRO A 228	-5.559	8.224	13.489	1.00	39.78
	1722	N	ASP A 229	-5.338	6.739	15.170	1.00	38.84
	1723	CA	ASP A 229	-6.358	7.336	16.024	1.00	37.34
	1724	CB	ASP A 229	-7.158	6.234	16.732	1.00	34.82
10	1725	CG	ASP A 229	-8.247	5.649	15.864	1.00	34.97
	1726	OD1	ASP A 229	-8.868	4.651	16.279	1.00	49.11
	1727	OD2	ASP A 229	-8.497	6.188	14.771	1.00	48.81
	1728	C	ASP A 229	-5.743	8.258	17.075	1.00	35.86
	1729	O	ASP A 229	-6.459	8.814	17.901	1.00	38.47
15	1730	N	PHE A 230	-4.423	8.422	17.043	1.00	31.52
	1731	CA	PHE A 230	-3.732	9.257	18.026	1.00	29.58
	1732	CB	PHE A 230	-2.245	8.877	18.112	1.00	30.24
	1733	CG	PHE A 230	-1.656	8.990	19.507	1.00	39.74
	1734	CD1	PHE A 230	-2.055	8.123	20.521	1.00	35.52
20	1735	CD2	PHE A 230	-0.676	9.937	19.796	1.00	36.37
	1736	CE1	PHE A 230	-1.482	8.192	21.800	1.00	28.22
	1737	CE2	PHE A 230	-0.099	10.014	21.068	1.00	28.28
	1738	CZ	PHE A 230	-0.504	9.138	22.068	1.00	28.51
	1739	C	PHE A 230	-3.866	10.744	17.709	1.00	31.09
25	1740	O	PHE A 230	-3.033	11.327	17.011	1.00	31.82
	1741	N	ASP A 231	-4.924	11.343	18.246	1.00	30.72
	1742	CA	ASP A 231	-5.245	12.752	18.060	1.00	32.63
	1743	CB	ASP A 231	-6.742	12.955	18.305	1.00	35.43
	1744	CG	ASP A 231	-7.201	12.362	19.639	1.00	41.36
30	1745	OD1	ASP A 231	-8.426	12.353	19.910	1.00	51.61
	1746	OD2	ASP A 231	-6.333	11.905	20.422	1.00	31.99
	1747	C	ASP A 231	-4.443	13.634	19.011	1.00	36.99
	1748	O	ASP A 231	-3.603	13.145	19.766	1.00	37.67
	1749	N	GLU A 232	-4.709	14.938	18.960	1.00	40.17
35	1750	CA	GLU A 232	-4.033	15.898	19.822	1.00	36.69
	1751	CB	GLU A 232	-4.459	17.325	19.459	1.00	27.12
	1752	CG	GLU A 232	-3.880	18.399	20.370	1.00	35.46
	1753	CD	GLU A 232	-4.364	19.805	20.039	1.00	35.04
	1754	OE1	GLU A 232	-5.581	20.066	20.113	1.00	37.13
40	1755	OE2	GLU A 232	-3.525	20.662	19.709	1.00	31.43
	1756	C	GLU A 232	-4.389	15.595	21.275	1.00	35.17
	1757	O	GLU A 232	-3.542	15.670	22.160	1.00	34.55
	1758	N	ALA A 233	-5.646	15.237	21.514	1.00	34.03

	1759	CA	ALA A 233	-6.111	14.920	22.858	1.00	35.23
	1760	CB	ALA A 233	-7.558	14.475	22.803	1.00	30.01
	1761	C	ALA A 233	-5.252	13.836	23.507	1.00	39.77
	1762	O	ALA A 233	-4.779	13.989	24.633	1.00	45.65
5	1763	N	ALA A 234	-5.054	12.737	22.789	1.00	37.20
	1764	CA	ALA A 234	-4.253	11.632	23.288	1.00	36.19
	1765	CB	ALA A 234	-4.217	10.514	22.255	1.00	38.99
	1766	C	ALA A 234	-2.833	12.089	23.627	1.00	37.57
	1767	O	ALA A 234	-2.263	11.662	24.631	1.00	37.82
10	1768	N	LEU A 235	-2.261	12.951	22.789	1.00	34.88
	1769	CA	LEU A 235	-0.915	13.447	23.025	1.00	31.18
	1770	CB	LEU A 235	-0.473	14.383	21.903	1.00	16.92
	1771	CG	LEU A 235	1.028	14.580	21.629	1.00	16.92
	1772	CD1	LEU A 235	1.255	15.988	21.115	1.00	17.38
15	1773	CD2	LEU A 235	1.849	14.366	22.875	1.00	23.73
	1774	C	LEU A 235	-0.952	14.216	24.331	1.00	35.86
	1775	O	LEU A 235	-0.049	14.104	25.154	1.00	38.82
	1776	N	GLN A 236	-2.001	15.005	24.523	1.00	37.65
	1777	CA	GLN A 236	-2.133	15.774	25.752	1.00	38.39
20	1778	CB	GLN A 236	-3.398	16.635	25.696	1.00	50.00
	1779	CG	GLN A 236	-3.284	17.844	24.771	1.00	52.97
	1780	CD	GLN A 236	-4.594	18.605	24.620	1.00	59.21
	1781	OE1	GLN A 236	-4.610	19.738	24.136	1.00	62.28
	1782	NE2	GLN A 236	-5.699	17.983	25.026	1.00	61.76
25	1783	C	GLN A 236	-2.179	14.806	26.934	1.00	39.03
	1784	O	GLN A 236	-1.561	15.046	27.974	1.00	38.78
	1785	N	GLU A 237	-2.913	13.710	26.760	1.00	39.68
	1786	CA	GLU A 237	-3.022	12.675	27.786	1.00	35.56
	1787	CB	GLU A 237	-3.891	11.518	27.297	1.00	41.41
30	1788	CG	GLU A 237	-5.374	11.719	27.515	1.00	56.97
	1789	CD	GLU A 237	-5.777	11.498	28.960	1.00	67.71
	1790	OE1	GLU A 237	-5.188	12.151	29.846	1.00	76.95
	1791	OE2	GLU A 237	-6.682	10.673	29.209	1.00	81.30
	1792	C	GLU A 237	-1.631	12.151	28.096	1.00	29.79
35	1793	O	GLU A 237	-1.213	12.137	29.245	1.00	26.60
	1794	N	ALA A 238	-0.919	11.712	27.064	1.00	29.71
	1795	CA	ALA A 238	0.432	11.210	27.245	1.00	30.48
	1796	CB	ALA A 238	1.072	10.925	25.894	1.00	17.71
	1797	C	ALA A 238	1.253	12.247	27.993	1.00	32.85
40	1798	O	ALA A 238	1.990	11.916	28.918	1.00	39.01
	1799	N	ILE A 239	1.113	13.508	27.594	1.00	34.48
	1800	CA	ILE A 239	1.862	14.592	28.215	1.00	32.58
	1801	CB	ILE A 239	1.761	15.875	27.390	1.00	20.63

	1802	CG2	ILE A 239	2.309	17.057	28.188	1.00	31.10
	1803	CG1	ILE A 239	2.547	15.698	26.093	1.00	16.92
	1804	CD1	ILE A 239	2.717	16.967	25.299	1.00	28.23
	1805	C	ILE A 239	1.446	14.889	29.640	1.00	30.58
5	1806	O	ILE A 239	2.272	15.270	30.462	1.00	27.47
	1807	N	LEU A 240	0.165	14.745	29.934	1.00	30.48
	1808	CA	LEU A 240	-0.290	14.977	31.291	1.00	34.89
	1809	CB	LEU A 240	-1.816	14.989	31.356	1.00	48.13
	1810	CG	LEU A 240	-2.523	16.290	30.988	1.00	43.96
10	1811	CD1	LEU A 240	-4.015	16.091	31.098	1.00	40.59
	1812	CD2	LEU A 240	-2.077	17.399	31.918	1.00	43.57
	1813	C	LEU A 240	0.254	13.849	32.163	1.00	31.63
	1814	O	LEU A 240	0.977	14.086	33.130	1.00	33.47
	1815	N	ALA A 241	-0.088	12.618	31.800	1.00	33.00
15	1816	CA	ALA A 241	0.353	11.440	32.536	1.00	35.65
	1817	CB	ALA A 241	-0.309	10.188	31.965	1.00	36.36
	1818	C	ALA A 241	1.860	11.284	32.493	1.00	40.07
	1819	O	ALA A 241	2.374	10.215	32.789	1.00	43.62
	1820	N	TYR A 242	2.565	12.347	32.128	1.00	46.16
20	1821	CA	TYR A 242	4.018	12.297	32.036	1.00	49.44
	1822	CB	TYR A 242	4.550	13.607	31.461	1.00	42.71
	1823	CG	TYR A 242	6.049	13.671	31.333	1.00	37.89
	1824	CD1	TYR A 242	6.790	12.555	30.962	1.00	38.49
	1825	CE1	TYR A 242	8.173	12.630	30.821	1.00	37.07
25	1826	CD2	TYR A 242	6.724	14.863	31.557	1.00	33.74
	1827	CE2	TYR A 242	8.096	14.953	31.416	1.00	31.74
	1828	CZ	TYR A 242	8.817	13.840	31.050	1.00	33.16
	1829	OH	TYR A 242	10.181	13.954	30.909	1.00	32.83
	1830	C	TYR A 242	4.668	11.989	33.378	1.00	56.18
30	1831	O	TYR A 242	4.608	10.847	33.840	1.00	77.34
	1832	N	ASN A 243	5.294	12.978	34.010	1.00	62.00
	1833	CA	ASN A 243	5.936	12.715	35.296	1.00	65.83
	1834	CB	ASN A 243	6.915	13.836	35.662	1.00	65.24
	1835	CG	ASN A 243	8.271	13.304	36.118	1.00	65.31
35	1836	OD1	ASN A 243	8.971	12.630	35.366	1.00	63.84
	1837	ND2	ASN A 243	8.643	13.607	37.354	1.00	65.91
	1838	C	ASN A 243	4.857	12.567	36.367	1.00	69.21
	1839	O	ASN A 243	3.934	13.388	36.456	1.00	69.74
	1840	N	ARG A 244	4.971	11.499	37.159	1.00	68.62
40	1841	CA	ARG A 244	4.010	11.193	38.221	1.00	71.05
	1842	CB	ARG A 244	2.782	10.491	37.626	1.00	71.10
	1843	CG	ARG A 244	1.687	10.186	38.633	1.00	72.04
	1844	CD	ARG A 244	0.844	11.415	38.956	1.00	73.39

	1845	NE	ARG	A	244	-0.253	11.619	38.003	1.00	72.71
	1846	CZ	ARG	A	244	-0.133	12.167	36.794	1.00	71.35
	1847	NH1	ARG	A	244	1.049	12.590	36.350	1.00	69.95
	1848	NH2	ARG	A	244	-1.211	12.291	36.025	1.00	70.30
5	1849	C	ARG	A	244	4.637	10.298	39.301	1.00	73.21
	1850	OT	ARG	A	244	4.587	10.685	40.491	1.00	73.64
	1851	OXT	ARG	A	244	5.165	9.216	38.948	1.00	73.64
	1	CB	GLU	B	14	-7.567	-27.032	31.483	1.00	65.83
	2	CG	GLU	B	14	-7.608	-27.397	32.959	1.00	66.40
10	3	CD	GLU	B	14	-6.303	-27.060	33.682	1.00	67.15
	4	OE1	GLU	B	14	-6.175	-27.398	34.883	1.00	68.21
	5	OE2	GLU	B	14	-5.402	-26.456	33.054	1.00	66.67
	6	C	GLU	B	14	-6.401	-25.362	30.042	1.00	63.83
	7	O	GLU	B	14	-6.713	-25.766	28.922	1.00	63.93
15	8	N	GLU	B	14	-8.653	-24.853	31.019	1.00	67.24
	9	CA	GLU	B	14	-7.346	-25.541	31.225	1.00	65.39
	10	N	VAL	B	15	-5.238	-24.767	30.299	1.00	48.09
	11	CA	VAL	B	15	-4.257	-24.523	29.244	1.00	46.83
	12	CB	VAL	B	15	-4.816	-23.505	28.199	1.00	46.56
20	13	CG1	VAL	B	15	-5.308	-22.250	28.906	1.00	51.75
	14	CG2	VAL	B	15	-3.749	-23.144	27.174	1.00	50.29
	15	C	VAL	B	15	-2.908	-24.023	29.767	1.00	43.02
	16	O	VAL	B	15	-2.812	-23.367	30.815	1.00	43.85
	17	N	PRO	B	16	-1.839	-24.349	29.042	1.00	43.32
25	18	CD	PRO	B	16	-1.762	-25.424	28.043	1.00	43.32
	19	CA	PRO	B	16	-0.502	-23.921	29.444	1.00	45.94
	20	CB	PRO	B	16	0.412	-24.872	28.673	1.00	46.50
	21	CG	PRO	B	16	-0.468	-26.072	28.407	1.00	46.71
	22	C	PRO	B	16	-0.261	-22.466	29.060	1.00	46.22
30	23	O	PRO	B	16	-0.952	-21.912	28.200	1.00	44.84
	24	N	THR	B	17	0.730	-21.854	29.694	1.00	47.29
	25	CA	THR	B	17	1.053	-20.468	29.406	1.00	43.32
	26	CB	THR	B	17	0.862	-19.591	30.631	1.00	39.41
	27	OG1	THR	B	17	-0.432	-19.839	31.193	1.00	43.75
35	28	CG2	THR	B	17	0.995	-18.121	30.249	1.00	37.92
	29	C	THR	B	17	2.497	-20.319	28.998	1.00	41.03
	30	O	THR	B	17	3.375	-20.974	29.569	1.00	43.88
	31	N	GLN	B	18	2.749	-19.465	28.011	1.00	41.44
	32	CA	GLN	B	18	4.121	-19.221	27.597	1.00	41.88
40	33	CB	GLN	B	18	4.201	-18.107	26.550	1.00	46.62
	34	CG	GLN	B	18	3.646	-18.426	25.176	1.00	52.25
	35	CD	GLN	B	18	4.106	-17.423	24.126	1.00	57.97
	36	OE1	GLN	B	18	5.296	-17.325	23.820	1.00	58.34

	37	NE2	GLN	B	18	3.164	-16.672	23.575	1.00	52.89
	38	C	GLN	B	18	4.782	-18.733	28.880	1.00	39.78
	39	O	GLN	B	18	4.228	-17.871	29.575	1.00	34.46
	40	N	VAL	B	19	5.944	-19.283	29.209	1.00	41.79
5	41	CA	VAL	B	19	6.636	-18.869	30.422	1.00	43.01
	42	CB	VAL	B	19	6.737	-20.036	31.442	1.00	43.44
	43	CG1	VAL	B	19	7.393	-21.241	30.800	1.00	47.93
	44	CG2	VAL	B	19	7.526	-19.595	32.661	1.00	37.93
	45	C	VAL	B	19	8.031	-18.343	30.097	1.00	41.23
10	46	O	VAL	B	19	8.857	-19.055	29.529	1.00	42.44
	47	N	PRO	B	20	8.310	-17.077	30.456	1.00	40.76
	48	CD	PRO	B	20	7.467	-16.218	31.305	1.00	38.76
	49	CA	PRO	B	20	9.605	-16.435	30.206	1.00	38.00
	50	CB	PRO	B	20	9.500	-15.127	30.993	1.00	36.72
15	51	CG	PRO	B	20	8.495	-15.447	32.065	1.00	35.57
	52	C	PRO	B	20	10.809	-17.272	30.620	1.00	35.22
	53	O	PRO	B	20	10.880	-17.750	31.746	1.00	32.45
	54	N	ALA	B	21	11.753	-17.439	29.700	1.00	30.30
	55	CA	ALA	B	21	12.950	-18.220	29.970	1.00	23.48
20	56	CB	ALA	B	21	13.571	-18.661	28.663	1.00	21.08
	57	C	ALA	B	21	13.965	-17.432	30.800	1.00	22.21
	58	O	ALA	B	21	14.627	-17.982	31.679	1.00	24.75
	59	N	HIS	B	22	14.096	-16.144	30.499	1.00	22.28
	60	CA	HIS	B	22	15.003	-15.271	31.229	1.00	23.83
25	61	CB	HIS	B	22	16.168	-14.817	30.348	1.00	17.45
	62	CG	HIS	B	22	17.110	-13.876	31.033	1.00	22.21
	63	CD2	HIS	B	22	16.976	-13.135	32.160	1.00	18.61
	64	ND1	HIS	B	22	18.376	-13.611	30.554	1.00	22.86
	65	CE1	HIS	B	22	18.980	-12.751	31.356	1.00	27.15
30	66	NE2	HIS	B	22	18.152	-12.445	32.340	1.00	23.08
	67	C	HIS	B	22	14.170	-14.080	31.636	1.00	24.54
	68	O	HIS	B	22	13.510	-13.471	30.802	1.00	24.16
	69	N	ILE	B	23	14.188	-13.758	32.924	1.00	25.14
	70	CA	ILE	B	23	13.409	-12.644	33.423	1.00	23.91
35	71	CB	ILE	B	23	12.379	-13.091	34.482	1.00	16.92
	72	CG2	ILE	B	23	11.657	-11.879	35.040	1.00	16.92
	73	CG1	ILE	B	23	11.354	-14.041	33.852	1.00	16.92
	74	CD1	ILE	B	23	10.240	-14.494	34.799	1.00	16.92
	75	C	ILE	B	23	14.275	-11.574	34.039	1.00	25.13
40	76	O	ILE	B	23	15.220	-11.871	34.760	1.00	27.80
	77	N	GLY	B	24	13.940	-10.323	33.735	1.00	25.44
	78	CA	GLY	B	24	14.667	-9.198	34.280	1.00	27.69
	79	C	GLY	B	24	13.802	-8.587	35.359	1.00	29.71

	80	O	GLY B	24	12.613	-8.354	35.146	1.00	29.35
	81	N	ILE B	25	14.376	-8.344	36.530	1.00	29.96
	82	CA	ILE B	25	13.597	-7.755	37.600	1.00	32.73
	83	CB	ILE B	25	13.376	-8.743	38.741	1.00	32.52
5	84	CG2	ILE B	25	12.382	-8.167	39.735	1.00	38.35
	85	CG1	ILE B	25	12.846	-10.055	38.180	1.00	29.69
	86	CD1	ILE B	25	12.368	-11.013	39.227	1.00	34.05
	87	C	ILE B	25	14.239	-6.516	38.179	1.00	34.24
	88	O	ILE B	25	15.373	-6.557	38.655	1.00	40.45
10	89	N	ILE B	26	13.506	-5.408	38.114	1.00	32.06
	90	CA	ILE B	26	13.955	-4.132	38.666	1.00	33.80
	91	CB	ILE B	26	13.754	-2.969	37.661	1.00	32.81
	92	CG2	ILE B	26	14.178	-1.662	38.291	1.00	24.54
	93	CG1	ILE B	26	14.567	-3.222	36.393	1.00	30.96
15	94	CD1	ILE B	26	14.390	-2.160	35.334	1.00	34.97
	95	C	ILE B	26	13.054	-3.915	39.885	1.00	36.67
	96	O	ILE B	26	11.920	-3.434	39.757	1.00	33.26
	97	N	MET B	27	13.553	-4.285	41.064	1.00	39.29
	98	CA	MET B	27	12.756	-4.165	42.274	1.00	40.87
20	99	CB	MET B	27	13.196	-5.198	43.324	1.00	36.66
	100	CG	MET B	27	14.684	-5.327	43.596	1.00	33.29
	101	SD	MET B	27	15.109	-7.089	43.851	1.00	28.20
	102	CE	MET B	27	16.507	-7.243	42.803	1.00	29.62
	103	C	MET B	27	12.687	-2.787	42.884	1.00	41.49
25	104	O	MET B	27	13.707	-2.156	43.172	1.00	44.33
	105	N	ASP B	28	11.448	-2.333	43.057	1.00	38.82
	106	CA	ASP B	28	11.135	-1.030	43.624	1.00	37.15
	107	CB	ASP B	28	10.613	-0.088	42.536	1.00	36.09
	108	CG	ASP B	28	11.704	0.755	41.931	1.00	37.61
30	109	OD1	ASP B	28	12.621	0.189	41.305	1.00	40.92
	110	OD2	ASP B	28	11.646	1.990	42.091	1.00	43.44
	111	C	ASP B	28	10.071	-1.183	44.696	1.00	37.00
	112	O	ASP B	28	9.342	-2.176	44.716	1.00	40.30
	113	N	GLY B	29	9.989	-0.198	45.584	1.00	32.98
35	114	CA	GLY B	29	8.997	-0.237	46.639	1.00	31.71
	115	C	GLY B	29	9.576	-0.501	48.012	1.00	34.52
	116	O	GLY B	29	8.905	-0.295	49.015	1.00	35.45
	117	N	ASN B	30	10.822	-0.959	48.061	1.00	35.21
	118	CA	ASN B	30	11.479	-1.259	49.322	1.00	34.55
40	119	CB	ASN B	30	12.982	-1.388	49.101	1.00	21.98
	120	CG	ASN B	30	13.372	-2.739	48.528	1.00	23.62
	121	OD1	ASN B	30	14.537	-2.979	48.222	1.00	20.30
	122	ND2	ASN B	30	12.397	-3.634	48.392	1.00	20.74

	123	C	ASN	B	30	11.195	-0.224	50.395	1.00	38.93
	124	O	ASN	B	30	10.527	-0.521	51.381	1.00	42.50
	125	N	GLY	B	31	11.693	0.992	50.199	1.00	38.13
	126	CA	GLY	B	31	11.481	2.053	51.173	1.00	37.44
5	127	C	GLY	B	31	10.033	2.484	51.353	1.00	37.86
	128	O	GLY	B	31	9.592	2.784	52.460	1.00	33.07
	129	N	ARG	B	32	9.291	2.532	50.256	1.00	41.86
	130	CA	ARG	B	32	7.890	2.920	50.300	1.00	43.79
	131	CB	ARG	B	32	7.331	2.969	48.876	1.00	50.98
10	132	CG	ARG	B	32	5.999	3.679	48.722	1.00	67.82
	133	CD	ARG	B	32	5.606	3.727	47.254	1.00	72.94
	134	NE	ARG	B	32	4.186	4.006	47.062	1.00	79.64
	135	CZ	ARG	B	32	3.538	3.824	45.914	1.00	90.52
	136	NH1	ARG	B	32	4.186	3.365	44.849	1.00	100.13
15	137	NH2	ARG	B	32	2.241	4.091	45.830	1.00	94.94
	138	C	ARG	B	32	7.171	1.867	51.135	1.00	41.07
	139	O	ARG	B	32	6.348	2.194	51.983	1.00	39.65
	140	N	TRP	B	33	7.510	0.605	50.885	1.00	39.29
	141	CA	TRP	B	33	6.948	-0.546	51.593	1.00	37.27
20	142	CB	TRP	B	33	7.593	-1.834	51.081	1.00	28.51
	143	CG	TRP	B	33	7.184	-3.076	51.818	1.00	29.95
	144	CD2	TRP	B	33	7.882	-3.701	52.900	1.00	34.19
	145	CE2	TRP	B	33	7.137	-4.836	53.277	1.00	29.68
	146	CE3	TRP	B	33	9.065	-3.407	53.590	1.00	47.07
25	147	CD1	TRP	B	33	6.076	-3.835	51.592	1.00	35.81
	148	NE1	TRP	B	33	6.040	-4.896	52.462	1.00	31.40
	149	CZ2	TRP	B	33	7.536	-5.684	54.316	1.00	27.96
	150	CZ3	TRP	B	33	9.460	-4.251	54.624	1.00	47.40
	151	CH2	TRP	B	33	8.696	-5.375	54.976	1.00	33.44
30	152	C	TRP	B	33	7.230	-0.428	53.085	1.00	35.31
	153	O	TRP	B	33	6.345	-0.603	53.918	1.00	35.16
	154	N	ALA	B	34	8.485	-0.151	53.408	1.00	30.64
	155	CA	ALA	B	34	8.907	-0.006	54.791	1.00	26.94
	156	CB	ALA	B	34	10.420	0.130	54.849	1.00	21.71
35	157	C	ALA	B	34	8.249	1.214	55.431	1.00	29.54
	158	O	ALA	B	34	7.619	1.118	56.487	1.00	30.57
	159	N	LYS	B	35	8.397	2.359	54.773	1.00	30.23
	160	CA	LYS	B	35	7.851	3.612	55.263	1.00	32.86
	161	CB	LYS	B	35	8.129	4.725	54.249	1.00	42.27
40	162	CG	LYS	B	35	8.577	6.048	54.859	1.00	58.11
	163	CD	LYS	B	35	8.488	7.167	53.834	1.00	74.59
	164	CE	LYS	B	35	7.059	7.302	53.311	1.00	85.25
	165	NZ	LYS	B	35	6.928	8.270	52.191	1.00	84.42



	166	C	LYS	B	35	6.353	3.523	55.551	1.00	38.17
	167	O	LYS	B	35	5.835	4.257	56.390	1.00	41.62
	168	N	LYS	B	36	5.652	2.624	54.870	1.00	41.65
	169	CA	LYS	B	36	4.219	2.498	55.094	1.00	43.49
5	170	CB	LYS	B	36	3.519	1.935	53.850	1.00	52.09
	171	CG	LYS	B	36	3.680	0.428	53.648	1.00	61.96
	172	CD	LYS	B	36	2.834	-0.098	52.468	1.00	65.82
	173	CE	LYS	B	36	2.974	-1.623	52.289	1.00	62.88
	174	NZ	LYS	B	36	2.084	-2.191	51.225	1.00	66.92
10	175	C	LYS	B	36	3.926	1.613	56.300	1.00	44.16
	176	O	LYS	B	36	2.857	1.706	56.895	1.00	46.34
	177	N	ARG	B	37	4.877	0.762	56.668	1.00	44.81
	178	CA	ARG	B	37	4.691	-0.129	57.803	1.00	46.91
	179	CB	ARG	B	37	5.305	-1.498	57.521	1.00	54.16
15	180	CG	ARG	B	37	4.652	-2.223	56.372	1.00	51.20
	181	CD	ARG	B	37	5.258	-3.588	56.141	1.00	52.57
	182	NE	ARG	B	37	4.915	-4.074	54.808	1.00	61.49
	183	CZ	ARG	B	37	3.675	-4.307	54.387	1.00	65.32
	184	NH1	ARG	B	37	2.653	-4.107	55.206	1.00	68.41
20	185	NH2	ARG	B	37	3.454	-4.713	53.140	1.00	59.01
	186	C	ARG	B	37	5.280	0.418	59.087	1.00	46.38
	187	O	ARG	B	37	5.519	-0.331	60.024	1.00	45.99
	188	N	MET	B	38	5.526	1.721	59.135	1.00	46.89
	189	CA	MET	B	38	6.069	2.346	60.338	1.00	49.02
25	190	CB	MET	B	38	5.216	1.987	61.564	1.00	46.95
	191	CG	MET	B	38	3.709	2.133	61.400	1.00	54.51
	192	SD	MET	B	38	3.148	3.835	61.214	1.00	62.23
	193	CE	MET	B	38	3.372	4.473	62.901	1.00	68.23
	194	C	MET	B	38	7.517	1.960	60.652	1.00	49.28
30	195	O	MET	B	38	8.062	2.406	61.662	1.00	50.06
	196	N	GLN	B	39	8.148	1.139	59.821	1.00	49.00
	197	CA	GLN	B	39	9.521	0.750	60.118	1.00	48.43
	198	CB	GLN	B	39	9.673	-0.769	60.007	1.00	40.73
	199	CG	GLN	B	39	8.855	-1.431	58.920	1.00	51.03
35	200	CD	GLN	B	39	8.846	-2.945	59.070	1.00	54.07
	201	OE1	GLN	B	39	9.897	-3.586	59.055	1.00	57.42
	202	NE2	GLN	B	39	7.656	-3.520	59.225	1.00	38.98
	203	C	GLN	B	39	10.589	1.455	59.298	1.00	50.38
	204	O	GLN	B	39	10.310	2.002	58.239	1.00	52.17
40	205	N	PRO	B	40	11.837	1.455	59.792	1.00	51.48
	206	CD	PRO	B	40	12.308	0.759	61.004	1.00	50.84
	207	CA	PRO	B	40	12.958	2.100	59.108	1.00	49.78
	208	CB	PRO	B	40	14.174	1.500	59.810	1.00	50.09

	209	CG	PRO	B	40	13.700	1.333	61.197	1.00	50.00
	210	C	PRO	B	40	12.980	1.852	57.609	1.00	46.59
	211	O	PRO	B	40	13.026	0.716	57.157	1.00	44.73
	212	N	ARG	B	41	12.941	2.927	56.843	1.00	44.90
5	213	CA	ARG	B	41	12.983	2.835	55.396	1.00	46.18
	214	CB	ARG	B	41	13.440	4.185	54.833	1.00	48.57
	215	CG	ARG	B	41	13.629	4.274	53.318	1.00	54.03
	216	CD	ARG	B	41	14.399	5.551	52.960	1.00	54.03
	217	NE	ARG	B	41	13.591	6.673	52.454	1.00	58.63
10	218	CZ	ARG	B	41	12.407	7.078	52.928	1.00	55.36
	219	NH1	ARG	B	41	11.820	6.454	53.945	1.00	56.78
	220	NH2	ARG	B	41	11.816	8.145	52.397	1.00	41.95
	221	C	ARG	B	41	13.968	1.735	54.998	1.00	49.28
	222	O	ARG	B	41	13.690	0.912	54.124	1.00	51.60
15	223	N	VAL	B	42	15.110	1.713	55.674	1.00	46.21
	224	CA	VAL	B	42	16.178	0.757	55.390	1.00	45.66
	225	CB	VAL	B	42	17.439	1.116	56.248	1.00	36.84
	226	CG1	VAL	B	42	17.513	0.234	57.479	1.00	30.96
	227	CG2	VAL	B	42	18.706	1.024	55.403	1.00	31.91
20	228	C	VAL	B	42	15.831	-0.744	55.536	1.00	49.01
	229	O	VAL	B	42	16.461	-1.591	54.901	1.00	53.47
	230	N	PHE	B	43	14.840	-1.078	56.360	1.00	46.72
	231	CA	PHE	B	43	14.455	-2.483	56.532	1.00	44.27
	232	CB	PHE	B	43	13.378	-2.646	57.610	1.00	37.66
25	233	CG	PHE	B	43	13.904	-2.642	59.017	1.00	36.94
	234	CD1	PHE	B	43	15.273	-2.694	59.276	1.00	36.78
	235	CD2	PHE	B	43	13.018	-2.601	60.095	1.00	39.68
	236	CE1	PHE	B	43	15.750	-2.702	60.589	1.00	29.77
	237	CE2	PHE	B	43	13.484	-2.611	61.406	1.00	31.31
30	238	CZ	PHE	B	43	14.853	-2.661	61.653	1.00	29.07
	239	C	PHE	B	43	13.894	-3.020	55.230	1.00	46.39
	240	O	PHE	B	43	14.177	-4.156	54.843	1.00	46.33
	241	N	GLY	B	44	13.083	-2.189	54.576	1.00	46.54
	242	CA	GLY	B	44	12.458	-2.555	53.316	1.00	43.50
35	243	C	GLY	B	44	13.381	-3.356	52.426	1.00	40.10
	244	O	GLY	B	44	12.959	-4.306	51.766	1.00	40.32
	245	N	HIS	B	45	14.649	-2.969	52.413	1.00	33.52
	246	CA	HIS	B	45	15.636	-3.662	51.614	1.00	30.60
	247	CB	HIS	B	45	16.964	-2.919	51.679	1.00	16.92
40	248	CG	HIS	B	45	16.942	-1.595	50.981	1.00	28.29
	249	CD2	HIS	B	45	17.815	-1.027	50.116	1.00	34.82
	250	ND1	HIS	B	45	15.934	-0.675	51.165	1.00	34.82
	251	CE1	HIS	B	45	16.187	0.405	50.446	1.00	39.36

	252	NE2	HIS	B	45	17.325	0.217	49.800	1.00	40.10
	253	C	HIS	B	45	15.798	-5.109	52.071	1.00	34.04
	254	O	HIS	B	45	15.837	-6.011	51.239	1.00	33.04
	255	N	LYS	B	46	15.881	-5.354	53.376	1.00	37.67
5	256	CA	LYS	B	46	16.018	-6.734	53.821	1.00	36.56
	257	CB	LYS	B	46	16.052	-6.850	55.337	1.00	27.77
	258	CG	LYS	B	46	16.277	-8.288	55.800	1.00	36.67
	259	CD	LYS	B	46	16.525	-8.385	57.301	1.00	47.11
	260	CE	LYS	B	46	17.756	-7.581	57.721	1.00	45.30
10	261	NZ	LYS	B	46	17.972	-7.582	59.198	1.00	54.67
	262	C	LYS	B	46	14.823	-7.497	53.296	1.00	35.24
	263	O	LYS	B	46	14.970	-8.572	52.714	1.00	34.48
	264	N	ALA	B	47	13.637	-6.929	53.497	1.00	34.22
	265	CA	ALA	B	47	12.404	-7.552	53.019	1.00	33.65
15	266	CB	ALA	B	47	11.205	-6.669	53.346	1.00	22.25
	267	C	ALA	B	47	12.493	-7.785	51.506	1.00	33.26
	268	O	ALA	B	47	12.057	-8.822	51.001	1.00	35.94
	269	N	GLY	B	48	13.048	-6.812	50.787	1.00	31.73
	270	CA	GLY	B	48	13.192	-6.973	49.360	1.00	31.22
20	271	C	GLY	B	48	13.881	-8.307	49.194	1.00	28.17
	272	O	GLY	B	48	13.376	-9.202	48.520	1.00	30.21
	273	N	MET	B	49	15.027	-8.448	49.848	1.00	26.41
	274	CA	MET	B	49	15.801	-9.677	49.787	1.00	26.13
	275	CB	MET	B	49	17.005	-9.594	50.735	1.00	26.11
25	276	CG	MET	B	49	17.778	-10.911	50.907	1.00	31.14
	277	SD	MET	B	49	19.315	-10.778	51.891	1.00	30.86
	278	CE	MET	B	49	18.675	-10.085	53.433	1.00	27.72
	279	C	MET	B	49	14.951	-10.894	50.128	1.00	26.86
	280	O	MET	B	49	15.075	-11.936	49.493	1.00	25.74
30	281	N	GLU	B	50	14.087	-10.773	51.128	1.00	26.86
	282	CA	GLU	B	50	13.237	-11.896	51.495	1.00	29.13
	283	CB	GLU	B	50	12.354	-11.527	52.680	1.00	35.38
	284	CG	GLU	B	50	13.166	-11.100	53.881	1.00	42.20
	285	CD	GLU	B	50	12.729	-11.778	55.161	1.00	55.85
35	286	OE1	GLU	B	50	12.645	-13.028	55.166	1.00	54.70
	287	OE2	GLU	B	50	12.483	-11.058	56.160	1.00	62.59
	288	C	GLU	B	50	12.380	-12.318	50.308	1.00	33.72
	289	O	GLU	B	50	12.349	-13.491	49.937	1.00	40.50
	290	N	ALA	B	51	11.690	-11.363	49.700	1.00	30.97
40	291	CA	ALA	B	51	10.863	-11.686	48.551	1.00	29.01
	292	CB	ALA	B	51	10.080	-10.470	48.108	1.00	33.60
	293	C	ALA	B	51	11.741	-12.187	47.414	1.00	28.16
	294	O	ALA	B	51	11.291	-12.981	46.599	1.00	28.15

	295	N	LEU	B	52	12.989	-11.729	47.350	1.00	26.73
	296	CA	LEU	B	52	13.871	-12.182	46.283	1.00	26.65
	297	CB	LEU	B	52	15.269	-11.582	46.415	1.00	16.92
	298	CG	LEU	B	52	16.111	-11.451	45.134	1.00	16.92
5	299	CD1	LEU	B	52	17.580	-11.336	45.515	1.00	16.92
	300	CD2	LEU	B	52	15.919	-12.650	44.221	1.00	22.52
	301	C	LEU	B	52	13.970	-13.691	46.394	1.00	32.69
	302	O	LEU	B	52	13.887	-14.399	45.393	1.00	34.28
	303	N	GLN	B	53	14.138	-14.174	47.625	1.00	32.34
10	304	CA	GLN	B	53	14.247	-15.608	47.894	1.00	28.24
	305	CB	GLN	B	53	14.446	-15.866	49.386	1.00	22.43
	306	CG	GLN	B	53	14.716	-17.328	49.719	1.00	16.92
	307	CD	GLN	B	53	16.175	-17.707	49.539	1.00	16.92
	308	OE1	GLN	B	53	16.922	-17.042	48.819	1.00	26.60
15	309	NE2	GLN	B	53	16.584	-18.785	50.190	1.00	16.92
	310	C	GLN	B	53	12.990	-16.335	47.436	1.00	31.47
	311	O	GLN	B	53	13.063	-17.377	46.792	1.00	30.88
	312	N	THR	B	54	11.840	-15.777	47.789	1.00	32.71
	313	CA	THR	B	54	10.550	-16.339	47.418	1.00	29.40
20	314	CB	THR	B	54	9.417	-15.508	47.985	1.00	22.85
	315	OG1	THR	B	54	9.443	-15.579	49.414	1.00	33.45
	316	CG2	THR	B	54	8.082	-16.000	47.447	1.00	16.92
	317	C	THR	B	54	10.357	-16.373	45.916	1.00	32.23
	318	O	THR	B	54	9.987	-17.399	45.358	1.00	35.38
25	319	N	VAL	B	55	10.582	-15.238	45.267	1.00	33.35
	320	CA	VAL	B	55	10.420	-15.143	43.824	1.00	32.18
	321	CB	VAL	B	55	10.600	-13.679	43.326	1.00	26.17
	322	CG1	VAL	B	55	10.591	-13.631	41.814	1.00	16.92
	323	CG2	VAL	B	55	9.480	-12.809	43.860	1.00	28.32
30	324	C	VAL	B	55	11.418	-16.037	43.111	1.00	32.33
	325	O	VAL	B	55	11.038	-16.831	42.253	1.00	31.60
	326	N	THR	B	56	12.690	-15.912	43.479	1.00	31.81
	327	CA	THR	B	56	13.752	-16.698	42.862	1.00	36.75
	328	CB	THR	B	56	15.119	-16.341	43.487	1.00	33.23
35	329	OG1	THR	B	56	16.174	-16.929	42.718	1.00	35.26
	330	CG2	THR	B	56	15.204	-16.857	44.905	1.00	48.73
	331	C	THR	B	56	13.486	-18.204	42.991	1.00	40.46
	332	O	THR	B	56	13.852	-18.991	42.123	1.00	43.12
	333	N	LYS	B	57	12.833	-18.590	44.079	1.00	42.26
40	334	CA	LYS	B	57	12.503	-19.986	44.342	1.00	43.45
	335	CB	LYS	B	57	12.229	-20.150	45.836	1.00	47.22
	336	CG	LYS	B	57	12.508	-21.512	46.413	1.00	47.96
	337	CD	LYS	B	57	12.483	-21.430	47.932	1.00	49.91

	338	CE	LYS B	57	11.172	-20.838	48.431	1.00	55.23
	339	NZ	LYS B	57	11.143	-20.634	49.907	1.00	63.19
	340	C	LYS B	57	11.259	-20.335	43.523	1.00	44.75
	341	O	LYS B	57	11.263	-21.268	42.724	1.00	48.17
5	342	N	ALA B	58	10.198	-19.566	43.724	1.00	44.02
	343	CA	ALA B	58	8.952	-19.767	43.004	1.00	45.02
	344	CB	ALA B	58	8.020	-18.608	43.269	1.00	31.05
	345	C	ALA B	58	9.216	-19.879	41.512	1.00	45.60
	346	O	ALA B	58	8.684	-20.754	40.841	1.00	47.49
10	347	N	ALA B	59	10.044	-18.978	40.999	1.00	43.55
	348	CA	ALA B	59	10.381	-18.949	39.581	1.00	44.39
	349	CB	ALA B	59	11.187	-17.701	39.269	1.00	36.73
	350	C	ALA B	59	11.158	-20.182	39.164	1.00	48.03
	351	O	ALA B	59	11.173	-20.549	37.993	1.00	49.73
15	352	N	ASN B	60	11.809	-20.820	40.130	1.00	50.14
	353	CA	ASN B	60	12.600	-22.014	39.854	1.00	50.72
	354	CB	ASN B	60	13.591	-22.261	40.998	1.00	56.81
	355	CG	ASN B	60	14.507	-23.437	40.737	1.00	59.09
	356	OD1	ASN B	60	15.222	-23.477	39.738	1.00	50.39
20	357	ND2	ASN B	60	14.493	-24.403	41.645	1.00	68.87
	358	C	ASN B	60	11.709	-23.238	39.660	1.00	48.92
	359	O	ASN B	60	11.954	-24.055	38.769	1.00	49.57
	360	N	LYS B	61	10.671	-23.353	40.489	1.00	44.16
	361	CA	LYS B	61	9.749	-24.477	40.403	1.00	42.23
25	362	CB	LYS B	61	8.810	-24.502	41.608	1.00	38.81
	363	CG	LYS B	61	7.504	-23.750	41.382	1.00	49.61
	364	CD	LYS B	61	6.440	-24.149	42.397	1.00	61.71
	365	CE	LYS B	61	5.080	-23.562	42.030	1.00	76.26
	366	NZ	LYS B	61	3.992	-23.993	42.958	1.00	77.30
30	367	C	LYS B	61	8.910	-24.362	39.143	1.00	41.26
	368	O	LYS B	61	8.286	-25.321	38.702	1.00	38.34
	369	N	LEU B	62	8.894	-23.170	38.570	1.00	43.33
	370	CA	LEU B	62	8.107	-22.921	37.379	1.00	40.43
	371	CB	LEU B	62	7.451	-21.541	37.478	1.00	41.05
35	372	CG	LEU B	62	6.153	-21.307	36.709	1.00	43.45
	373	CD1	LEU B	62	5.121	-22.374	37.061	1.00	49.97
	374	CD2	LEU B	62	5.626	-19.933	37.055	1.00	41.95
	375	C	LEU B	62	8.960	-23.026	36.124	1.00	37.78
	376	O	LEU B	62	8.490	-22.753	35.027	1.00	36.77
40	377	N	GLY B	63	10.219	-23.404	36.292	1.00	34.00
	378	CA	GLY B	63	11.087	-23.573	35.142	1.00	34.47
	379	C	GLY B	63	11.736	-22.368	34.483	1.00	34.70
	380	O	GLY B	63	12.311	-22.494	33.400	1.00	37.15

	381	N	VAL B	64	11.649	-21.194	35.085	1.00	32.50
	382	CA	VAL B	64	12.307	-20.051	34.475	1.00	33.85
	383	CB	VAL B	64	12.074	-18.780	35.297	1.00	38.31
	384	CG1	VAL B	64	12.953	-17.652	34.783	1.00	45.70
5	385	CG2	VAL B	64	10.611	-18.390	35.224	1.00	30.49
	386	C	VAL B	64	13.798	-20.376	34.449	1.00	32.11
	387	O	VAL B	64	14.384	-20.691	35.478	1.00	35.71
	388	N	LYS B	65	14.412	-20.317	33.277	1.00	30.11
	389	CA	LYS B	65	15.830	-20.629	33.178	1.00	32.19
10	390	CB	LYS B	65	16.276	-20.642	31.720	1.00	34.45
	391	CG	LYS B	65	16.629	-22.024	31.194	1.00	28.19
	392	CD	LYS B	65	15.416	-22.950	31.165	1.00	32.70
	393	CE	LYS B	65	15.722	-24.264	30.438	1.00	50.92
	394	NZ	LYS B	65	16.090	-24.081	28.994	1.00	60.18
15	395	C	LYS B	65	16.738	-19.695	33.963	1.00	32.24
	396	O	LYS B	65	17.634	-20.152	34.667	1.00	32.31
	397	N	VAL B	66	16.515	-18.389	33.843	1.00	29.19
	398	CA	VAL B	66	17.342	-17.402	34.547	1.00	27.66
	399	CB	VAL B	66	18.647	-17.103	33.727	1.00	30.38
20	400	CG1	VAL B	66	18.369	-17.285	32.254	1.00	29.01
	401	CG2	VAL B	66	19.170	-15.681	34.002	1.00	16.92
	402	C	VAL B	66	16.623	-16.087	34.846	1.00	22.57
	403	O	VAL B	66	15.637	-15.758	34.199	1.00	18.50
	404	N	ILE B	67	17.099	-15.360	35.855	1.00	23.89
25	405	CA	ILE B	67	16.533	-14.054	36.196	1.00	31.24
	406	CB	ILE B	67	15.389	-14.129	37.259	1.00	30.49
	407	CG2	ILE B	67	14.278	-15.044	36.761	1.00	32.00
	408	CG1	ILE B	67	15.920	-14.612	38.604	1.00	35.49
	409	CD1	ILE B	67	14.844	-14.690	39.664	1.00	44.48
30	410	C	ILE B	67	17.628	-13.112	36.685	1.00	32.32
	411	O	ILE B	67	18.497	-13.490	37.483	1.00	36.35
	412	N	THR B	68	17.589	-11.890	36.160	1.00	27.06
	413	CA	THR B	68	18.553	-10.854	36.497	1.00	22.58
	414	CB	THR B	68	19.178	-10.256	35.239	1.00	20.26
35	415	OG1	THR B	68	19.880	-11.283	34.524	1.00	31.06
	416	CG2	THR B	68	20.128	-9.135	35.606	1.00	16.92
	417	C	THR B	68	17.854	-9.756	37.281	1.00	26.08
	418	O	THR B	68	17.017	-9.027	36.751	1.00	28.24
	419	N	VAL B	69	18.210	-9.663	38.557	1.00	25.72
40	420	CA	VAL B	69	17.631	-8.698	39.475	1.00	22.44
	421	CB	VAL B	69	17.459	-9.329	40.845	1.00	20.89
	422	CG1	VAL B	69	16.430	-10.430	40.788	1.00	16.92
	423	CG2	VAL B	69	18.784	-9.901	41.301	1.00	16.92

	424	C	VAL	B	69	18.536	-7.495	39.614	1.00	23.00
	425	O	VAL	B	69	19.720	-7.635	39.923	1.00	23.85
	426	N	TYR	B	70	17.977	-6.313	39.375	1.00	25.89
	427	CA	TYR	B	70	18.732	-5.066	39.489	1.00	26.71
5	428	CB	TYR	B	70	17.978	-3.926	38.798	1.00	22.08
	429	CG	TYR	B	70	18.861	-2.795	38.312	1.00	16.92
	430	CD1	TYR	B	70	20.240	-2.807	38.539	1.00	16.92
	431	CE1	TYR	B	70	21.056	-1.781	38.067	1.00	16.92
	432	CD2	TYR	B	70	18.320	-1.720	37.597	1.00	18.76
10	433	CE2	TYR	B	70	19.125	-0.689	37.121	1.00	20.19
	434	CZ	TYR	B	70	20.490	-0.728	37.359	1.00	23.85
	435	OH	TYR	B	70	21.290	0.283	36.889	1.00	28.88
	436	C	TYR	B	70	18.895	-4.756	40.981	1.00	27.42
	437	O	TYR	B	70	18.045	-4.077	41.579	1.00	29.24
15	438	N	ALA	B	71	19.991	-5.258	41.560	1.00	26.20
	439	CA	ALA	B	71	20.303	-5.103	42.984	1.00	27.77
	440	CB	ALA	B	71	21.123	-6.301	43.448	1.00	21.40
	441	C	ALA	B	71	20.996	-3.798	43.418	1.00	33.28
	442	O	ALA	B	71	20.758	-3.301	44.519	1.00	35.06
20	443	N	PHE	B	72	21.867	-3.247	42.580	1.00	34.13
	444	CA	PHE	B	72	22.533	-1.999	42.938	1.00	35.25
	445	CB	PHE	B	72	23.672	-2.263	43.937	1.00	28.54
	446	CG	PHE	B	72	24.179	-1.017	44.624	1.00	32.61
	447	CD1	PHE	B	72	23.480	-0.458	45.694	1.00	33.56
25	448	CD2	PHE	B	72	25.332	-0.374	44.179	1.00	35.80
	449	CE1	PHE	B	72	23.924	0.726	46.309	1.00	28.42
	450	CE2	PHE	B	72	25.777	0.807	44.788	1.00	32.48
	451	CZ	PHE	B	72	25.070	1.355	45.854	1.00	31.11
	452	C	PHE	B	72	23.079	-1.313	41.689	1.00	40.63
30	453	O	PHE	B	72	24.052	-1.770	41.102	1.00	43.32
	454	N	SER	B	73	22.447	-0.217	41.279	1.00	47.02
	455	CA	SER	B	73	22.893	0.514	40.093	1.00	49.68
	456	CB	SER	B	73	21.794	1.441	39.575	1.00	43.74
	457	OG	SER	B	73	21.824	2.681	40.257	1.00	33.26
35	458	C	SER	B	73	24.119	1.351	40.423	1.00	52.36
	459	O	SER	B	73	24.433	1.577	41.593	1.00	53.00
	460	N	THR	B	74	24.804	1.816	39.386	1.00	57.20
	461	CA	THR	B	74	25.996	2.630	39.573	1.00	62.04
	462	CB	THR	B	74	26.707	2.904	38.214	1.00	67.14
40	463	OG1	THR	B	74	26.682	1.723	37.404	1.00	74.37
	464	CG2	THR	B	74	28.159	3.292	38.440	1.00	71.77
	465	C	THR	B	74	25.569	3.956	40.199	1.00	62.95
	466	O	THR	B	74	26.316	4.582	40.951	1.00	62.39

	467	N	GLU	B	75	24.340	4.360	39.900	1.00	63.63
	468	CA	GLU	B	75	23.804	5.621	40.394	1.00	66.15
	469	CB	GLU	B	75	22.783	6.165	39.389	1.00	75.90
	470	CG	GLU	B	75	22.350	7.593	39.651	1.00	93.53
5	471	CD	GLU	B	75	21.286	8.057	38.686	1.00	103.81
	472	OE1	GLU	B	75	20.236	7.384	38.593	1.00	110.70
	473	OE2	GLU	B	75	21.500	9.094	38.023	1.00	111.36
	474	C	GLU	B	75	23.168	5.533	41.779	1.00	66.40
	475	O	GLU	B	75	22.464	6.450	42.203	1.00	68.91
10	476	N	ASN	B	76	23.415	4.439	42.490	1.00	64.57
	477	CA	ASN	B	76	22.845	4.281	43.825	1.00	59.63
	478	CB	ASN	B	76	22.419	2.827	44.067	1.00	53.70
	479	CG	ASN	B	76	21.031	2.531	43.539	1.00	46.89
	480	OD1	ASN	B	76	20.101	3.305	43.752	1.00	50.66
15	481	ND2	ASN	B	76	20.880	1.402	42.861	1.00	40.20
	482	C	ASN	B	76	23.774	4.727	44.950	1.00	56.27
	483	O	ASN	B	76	23.319	4.953	46.071	1.00	55.41
	484	N	TRP	B	77	25.067	4.860	44.657	1.00	53.67
	485	CA	TRP	B	77	26.026	5.270	45.679	1.00	51.94
20	486	CB	TRP	B	77	27.460	5.237	45.132	1.00	48.90
	487	CG	TRP	B	77	27.920	3.896	44.617	1.00	51.60
	488	CD2	TRP	B	77	28.576	2.859	45.365	1.00	51.70
	489	CE2	TRP	B	77	28.839	1.797	44.467	1.00	52.11
	490	CE3	TRP	B	77	28.968	2.722	46.706	1.00	43.86
25	491	CD1	TRP	B	77	27.812	3.431	43.338	1.00	52.12
	492	NE1	TRP	B	77	28.362	2.173	43.240	1.00	53.74
	493	CZ2	TRP	B	77	29.476	0.616	44.865	1.00	43.91
	494	CZ3	TRP	B	77	29.603	1.540	47.101	1.00	37.41
	495	CH2	TRP	B	77	29.850	0.506	46.180	1.00	35.61
30	496	C	TRP	B	77	25.701	6.676	46.181	1.00	50.29
	497	O	TRP	B	77	26.194	7.112	47.226	1.00	54.30
	498	N	THR	B	78	24.858	7.369	45.428	1.00	46.30
	499	CA	THR	B	78	24.434	8.726	45.751	1.00	40.87
	500	CB	THR	B	78	23.518	9.268	44.646	1.00	40.94
35	501	OG1	THR	B	78	24.257	9.344	43.421	1.00	41.23
	502	CG2	THR	B	78	22.972	10.641	45.013	1.00	43.72
	503	C	THR	B	78	23.685	8.805	47.076	1.00	39.63
	504	O	THR	B	78	23.558	9.881	47.661	1.00	43.77
	505	N	ARG	B	79	23.194	7.662	47.548	1.00	33.93
40	506	CA	ARG	B	79	22.424	7.593	48.792	1.00	29.09
	507	CB	ARG	B	79	21.698	6.246	48.855	1.00	22.71
	508	CG	ARG	B	79	20.705	6.102	47.730	1.00	24.31
	509	CD	ARG	B	79	20.027	4.767	47.718	1.00	23.41



	510	NE	ARG	B	79	18.813	4.835	46.916	1.00	19.61
	511	CZ	ARG	B	79	17.945	3.839	46.780	1.00	25.88
	512	NH1	ARG	B	79	18.159	2.683	47.396	1.00	35.60
	513	NH2	ARG	B	79	16.858	4.004	46.037	1.00	23.97
5	514	C	ARG	B	79	23.217	7.830	50.076	1.00	31.63
	515	O	ARG	B	79	24.447	7.732	50.094	1.00	31.85
	516	N	PRO	B	80	22.513	8.167	51.171	1.00	30.10
	517	CD	PRO	B	80	21.059	8.319	51.358	1.00	30.04
	518	CA	PRO	B	80	23.233	8.402	52.423	1.00	31.57
10	519	CB	PRO	B	80	22.113	8.754	53.414	1.00	29.71
	520	CG	PRO	B	80	20.904	8.083	52.840	1.00	29.28
	521	C	PRO	B	80	24.041	7.168	52.824	1.00	38.32
	522	O	PRO	B	80	23.487	6.083	53.011	1.00	42.42
	523	N	ASP	B	81	25.356	7.351	52.935	1.00	41.93
15	524	CA	ASP	B	81	26.284	6.284	53.299	1.00	45.58
	525	CB	ASP	B	81	27.427	6.850	54.150	1.00	63.07
	526	CG	ASP	B	81	28.116	8.043	53.504	1.00	67.38
	527	OD1	ASP	B	81	28.509	7.948	52.321	1.00	73.52
	528	OD2	ASP	B	81	28.274	9.075	54.189	1.00	72.51
20	529	C	ASP	B	81	25.616	5.136	54.055	1.00	44.34
	530	O	ASP	B	81	25.671	3.984	53.626	1.00	45.14
	531	N	GLN	B	82	24.981	5.456	55.178	1.00	43.19
	532	CA	GLN	B	82	24.316	4.443	55.981	1.00	46.00
	533	CB	GLN	B	82	23.492	5.110	57.076	1.00	45.03
25	534	CG	GLN	B	82	24.289	5.374	58.335	1.00	34.60
	535	CD	GLN	B	82	24.607	4.099	59.104	1.00	16.92
	536	OE1	GLN	B	82	23.720	3.476	59.693	1.00	26.54
	537	NE2	GLN	B	82	25.875	3.703	59.098	1.00	16.92
	538	C	GLN	B	82	23.448	3.473	55.187	1.00	47.51
30	539	O	GLN	B	82	23.598	2.260	55.322	1.00	51.03
	540	N	GLU	B	83	22.541	3.998	54.367	1.00	44.67
	541	CA	GLU	B	83	21.667	3.142	53.565	1.00	37.68
	542	CB	GLU	B	83	20.754	3.979	52.664	1.00	35.83
	543	CG	GLU	B	83	19.621	3.191	52.003	1.00	39.43
35	544	CD	GLU	B	83	18.718	4.065	51.137	1.00	43.90
	545	OE1	GLU	B	83	17.556	3.666	50.877	1.00	48.19
	546	OE2	GLU	B	83	19.176	5.149	50.706	1.00	48.89
	547	C	GLU	B	83	22.517	2.232	52.700	1.00	32.89
	548	O	GLU	B	83	22.222	1.054	52.566	1.00	32.08
40	549	N	VAL	B	84	23.571	2.787	52.109	1.00	30.13
	550	CA	VAL	B	84	24.464	1.998	51.273	1.00	31.93
	551	CB	VAL	B	84	25.503	2.884	50.546	1.00	35.84
	552	CG1	VAL	B	84	26.379	2.025	49.640	1.00	39.26

	553	CG2	VAL	B	84	24.792	3.946	49.722	1.00	34.99
	554	C	VAL	B	84	25.177	1.016	52.196	1.00	33.63
	555	O	VAL	B	84	25.276	-0.178	51.903	1.00	34.73
	556	N	LYS	B	85	25.667	1.533	53.319	1.00	33.74
5	557	CA	LYS	B	85	26.341	0.716	54.322	1.00	35.59
	558	CB	LYS	B	85	26.496	1.544	55.612	1.00	48.55
	559	CG	LYS	B	85	26.571	0.767	56.928	1.00	59.03
	560	CD	LYS	B	85	27.942	0.170	57.196	1.00	67.33
	561	CE	LYS	B	85	27.943	-0.586	58.525	1.00	72.93
10	562	NZ	LYS	B	85	29.237	-1.290	58.785	1.00	68.29
	563	C	LYS	B	85	25.464	-0.525	54.545	1.00	33.73
	564	O	LYS	B	85	25.918	-1.655	54.380	1.00	32.87
	565	N	PHE	B	86	24.200	-0.280	54.882	1.00	34.91
	566	CA	PHE	B	86	23.192	-1.314	55.132	1.00	38.00
15	567	CB	PHE	B	86	21.840	-0.640	55.405	1.00	29.90
	568	CG	PHE	B	86	20.701	-1.600	55.644	1.00	28.19
	569	CD1	PHE	B	86	20.164	-1.758	56.918	1.00	28.34
	570	CD2	PHE	B	86	20.112	-2.289	54.586	1.00	30.14
	571	CE1	PHE	B	86	19.052	-2.581	57.133	1.00	16.92
20	572	CE2	PHE	B	86	19.004	-3.114	54.792	1.00	31.79
	573	CZ	PHE	B	86	18.472	-3.258	56.067	1.00	23.42
	574	C	PHE	B	86	23.039	-2.310	53.982	1.00	41.33
	575	O	PHE	B	86	23.232	-3.512	54.170	1.00	44.39
	576	N	ILE	B	87	22.674	-1.811	52.800	1.00	42.94
25	577	CA	ILE	B	87	22.479	-2.661	51.624	1.00	44.91
	578	CB	ILE	B	87	22.225	-1.831	50.348	1.00	33.27
	579	CG2	ILE	B	87	21.956	-2.748	49.176	1.00	35.47
	580	CG1	ILE	B	87	21.018	-0.925	50.538	1.00	33.55
	581	CD1	ILE	B	87	20.762	-0.027	49.357	1.00	34.35
30	582	C	ILE	B	87	23.683	-3.552	51.354	1.00	49.45
	583	O	ILE	B	87	23.559	-4.774	51.312	1.00	51.81
	584	N	MET	B	88	24.845	-2.933	51.174	1.00	49.47
	585	CA	MET	B	88	26.064	-3.680	50.892	1.00	49.30
	586	CB	MET	B	88	27.269	-2.737	50.822	1.00	50.22
35	587	CG	MET	B	88	27.187	-1.661	49.738	1.00	45.64
	588	SD	MET	B	88	26.855	-2.262	48.067	1.00	36.68
	589	CE	MET	B	88	28.205	-3.366	47.823	1.00	32.68
	590	C	MET	B	88	26.352	-4.815	51.881	1.00	47.36
	591	O	MET	B	88	27.187	-5.678	51.614	1.00	47.71
40	592	N	ASN	B	89	25.676	-4.835	53.022	1.00	47.87
	593	CA	ASN	B	89	25.925	-5.919	53.958	1.00	53.55
	594	CB	ASN	B	89	25.943	-5.421	55.400	1.00	59.69
	595	CG	ASN	B	89	26.446	-6.481	56.358	1.00	60.29

	596	OD1	ASN	B	89	27.611	-6.880	56.300	1.00	58.66
	597	ND2	ASN	B	89	25.567	-6.956	57.233	1.00	59.82
	598	C	ASN	B	89	24.874	-7.011	53.814	1.00	54.69
	599	O	ASN	B	89	24.876	-7.996	54.555	1.00	55.77
5	600	N	LEU	B	90	23.971	-6.821	52.856	1.00	53.91
	601	CA	LEU	B	90	22.919	-7.792	52.593	1.00	50.26
	602	CB	LEU	B	90	21.804	-7.158	51.759	1.00	44.32
	603	CG	LEU	B	90	20.892	-6.161	52.478	1.00	38.54
	604	CD1	LEU	B	90	19.928	-5.544	51.488	1.00	43.04
10	605	CD2	LEU	B	90	20.129	-6.869	53.578	1.00	42.59
	606	C	LEU	B	90	23.492	-9.013	51.879	1.00	47.14
	607	O	LEU	B	90	22.974	-10.121	52.027	1.00	44.55
	608	N	PRO	B	91	24.556	-8.825	51.072	1.00	46.27
	609	CD	PRO	B	91	25.020	-7.553	50.489	1.00	44.80
15	610	CA	PRO	B	91	25.162	-9.958	50.366	1.00	46.47
	611	CB	PRO	B	91	26.199	-9.285	49.470	1.00	43.34
	612	CG	PRO	B	91	25.545	-7.993	49.145	1.00	45.54
	613	C	PRO	B	91	25.795	-10.958	51.346	1.00	47.41
	614	O	PRO	B	91	26.062	-12.107	51.000	1.00	46.38
20	615	N	VAL	B	92	26.033	-10.507	52.573	1.00	47.94
	616	CA	VAL	B	92	26.619	-11.363	53.598	1.00	45.52
	617	CB	VAL	B	92	27.367	-10.537	54.639	1.00	34.17
	618	CG1	VAL	B	92	28.018	-11.454	55.632	1.00	38.02
	619	CG2	VAL	B	92	28.404	-9.666	53.957	1.00	38.64
25	620	C	VAL	B	92	25.512	-12.154	54.286	1.00	45.50
	621	O	VAL	B	92	25.576	-13.379	54.364	1.00	44.68
	622	N	GLU	B	93	24.499	-11.447	54.782	1.00	42.90
	623	CA	GLU	B	93	23.367	-12.099	55.418	1.00	42.53
	624	CB	GLU	B	93	22.252	-11.101	55.707	1.00	49.87
30	625	CG	GLU	B	93	22.684	-9.832	56.407	1.00	57.60
	626	CD	GLU	B	93	21.498	-9.061	56.963	1.00	61.78
	627	OE1	GLU	B	93	21.693	-7.934	57.473	1.00	71.50
	628	OE2	GLU	B	93	20.367	-9.592	56.892	1.00	52.19
	629	C	GLU	B	93	22.844	-13.111	54.412	1.00	43.12
35	630	O	GLU	B	93	22.582	-14.263	54.742	1.00	45.85
	631	N	PHE	B	94	22.694	-12.661	53.172	1.00	45.41
	632	CA	PHE	B	94	22.203	-13.515	52.101	1.00	46.26
	633	CB	PHE	B	94	22.269	-12.780	50.761	1.00	42.53
	634	CG	PHE	B	94	21.575	-13.507	49.645	1.00	32.85
40	635	CD1	PHE	B	94	20.180	-13.595	49.617	1.00	28.47
	636	CD2	PHE	B	94	22.311	-14.148	48.649	1.00	28.12
	637	CE1	PHE	B	94	19.523	-14.314	48.617	1.00	19.92
	638	CE2	PHE	B	94	21.666	-14.870	47.644	1.00	31.07

	639	CZ	PHE B	94	20.267	-14.951	47.632	1.00	25.79
	640	C	PHE B	94	23.016	-14.802	52.013	1.00	45.67
	641	O	PHE B	94	22.462	-15.898	52.067	1.00	41.22
	642	N	TYR B	95	24.331	-14.665	51.880	1.00	44.67
5	643	CA	TYR B	95	25.205	-15.826	51.785	1.00	42.71
	644	CB	TYR B	95	26.652	-15.400	51.558	1.00	44.48
	645	CG	TYR B	95	27.613	-16.569	51.484	1.00	45.34
	646	CD1	TYR B	95	27.472	-17.547	50.504	1.00	46.34
	647	CE1	TYR B	95	28.354	-18.615	50.419	1.00	50.00
10	648	CD2	TYR B	95	28.666	-16.693	52.384	1.00	46.57
	649	CE2	TYR B	95	29.550	-17.757	52.307	1.00	49.96
	650	CZ	TYR B	95	29.391	-18.713	51.321	1.00	53.17
	651	OH	TYR B	95	30.274	-19.760	51.222	1.00	55.77
	652	C	TYR B	95	25.152	-16.688	53.033	1.00	41.47
15	653	O	TYR B	95	24.971	-17.904	52.954	1.00	41.86
	654	N	ASP B	96	25.326	-16.058	54.189	1.00	38.09
	655	CA	ASP B	96	25.301	-16.798	55.437	1.00	34.86
	656	CB	ASP B	96	25.352	-15.872	56.650	1.00	28.63
	657	CG	ASP B	96	26.761	-15.439	56.993	1.00	32.06
20	658	OD1	ASP B	96	27.720	-16.122	56.552	1.00	29.64
	659	OD2	ASP B	96	26.902	-14.423	57.717	1.00	33.25
	660	C	ASP B	96	24.084	-17.678	55.566	1.00	31.39
	661	O	ASP B	96	24.219	-18.890	55.686	1.00	31.77
	662	N	ASN B	97	22.893	-17.094	55.528	1.00	26.14
25	663	CA	ASN B	97	21.711	-17.920	55.702	1.00	29.32
	664	CB	ASN B	97	21.101	-17.615	57.077	1.00	34.58
	665	CG	ASN B	97	20.908	-16.131	57.320	1.00	33.64
	666	OD1	ASN B	97	20.735	-15.692	58.466	1.00	31.70
	667	ND2	ASN B	97	20.918	-15.347	56.241	1.00	25.32
30	668	C	ASN B	97	20.621	-17.970	54.624	1.00	33.75
	669	O	ASN B	97	19.577	-18.588	54.840	1.00	31.16
	670	N	TYR B	98	20.849	-17.354	53.466	1.00	37.18
	671	CA	TYR B	98	19.855	-17.410	52.391	1.00	35.12
	672	CB	TYR B	98	19.536	-16.018	51.874	1.00	33.51
35	673	CG	TYR B	98	18.459	-15.359	52.664	1.00	29.03
	674	CD1	TYR B	98	18.768	-14.454	53.677	1.00	24.71
	675	CE1	TYR B	98	17.775	-13.896	54.464	1.00	19.15
	676	CD2	TYR B	98	17.129	-15.690	52.450	1.00	24.62
	677	CE2	TYR B	98	16.125	-15.147	53.227	1.00	22.79
40	678	CZ	TYR B	98	16.453	-14.249	54.238	1.00	25.75
	679	OH	TYR B	98	15.456	-13.721	55.032	1.00	31.99
	680	C	TYR B	98	20.307	-18.287	51.230	1.00	36.88
	681	O	TYR B	98	19.490	-18.929	50.554	1.00	38.14

	682	N	VAL B	99	21.617	-18.301	51.005	1.00	34.30
	683	CA	VAL B	99	22.230	-19.095	49.950	1.00	27.39
	684	CB	VAL B	99	23.713	-18.721	49.801	1.00	20.34
	685	CG1	VAL B	99	24.419	-19.715	48.906	1.00	16.92
5	686	CG2	VAL B	99	23.827	-17.314	49.234	1.00	19.75
	687	C	VAL B	99	22.093	-20.609	50.193	1.00	31.44
	688	O	VAL B	99	21.833	-21.366	49.257	1.00	35.10
	689	N	PRO B	100	22.263	-21.070	51.449	1.00	34.59
	690	CD	PRO B	100	22.547	-20.362	52.709	1.00	35.82
10	691	CA	PRO B	100	22.130	-22.504	51.698	1.00	33.54
	692	CB	PRO B	100	22.021	-22.573	53.212	1.00	31.42
	693	CG	PRO B	100	22.925	-21.500	53.636	1.00	35.80
	694	C	PRO B	100	20.891	-23.060	51.018	1.00	34.59
	695	O	PRO B	100	20.968	-24.041	50.282	1.00	36.94
15	696	N	GLU B	101	19.753	-22.415	51.259	1.00	33.67
	697	CA	GLU B	101	18.491	-22.852	50.677	1.00	31.97
	698	CB	GLU B	101	17.330	-22.029	51.222	1.00	16.92
	699	CG	GLU B	101	16.054	-22.273	50.446	1.00	16.92
	700	CD	GLU B	101	14.817	-21.788	51.160	1.00	26.55
20	701	OE1	GLU B	101	14.835	-20.646	51.681	1.00	21.07
	702	OE2	GLU B	101	13.825	-22.556	51.183	1.00	22.12
	703	C	GLU B	101	18.452	-22.804	49.159	1.00	33.18
	704	O	GLU B	101	17.995	-23.747	48.511	1.00	32.52
	705	N	LEU B	102	18.899	-21.696	48.584	1.00	33.81
25	706	CA	LEU B	102	18.898	-21.600	47.140	1.00	31.47
	707	CB	LEU B	102	19.539	-20.287	46.698	1.00	30.43
	708	CG	LEU B	102	18.763	-19.039	47.118	1.00	34.74
	709	CD1	LEU B	102	19.484	-17.801	46.628	1.00	25.10
	710	CD2	LEU B	102	17.359	-19.095	46.540	1.00	36.87
30	711	C	LEU B	102	19.689	-22.791	46.616	1.00	30.29
	712	O	LEU B	102	19.282	-23.454	45.658	1.00	33.60
	713	N	HIS B	103	20.805	-23.072	47.283	1.00	28.12
	714	CA	HIS B	103	21.692	-24.172	46.920	1.00	30.58
	715	CB	HIS B	103	22.936	-24.119	47.789	1.00	32.00
35	716	CG	HIS B	103	24.031	-25.026	47.325	1.00	35.36
	717	CD2	HIS B	103	24.655	-26.057	47.939	1.00	34.89
	718	ND1	HIS B	103	24.634	-24.892	46.092	1.00	38.53
	719	CE1	HIS B	103	25.585	-25.800	45.969	1.00	36.15
	720	NE2	HIS B	103	25.618	-26.519	47.076	1.00	34.36
40	721	C	HIS B	103	21.040	-25.551	47.056	1.00	31.60
	722	O	HIS B	103	21.344	-26.478	46.304	1.00	26.65
	723	N	ALA B	104	20.164	-25.693	48.039	1.00	30.94
	724	CA	ALA B	104	19.474	-26.948	48.232	1.00	28.23

	725	CB	ALA B 104	18.696	-26.927	49.521	1.00	23.85
	726	C	ALA B 104	18.527	-27.081	47.060	1.00	32.92
	727	O	ALA B 104	18.280	-28.179	46.579	1.00	40.90
	728	N	ASN B 105	18.006	-25.952	46.592	1.00	32.79
5	729	CA	ASN B 105	17.071	-25.966	45.471	1.00	29.90
	730	CB	ASN B 105	16.031	-24.850	45.637	1.00	42.45
	731	CG	ASN B 105	15.022	-25.161	46.733	1.00	48.96
	732	OD1	ASN B 105	14.256	-26.117	46.626	1.00	60.59
	733	ND2	ASN B 105	15.028	-24.364	47.794	1.00	37.91
10	734	C	ASN B 105	17.725	-25.894	44.089	1.00	24.31
	735	O	ASN B 105	17.084	-25.529	43.106	1.00	24.21
	736	N	ASN B 106	19.004	-26.251	44.026	1.00	21.42
	737	CA	ASN B 106	19.752	-26.280	42.771	1.00	21.95
	738	CB	ASN B 106	19.119	-27.303	41.820	1.00	16.92
15	739	CG	ASN B 106	20.030	-27.667	40.660	1.00	18.90
	740	OD1	ASN B 106	19.574	-28.162	39.629	1.00	20.83
	741	ND2	ASN B 106	21.331	-27.434	40.830	1.00	16.92
	742	C	ASN B 106	19.845	-24.933	42.059	1.00	26.82
	743	O	ASN B 106	19.892	-24.880	40.830	1.00	28.64
20	744	N	VAL B 107	19.874	-23.841	42.811	1.00	28.06
	745	CA	VAL B 107	19.963	-22.532	42.183	1.00	25.22
	746	CB	VAL B 107	19.211	-21.468	43.019	1.00	24.13
	747	CG1	VAL B 107	19.267	-20.107	42.330	1.00	37.12
	748	CG2	VAL B 107	17.770	-21.906	43.224	1.00	24.46
25	749	C	VAL B 107	21.430	-22.137	42.053	1.00	28.07
	750	O	VAL B 107	22.200	-22.306	42.994	1.00	33.25
	751	N	LYS B 108	21.825	-21.649	40.879	1.00	25.06
	752	CA	LYS B 108	23.204	-21.203	40.663	1.00	24.60
	753	CB	LYS B 108	23.677	-21.534	39.248	1.00	19.20
30	754	CG	LYS B 108	25.080	-21.041	38.929	1.00	17.42
	755	CD	LYS B 108	25.607	-21.710	37.664	1.00	18.52
	756	CE	LYS B 108	26.826	-21.005	37.081	1.00	23.17
	757	NZ	LYS B 108	27.981	-20.950	38.013	1.00	26.96
	758	C	LYS B 108	23.211	-19.695	40.873	1.00	28.32
35	759	O	LYS B 108	22.221	-19.020	40.589	1.00	32.57
	760	N	ILE B 109	24.311	-19.157	41.380	1.00	29.02
	761	CA	ILE B 109	24.355	-17.724	41.616	1.00	29.85
	762	CB	ILE B 109	24.461	-17.403	43.139	1.00	29.54
	763	CG2	ILE B 109	24.387	-15.893	43.359	1.00	24.76
40	764	CG1	ILE B 109	23.319	-18.076	43.906	1.00	26.25
	765	CD1	ILE B 109	23.250	-17.686	45.368	1.00	26.43
	766	C	ILE B 109	25.506	-17.055	40.874	1.00	31.25
	767	O	ILE B 109	26.648	-17.510	40.937	1.00	31.58

	768	N	GLN B 110	25.183	-15.980	40.158	1.00	34.94
	769	CA	GLN B 110	26.169	-15.218	39.407	1.00	35.94
	770	CB	GLN B 110	26.090	-15.551	37.920	1.00	43.90
	771	CG	GLN B 110	26.003	-17.034	37.624	1.00	52.49
5	772	CD	GLN B 110	26.115	-17.355	36.147	1.00	53.12
	773	OE1	GLN B 110	25.989	-18.516	35.741	1.00	42.83
	774	NE2	GLN B 110	26.363	-16.329	35.331	1.00	66.31
	775	C	GLN B 110	25.825	-13.757	39.615	1.00	35.02
	776	O	GLN B 110	24.671	-13.423	39.890	1.00	36.09
10	777	N	MET B 111	26.821	-12.889	39.495	1.00	34.95
	778	CA	MET B 111	26.595	-11.463	39.665	1.00	38.29
	779	CB	MET B 111	26.975	-11.034	41.091	1.00	54.75
	780	CG	MET B 111	28.387	-11.398	41.561	1.00	63.44
	781	SD	MET B 111	29.627	-10.096	41.304	1.00	75.55
15	782	CE	MET B 111	28.739	-8.620	41.902	1.00	63.96
	783	C	MET B 111	27.358	-10.646	38.625	1.00	39.52
	784	O	MET B 111	28.555	-10.836	38.435	1.00	42.08
	785	N	ILE B 112	26.649	-9.743	37.948	1.00	39.74
	786	CA	ILE B 112	27.241	-8.892	36.914	1.00	38.26
20	787	CB	ILE B 112	26.406	-8.909	35.616	1.00	37.80
	788	CG2	ILE B 112	26.317	-10.321	35.067	1.00	34.53
	789	CG1	ILE B 112	25.017	-8.330	35.897	1.00	42.15
	790	CD1	ILE B 112	24.175	-8.130	34.672	1.00	40.41
	791	C	ILE B 112	27.344	-7.435	37.348	1.00	33.52
25	792	O	ILE B 112	26.527	-6.947	38.129	1.00	28.71
	793	N	GLY B 113	28.349	-6.743	36.823	1.00	30.89
	794	CA	GLY B 113	28.521	-5.346	37.152	1.00	37.18
	795	C	GLY B 113	29.944	-5.002	37.505	1.00	39.38
	796	O	GLY B 113	30.810	-5.869	37.513	1.00	38.55
30	797	N	GLU B 114	30.178	-3.724	37.789	1.00	42.25
	798	CA	GLU B 114	31.497	-3.235	38.166	1.00	50.83
	799	CB	GLU B 114	31.548	-1.705	38.044	1.00	64.49
	800	CG	GLU B 114	31.688	-1.180	36.608	1.00	73.99
	801	CD	GLU B 114	30.510	-0.333	36.161	1.00	75.69
35	802	OE1	GLU B 114	29.453	-0.904	35.805	1.00	75.15
	803	OE2	GLU B 114	30.644	0.910	36.170	1.00	71.34
	804	C	GLU B 114	31.753	-3.672	39.605	1.00	55.84
	805	O	GLU B 114	31.591	-2.905	40.551	1.00	57.72
	806	N	THR B 115	32.161	-4.925	39.745	1.00	57.14
40	807	CA	THR B 115	32.419	-5.530	41.042	1.00	58.68
	808	CB	THR B 115	32.550	-7.038	40.891	1.00	53.84
	809	OG1	THR B 115	33.791	-7.332	40.244	1.00	53.59
	810	CG2	THR B 115	31.409	-7.589	40.043	1.00	49.34

	811	C	THR B 115	33.675	-5.034	41.742	1.00	63.08
	812	O	THR B 115	34.010	-5.514	42.820	1.00	63.55
	813	N	ASP B 116	34.368	-4.070	41.147	1.00	67.68
	814	CA	ASP B 116	35.604	-3.566	41.736	1.00	72.55
5	815	CB	ASP B 116	36.591	-3.200	40.623	1.00	76.81
	816	CG	ASP B 116	37.050	-4.415	39.831	1.00	82.99
	817	OD1	ASP B 116	36.200	-5.066	39.186	1.00	84.93
	818	OD2	ASP B 116	38.262	-4.723	39.860	1.00	75.26
	819	C	ASP B 116	35.487	-2.406	42.721	1.00	74.26
10	820	O	ASP B 116	36.442	-2.109	43.438	1.00	76.40
	821	N	ARG B 117	34.332	-1.750	42.766	1.00	75.22
	822	CA	ARG B 117	34.145	-0.633	43.694	1.00	76.00
	823	CB	ARG B 117	33.392	0.514	43.009	1.00	91.55
	824	CG	ARG B 117	33.692	0.656	41.521	1.00	106.10
15	825	CD	ARG B 117	32.965	1.850	40.908	1.00	116.76
	826	NE	ARG B 117	32.740	1.680	39.472	1.00	125.02
	827	CZ	ARG B 117	33.691	1.402	38.584	1.00	129.50
	828	NH1	ARG B 117	34.951	1.258	38.975	1.00	133.15
	829	NH2	ARG B 117	33.381	1.264	37.300	1.00	131.90
20	830	C	ARG B 117	33.348	-1.124	44.904	1.00	73.15
	831	O	ARG B 117	32.938	-0.339	45.765	1.00	75.52
	832	N	LEU B 118	33.145	-2.436	44.958	1.00	65.43
	833	CA	LEU B 118	32.390	-3.059	46.033	1.00	59.80
	834	CB	LEU B 118	31.834	-4.402	45.573	1.00	53.32
25	835	CG	LEU B 118	30.831	-4.440	44.427	1.00	51.22
	836	CD1	LEU B 118	30.449	-5.893	44.140	1.00	43.14
	837	CD2	LEU B 118	29.599	-3.618	44.800	1.00	48.18
	838	C	LEU B 118	33.193	-3.303	47.294	1.00	55.75
	839	O	LEU B 118	34.401	-3.496	47.253	1.00	56.56
30	840	N	PRO B 119	32.516	-3.288	48.443	1.00	50.27
	841	CD	PRO B 119	31.151	-2.765	48.619	1.00	47.23
	842	CA	PRO B 119	33.158	-3.526	49.735	1.00	48.03
	843	CB	PRO B 119	32.010	-3.336	50.716	1.00	44.88
	844	CG	PRO B 119	31.170	-2.284	50.039	1.00	43.34
35	845	C	PRO B 119	33.680	-4.965	49.725	1.00	50.30
	846	O	PRO B 119	33.089	-5.834	49.090	1.00	51.90
	847	N	LYS B 120	34.774	-5.223	50.427	1.00	52.17
	848	CA	LYS B 120	35.350	-6.564	50.445	1.00	56.36
	849	CB	LYS B 120	36.628	-6.583	51.284	1.00	63.53
40	850	CG	LYS B 120	37.423	-7.877	51.156	1.00	63.00
	851	CD	LYS B 120	38.405	-8.063	52.305	1.00	73.77
	852	CE	LYS B 120	37.665	-8.326	53.609	1.00	77.05
	853	NZ	LYS B 120	38.595	-8.673	54.713	1.00	69.29



	854	C	LYS	B	120	34.409	-7.647	50.967	1.00	55.74
	855	O	LYS	B	120	34.132	-8.625	50.272	1.00	56.30
	856	N	GLN	B	121	33.929	-7.479	52.196	1.00	55.41
	857	CA	GLN	B	121	33.045	-8.470	52.791	1.00	54.91
5	858	CB	GLN	B	121	32.572	-8.017	54.181	1.00	67.90
	859	CG	GLN	B	121	31.364	-7.087	54.199	1.00	74.11
	860	CD	GLN	B	121	31.694	-5.663	53.814	1.00	76.82
	861	OE1	GLN	B	121	30.807	-4.809	53.743	1.00	72.18
	862	NE2	GLN	B	121	32.971	-5.393	53.569	1.00	76.38
10	863	C	GLN	B	121	31.853	-8.729	51.881	1.00	52.21
	864	O	GLN	B	121	31.332	-9.841	51.826	1.00	53.09
	865	N	THR	B	122	31.434	-7.695	51.159	1.00	49.30
	866	CA	THR	B	122	30.305	-7.807	50.238	1.00	43.48
	867	CB	THR	B	122	29.897	-6.424	49.676	1.00	42.07
15	868	OG1	THR	B	122	29.714	-5.498	50.754	1.00	47.12
	869	CG2	THR	B	122	28.606	-6.536	48.875	1.00	43.57
	870	C	THR	B	122	30.719	-8.685	49.060	1.00	35.33
	871	O	THR	B	122	30.051	-9.667	48.715	1.00	27.53
	872	N	PHE	B	123	31.835	-8.307	48.449	1.00	33.58
20	873	CA	PHE	B	123	32.369	-9.018	47.304	1.00	35.10
	874	CB	PHE	B	123	33.697	-8.407	46.879	1.00	37.63
	875	CG	PHE	B	123	34.247	-8.991	45.623	1.00	44.54
	876	CD1	PHE	B	123	33.554	-8.857	44.422	1.00	53.52
	877	CD2	PHE	B	123	35.450	-9.683	45.634	1.00	46.30
25	878	CE1	PHE	B	123	34.054	-9.404	43.246	1.00	61.21
	879	CE2	PHE	B	123	35.960	-10.236	44.463	1.00	47.50
	880	CZ	PHE	B	123	35.261	-10.096	43.267	1.00	55.61
	881	C	PHE	B	123	32.581	-10.475	47.647	1.00	37.43
	882	O	PHE	B	123	31.977	-11.361	47.038	1.00	39.83
30	883	N	GLU	B	124	33.441	-10.716	48.629	1.00	37.07
	884	CA	GLU	B	124	33.742	-12.067	49.059	1.00	35.49
	885	CB	GLU	B	124	34.570	-12.027	50.334	1.00	33.74
	886	CG	GLU	B	124	36.000	-11.595	50.089	1.00	34.11
	887	CD	GLU	B	124	36.734	-11.266	51.368	1.00	43.15
35	888	OE1	GLU	B	124	37.959	-11.020	51.299	1.00	48.58
	889	OE2	GLU	B	124	36.086	-11.246	52.440	1.00	60.13
	890	C	GLU	B	124	32.481	-12.884	49.276	1.00	35.66
	891	O	GLU	B	124	32.440	-14.061	48.928	1.00	36.51
	892	N	ALA	B	125	31.449	-12.261	49.832	1.00	34.75
40	893	CA	ALA	B	125	30.195	-12.960	50.079	1.00	37.21
	894	CB	ALA	B	125	29.172	-12.005	50.655	1.00	34.20
	895	C	ALA	B	125	29.662	-13.570	48.793	1.00	40.90
	896	O	ALA	B	125	29.398	-14.771	48.719	1.00	44.51

	897	N	LEU B 126	29.511	-12.731	47.778	1.00	39.91
	898	CA	LEU B 126	28.996	-13.172	46.492	1.00	38.45
	899	CB	LEU B 126	28.728	-11.955	45.615	1.00	36.01
	900	CG	LEU B 126	27.613	-11.063	46.166	1.00	28.88
5	901	CD1	LEU B 126	27.787	-9.646	45.643	1.00	32.10
	902	CD2	LEU B 126	26.254	-11.653	45.794	1.00	22.64
	903	C	LEU B 126	29.942	-14.125	45.790	1.00	39.09
	904	O	LEU B 126	29.525	-15.137	45.243	1.00	41.65
	905	N	THR B 127	31.219	-13.792	45.799	1.00	36.98
10	906	CA	THR B 127	32.222	-14.636	45.174	1.00	42.37
	907	CB	THR B 127	33.619	-14.153	45.555	1.00	49.56
	908	OG1	THR B 127	33.776	-12.791	45.135	1.00	47.49
	909	CG2	THR B 127	34.679	-15.017	44.909	1.00	48.08
	910	C	THR B 127	32.043	-16.077	45.643	1.00	46.79
15	911	O	THR B 127	31.980	-17.007	44.836	1.00	50.37
	912	N	LYS B 128	31.956	-16.243	46.960	1.00	49.56
	913	CA	LYS B 128	31.775	-17.548	47.578	1.00	46.71
	914	CB	LYS B 128	31.838	-17.416	49.102	1.00	47.68
	915	CG	LYS B 128	33.254	-17.447	49.668	1.00	55.98
20	916	CD	LYS B 128	33.424	-16.501	50.851	1.00	60.97
	917	CE	LYS B 128	32.418	-16.782	51.957	1.00	65.54
	918	NZ	LYS B 128	32.461	-15.787	53.077	1.00	64.13
	919	C	LYS B 128	30.459	-18.193	47.167	1.00	45.28
	920	O	LYS B 128	30.442	-19.328	46.698	1.00	41.48
25	921	N	ALA B 129	29.358	-17.474	47.340	1.00	45.11
	922	CA	ALA B 129	28.048	-18.007	46.975	1.00	46.45
	923	CB	ALA B 129	26.981	-16.952	47.186	1.00	49.46
	924	C	ALA B 129	28.022	-18.489	45.526	1.00	44.27
	925	O	ALA B 129	27.205	-19.332	45.161	1.00	41.06
30	926	N	GLU B 130	28.912	-17.933	44.707	1.00	44.20
	927	CA	GLU B 130	29.017	-18.311	43.305	1.00	46.78
	928	CB	GLU B 130	29.772	-17.247	42.512	1.00	44.22
	929	CG	GLU B 130	29.114	-15.882	42.508	1.00	49.59
	930	CD	GLU B 130	29.785	-14.910	41.554	1.00	49.64
35	931	OE1	GLU B 130	30.982	-14.598	41.747	1.00	49.46
	932	OE2	GLU B 130	29.108	-14.459	40.606	1.00	53.99
	933	C	GLU B 130	29.811	-19.591	43.282	1.00	48.99
	934	O	GLU B 130	29.507	-20.526	42.544	1.00	48.82
	935	N	GLU B 131	30.846	-19.604	44.111	1.00	47.76
40	936	CA	GLU B 131	31.726	-20.747	44.256	1.00	41.07
	937	CB	GLU B 131	32.825	-20.415	45.262	1.00	33.82
	938	CG	GLU B 131	34.186	-20.370	44.643	1.00	48.83
	939	CD	GLU B 131	34.428	-21.588	43.773	1.00	53.69

	940	OE1	GLU	B	131	34.331	-22.724	44.296	1.00	54.79
	941	OE2	GLU	B	131	34.704	-21.410	42.564	1.00	67.98
	942	C	GLU	B	131	30.948	-21.974	44.727	1.00	39.85
	943	O	GLU	B	131	31.116	-23.079	44.208	1.00	39.50
5	944	N	LEU	B	132	30.089	-21.774	45.716	1.00	40.81
	945	CA	LEU	B	132	29.287	-22.859	46.257	1.00	40.93
	946	CB	LEU	B	132	28.427	-22.338	47.414	1.00	42.02
	947	CG	LEU	B	132	27.441	-23.310	48.072	1.00	37.20
	948	CD1	LEU	B	132	28.184	-24.539	48.543	1.00	40.73
10	949	CD2	LEU	B	132	26.740	-22.636	49.244	1.00	22.65
	950	C	LEU	B	132	28.390	-23.478	45.197	1.00	39.99
	951	O	LEU	B	132	28.364	-24.692	45.020	1.00	37.40
	952	N	THR	B	133	27.675	-22.624	44.475	1.00	43.53
	953	CA	THR	B	133	26.726	-23.057	43.454	1.00	43.29
15	954	CB	THR	B	133	25.540	-22.072	43.404	1.00	30.42
	955	OG1	THR	B	133	26.035	-20.725	43.410	1.00	32.09
	956	CG2	THR	B	133	24.640	-22.269	44.612	1.00	29.55
	957	C	THR	B	133	27.217	-23.303	42.020	1.00	40.62
	958	O	THR	B	133	26.401	-23.580	41.140	1.00	37.19
20	959	N	LYS	B	134	28.527	-23.220	41.789	1.00	34.90
	960	CA	LYS	B	134	29.093	-23.448	40.454	1.00	36.42
	961	CB	LYS	B	134	30.563	-23.860	40.531	1.00	20.34
	962	CG	LYS	B	134	31.536	-22.775	40.932	1.00	39.12
	963	CD	LYS	B	134	32.983	-23.301	40.954	1.00	44.98
25	964	CE	LYS	B	134	33.173	-24.428	41.970	1.00	44.22
	965	NZ	LYS	B	134	34.594	-24.857	42.103	1.00	45.46
	966	C	LYS	B	134	28.377	-24.534	39.668	1.00	44.36
	967	O	LYS	B	134	27.666	-24.259	38.706	1.00	48.76
	968	N	ASN	B	135	28.579	-25.775	40.092	1.00	49.25
30	969	CA	ASN	B	135	28.002	-26.924	39.414	1.00	49.89
	970	CB	ASN	B	135	28.665	-28.213	39.909	1.00	51.24
	971	CG	ASN	B	135	30.165	-28.078	40.062	1.00	56.46
	972	OD1	ASN	B	135	30.824	-27.386	39.285	1.00	47.82
	973	ND2	ASN	B	135	30.718	-28.752	41.064	1.00	67.17
35	974	C	ASN	B	135	26.491	-27.084	39.503	1.00	51.52
	975	O	ASN	B	135	25.963	-28.124	39.111	1.00	52.67
	976	N	ASN	B	136	25.783	-26.084	40.019	1.00	51.08
	977	CA	ASN	B	136	24.332	-26.206	40.094	1.00	50.58
	978	CB	ASN	B	136	23.745	-25.176	41.056	1.00	44.34
40	979	CG	ASN	B	136	23.673	-25.693	42.480	1.00	37.46
	980	OD1	ASN	B	136	23.038	-25.085	43.337	1.00	26.38
	981	ND2	ASN	B	136	24.322	-26.823	42.738	1.00	42.23
	982	C	ASN	B	136	23.717	-26.061	38.707	1.00	51.60

	983	O	ASN B 136	24.292	-25.425	37.825	1.00	53.87
	984	N	THR B 137	22.544	-26.649	38.510	1.00	50.58
	985	CA	THR B 137	21.913	-26.601	37.205	1.00	46.19
	986	CB	THR B 137	21.936	-27.981	36.568	1.00	44.64
5	987	OG1	THR B 137	21.269	-28.904	37.432	1.00	35.45
	988	CG2	THR B 137	23.354	-28.441	36.353	1.00	28.58
	989	C	THR B 137	20.475	-26.113	37.193	1.00	44.33
	990	O	THR B 137	19.697	-26.499	36.315	1.00	47.55
	991	N	GLY B 138	20.107	-25.273	38.152	1.00	40.76
10	992	CA	GLY B 138	18.743	-24.771	38.182	1.00	38.50
	993	C	GLY B 138	18.677	-23.358	37.647	1.00	37.87
	994	O	GLY B 138	19.532	-22.943	36.858	1.00	35.95
	995	N	LEU B 139	17.657	-22.618	38.064	1.00	37.09
	996	CA	LEU B 139	17.506	-21.231	37.641	1.00	37.28
15	997	CB	LEU B 139	16.337	-20.578	38.395	1.00	41.93
	998	CG	LEU B 139	15.975	-19.102	38.180	1.00	43.42
	999	CD1	LEU B 139	14.662	-18.827	38.888	1.00	36.62
	1000	CD2	LEU B 139	17.063	-18.175	38.706	1.00	40.37
	1001	C	LEU B 139	18.808	-20.537	38.012	1.00	35.36
20	1002	O	LEU B 139	19.455	-20.926	38.985	1.00	34.33
	1003	N	ILE B 140	19.204	-19.529	37.245	1.00	33.22
	1004	CA	ILE B 140	20.425	-18.814	37.573	1.00	32.63
	1005	CB	ILE B 140	21.300	-18.581	36.351	1.00	23.68
	1006	CG2	ILE B 140	22.611	-17.946	36.774	1.00	18.34
25	1007	CG1	ILE B 140	21.553	-19.903	35.642	1.00	19.23
	1008	CD1	ILE B 140	22.299	-19.751	34.357	1.00	16.92
	1009	C	ILE B 140	20.043	-17.466	38.143	1.00	33.01
	1010	O	ILE B 140	19.475	-16.629	37.450	1.00	37.44
	1011	N	LEU B 141	20.339	-17.261	39.420	1.00	29.19
30	1012	CA	LEU B 141	20.020	-15.997	40.060	1.00	27.02
	1013	CB	LEU B 141	19.847	-16.196	41.559	1.00	16.92
	1014	CG	LEU B 141	18.917	-15.186	42.219	1.00	17.32
	1015	CD1	LEU B 141	18.577	-15.645	43.627	1.00	16.92
	1016	CD2	LEU B 141	19.577	-13.827	42.221	1.00	16.92
35	1017	C	LEU B 141	21.160	-15.032	39.758	1.00	28.94
	1018	O	LEU B 141	22.206	-15.043	40.410	1.00	25.64
	1019	N	ASN B 142	20.934	-14.204	38.746	1.00	31.00
	1020	CA	ASN B 142	21.917	-13.242	38.292	1.00	33.31
	1021	CB	ASN B 142	21.749	-13.079	36.787	1.00	23.76
40	1022	CG	ASN B 142	23.033	-12.706	36.094	1.00	30.31
	1023	OD1	ASN B 142	24.057	-13.360	36.271	1.00	44.03
	1024	ND2	ASN B 142	22.985	-11.659	35.288	1.00	27.58
	1025	C	ASN B 142	21.759	-11.900	39.000	1.00	38.34

	1026	O	ASN B 142	20.721	-11.249	38.880	1.00	41.87
	1027	N	PHE B 143	22.788	-11.487	39.738	1.00	38.96
	1028	CA	PHE B 143	22.745	-10.219	40.468	1.00	38.15
	1029	CB	PHE B 143	23.466	-10.333	41.818	1.00	29.21
5	1030	CG	PHE B 143	22.646	-10.974	42.889	1.00	26.76
	1031	CD1	PHE B 143	22.916	-12.273	43.310	1.00	28.11
	1032	CD2	PHE B 143	21.581	-10.294	43.462	1.00	23.22
	1033	CE1	PHE B 143	22.135	-12.890	44.286	1.00	33.48
	1034	CE2	PHE B 143	20.790	-10.901	44.439	1.00	17.47
10	1035	CZ	PHE B 143	21.068	-12.203	44.852	1.00	19.85
	1036	C	PHE B 143	23.334	-9.027	39.740	1.00	40.69
	1037	O	PHE B 143	24.488	-9.052	39.330	1.00	42.36
	1038	N	ALA B 144	22.538	-7.975	39.593	1.00	40.34
	1039	CA	ALA B 144	23.019	-6.754	38.959	1.00	34.53
15	1040	CB	ALA B 144	21.893	-6.088	38.163	1.00	32.61
	1041	C	ALA B 144	23.501	-5.834	40.097	1.00	30.81
	1042	O	ALA B 144	22.709	-5.091	40.691	1.00	22.94
	1043	N	LEU B 145	24.796	-5.905	40.408	1.00	30.25
	1044	CA	LEU B 145	25.384	-5.101	41.477	1.00	32.00
20	1045	CB	LEU B 145	26.037	-6.015	42.501	1.00	29.70
	1046	CG	LEU B 145	24.928	-6.794	43.207	1.00	33.67
	1047	CD1	LEU B 145	25.428	-8.156	43.634	1.00	32.67
	1048	CD2	LEU B 145	24.407	-5.970	44.374	1.00	17.99
	1049	C	LEU B 145	26.386	-4.105	40.936	1.00	32.87
25	1050	O	LEU B 145	27.308	-4.470	40.214	1.00	34.08
	1051	N	ASN B 146	26.199	-2.844	41.316	1.00	36.56
	1052	CA	ASN B 146	27.025	-1.741	40.844	1.00	38.10
	1053	CB	ASN B 146	28.443	-1.818	41.416	1.00	32.16
	1054	CG	ASN B 146	29.242	-0.554	41.142	1.00	36.02
30	1055	OD1	ASN B 146	28.739	0.556	41.316	1.00	38.28
	1056	ND2	ASN B 146	30.490	-0.713	40.717	1.00	37.10
	1057	C	ASN B 146	27.051	-1.822	39.318	1.00	39.84
	1058	O	ASN B 146	28.062	-1.538	38.675	1.00	40.22
	1059	N	TYR B 147	25.907	-2.213	38.758	1.00	37.99
35	1060	CA	TYR B 147	25.720	-2.366	37.320	1.00	38.54
	1061	CB	TYR B 147	24.882	-3.615	37.029	1.00	36.21
	1062	CG	TYR B 147	24.382	-3.697	35.600	1.00	32.62
	1063	CD1	TYR B 147	25.147	-4.299	34.602	1.00	29.51
	1064	CE1	TYR B 147	24.712	-4.318	33.273	1.00	33.34
40	1065	CD2	TYR B 147	23.163	-3.118	35.233	1.00	32.87
	1066	CE2	TYR B 147	22.721	-3.130	33.908	1.00	33.52
	1067	CZ	TYR B 147	23.499	-3.731	32.934	1.00	36.75
	1068	OH	TYR B 147	23.067	-3.741	31.625	1.00	40.69

	1069	C	TYR B 147	25.025	-1.167	36.694	1.00	38.81
	1070	O	TYR B 147	24.027	-0.668	37.212	1.00	39.53
	1071	N	GLY B 148	25.553	-0.729	35.559	1.00	34.56
	1072	CA	GLY B 148	24.973	0.390	34.849	1.00	35.29
5	1073	C	GLY B 148	24.844	0.084	33.367	1.00	36.55
	1074	O	GLY B 148	25.821	-0.266	32.713	1.00	34.11
	1075	N	GLY B 149	23.635	0.216	32.836	1.00	35.88
	1076	CA	GLY B 149	23.406	-0.053	31.428	1.00	35.86
	1077	C	GLY B 149	24.445	0.531	30.489	1.00	33.73
10	1078	O	GLY B 149	25.268	-0.194	29.924	1.00	34.86
	1079	N	ARG B 150	24.411	1.845	30.308	1.00	29.19
	1080	CA	ARG B 150	25.358	2.498	29.418	1.00	28.55
	1081	CB	ARG B 150	25.124	4.009	29.408	1.00	21.40
	1082	CG	ARG B 150	23.737	4.438	28.938	1.00	21.80
15	1083	CD	ARG B 150	23.659	5.946	28.778	1.00	16.92
	1084	NE	ARG B 150	22.302	6.390	28.487	1.00	16.92
	1085	CZ	ARG B 150	21.961	7.656	28.252	1.00	19.59
	1086	NH1	ARG B 150	22.883	8.614	28.269	1.00	23.32
	1087	NH2	ARG B 150	20.692	7.974	28.008	1.00	21.38
20	1088	C	ARG B 150	26.790	2.197	29.847	1.00	30.06
	1089	O	ARG B 150	27.701	2.105	29.021	1.00	26.00
	1090	N	ALA B 151	26.983	2.043	31.148	1.00	35.94
	1091	CA	ALA B 151	28.304	1.745	31.673	1.00	37.38
	1092	CB	ALA B 151	28.254	1.688	33.194	1.00	52.48
25	1093	C	ALA B 151	28.823	0.419	31.108	1.00	35.17
	1094	O	ALA B 151	29.959	0.345	30.635	1.00	31.19
	1095	N	GLU B 152	27.990	-0.620	31.161	1.00	32.94
	1096	CA	GLU B 152	28.362	-1.938	30.655	1.00	35.48
	1097	CB	GLU B 152	27.220	-2.933	30.859	1.00	30.00
30	1098	CG	GLU B 152	27.365	-4.223	30.062	1.00	19.49
	1099	CD	GLU B 152	26.125	-5.100	30.149	1.00	22.76
	1100	OE1	GLU B 152	25.001	-4.547	30.160	1.00	21.18
	1101	OE2	GLU B 152	26.264	-6.344	30.191	1.00	25.44
	1102	C	GLU B 152	28.734	-1.900	29.179	1.00	38.76
35	1103	O	GLU B 152	29.749	-2.473	28.785	1.00	39.19
	1104	N	ILE B 153	27.914	-1.236	28.365	1.00	39.55
	1105	CA	ILE B 153	28.182	-1.146	26.929	1.00	38.31
	1106	CB	ILE B 153	27.053	-0.420	26.173	1.00	32.60
	1107	CG2	ILE B 153	27.348	-0.418	24.692	1.00	35.83
40	1108	CG1	ILE B 153	25.718	-1.111	26.425	1.00	37.55
	1109	CD1	ILE B 153	24.555	-0.452	25.731	1.00	34.30
	1110	C	ILE B 153	29.479	-0.399	26.648	1.00	40.62
	1111	O	ILE B 153	30.215	-0.747	25.729	1.00	37.23

	1112	N	THR B 154	29.747	0.631	27.446	1.00	45.36
	1113	CA	THR B 154	30.953	1.442	27.298	1.00	47.53
	1114	CB	THR B 154	30.937	2.624	28.270	1.00	36.71
	1115	OG1	THR B 154	29.670	3.278	28.194	1.00	34.10
5	1116	CG2	THR B 154	32.016	3.617	27.910	1.00	31.30
	1117	C	THR B 154	32.194	0.601	27.567	1.00	51.16
	1118	O	THR B 154	33.211	0.732	26.885	1.00	50.52
	1119	N	GLN B 155	32.099	-0.260	28.572	1.00	55.38
	1120	CA	GLN B 155	33.192	-1.143	28.946	1.00	57.33
10	1121	CB	GLN B 155	32.855	-1.851	30.264	1.00	67.23
	1122	CG	GLN B 155	33.707	-3.068	30.590	1.00	83.16
	1123	CD	GLN B 155	33.045	-4.380	30.180	1.00	90.67
	1124	OE1	GLN B 155	33.604	-5.461	30.385	1.00	95.55
	1125	NE2	GLN B 155	31.849	-4.291	29.603	1.00	94.98
15	1126	C	GLN B 155	33.418	-2.155	27.832	1.00	56.79
	1127	O	GLN B 155	34.555	-2.448	27.470	1.00	57.35
	1128	N	ALA B 156	32.327	-2.680	27.284	1.00	54.82
	1129	CA	ALA B 156	32.416	-3.655	26.210	1.00	52.43
	1130	CB	ALA B 156	31.051	-4.259	25.941	1.00	53.56
20	1131	C	ALA B 156	32.933	-2.962	24.964	1.00	52.01
	1132	O	ALA B 156	33.714	-3.527	24.203	1.00	50.83
	1133	N	LEU B 157	32.500	-1.725	24.766	1.00	53.20
	1134	CA	LEU B 157	32.907	-0.945	23.606	1.00	54.15
	1135	CB	LEU B 157	32.004	0.286	23.480	1.00	59.88
25	1136	CG	LEU B 157	32.116	1.171	22.238	1.00	68.36
	1137	CD1	LEU B 157	30.749	1.785	21.941	1.00	66.20
	1138	CD2	LEU B 157	33.190	2.240	22.442	1.00	73.25
	1139	C	LEU B 157	34.376	-0.535	23.711	1.00	53.24
	1140	O	LEU B 157	35.027	-0.250	22.709	1.00	53.64
30	1141	N	LYS B 158	34.889	-0.522	24.935	1.00	48.90
	1142	CA	LYS B 158	36.275	-0.156	25.196	1.00	43.03
	1143	CB	LYS B 158	36.395	0.368	26.632	1.00	51.76
	1144	CG	LYS B 158	37.738	0.976	27.006	1.00	50.73
	1145	CD	LYS B 158	37.553	2.108	28.020	1.00	59.64
35	1146	CE	LYS B 158	36.717	1.678	29.233	1.00	62.25
	1147	NZ	LYS B 158	36.406	2.801	30.175	1.00	58.23
	1148	C	LYS B 158	37.174	-1.374	24.983	1.00	38.44
	1149	O	LYS B 158	38.192	-1.288	24.304	1.00	36.00
	1150	N	LEU B 159	36.784	-2.505	25.566	1.00	39.17
40	1151	CA	LEU B 159	37.530	-3.755	25.432	1.00	39.21
	1152	CB	LEU B 159	36.780	-4.898	26.116	1.00	46.03
	1153	CG	LEU B 159	36.840	-5.020	27.635	1.00	49.65
	1154	CD1	LEU B 159	35.775	-5.991	28.124	1.00	52.44

	1155	CD2	LEU B 159	38.222	-5.492	28.034	1.00	50.53
	1156	C	LEU B 159	37.729	-4.121	23.964	1.00	38.04
	1157	O	LEU B 159	38.792	-4.599	23.576	1.00	32.72
	1158	N	ILE B 160	36.692	-3.913	23.157	1.00	39.18
5	1159	CA	ILE B 160	36.757	-4.219	21.732	1.00	39.26
	1160	CB	ILE B 160	35.382	-4.045	21.062	1.00	29.65
	1161	CG2	ILE B 160	35.493	-4.272	19.559	1.00	21.54
	1162	CG1	ILE B 160	34.383	-5.027	21.668	1.00	33.17
	1163	CD1	ILE B 160	32.981	-4.844	21.155	1.00	27.59
10	1164	C	ILE B 160	37.767	-3.303	21.042	1.00	42.75
	1165	O	ILE B 160	38.630	-3.767	20.304	1.00	41.60
	1166	N	SER B 161	37.662	-2.001	21.283	1.00	47.98
	1167	CA	SER B 161	38.593	-1.055	20.678	1.00	52.98
	1168	CB	SER B 161	38.154	0.387	20.942	1.00	51.83
15	1169	OG	SER B 161	36.966	0.699	20.235	1.00	47.45
	1170	C	SER B 161	39.987	-1.270	21.244	1.00	54.93
	1171	O	SER B 161	40.862	-0.420	21.103	1.00	59.36
	1172	N	GLN B 162	40.183	-2.407	21.902	1.00	54.75
	1173	CA	GLN B 162	41.471	-2.748	22.480	1.00	57.55
20	1174	CB	GLN B 162	41.327	-3.031	23.971	1.00	57.42
	1175	CG	GLN B 162	42.644	-3.337	24.667	1.00	59.30
	1176	CD	GLN B 162	43.554	-2.129	24.738	1.00	61.11
	1177	OE1	GLN B 162	43.922	-1.555	23.716	1.00	65.88
	1178	NE2	GLN B 162	43.923	-1.738	25.951	1.00	72.94
25	1179	C	GLN B 162	41.989	-3.987	21.764	1.00	60.23
	1180	O	GLN B 162	43.147	-4.047	21.358	1.00	61.01
	1181	N	ASP B 163	41.120	-4.980	21.616	1.00	61.53
	1182	CA	ASP B 163	41.482	-6.208	20.925	1.00	59.20
	1183	CB	ASP B 163	40.345	-7.229	21.037	1.00	59.79
30	1184	CG	ASP B 163	40.090	-7.668	22.465	1.00	63.02
	1185	OD1	ASP B 163	40.045	-6.796	23.354	1.00	72.81
	1186	OD2	ASP B 163	39.924	-8.883	22.701	1.00	61.86
	1187	C	ASP B 163	41.730	-5.850	19.459	1.00	57.70
	1188	O	ASP B 163	42.537	-6.482	18.782	1.00	55.82
35	1189	N	VAL B 164	41.025	-4.828	18.981	1.00	57.73
	1190	CA	VAL B 164	41.160	-4.365	17.606	1.00	59.37
	1191	CB	VAL B 164	40.087	-3.332	17.249	1.00	55.59
	1192	CG1	VAL B 164	40.362	-2.753	15.865	1.00	47.40
	1193	CG2	VAL B 164	38.724	-3.975	17.285	1.00	51.18
40	1194	C	VAL B 164	42.504	-3.694	17.443	1.00	62.08
	1195	O	VAL B 164	43.213	-3.914	16.461	1.00	65.19
	1196	N	LEU B 165	42.839	-2.853	18.411	1.00	63.92
	1197	CA	LEU B 165	44.104	-2.142	18.394	1.00	62.86



	1198	CB	LEU B 165	44.143	-1.140	19.547	1.00	45.47
	1199	CG	LEU B 165	45.282	-0.128	19.554	1.00	40.70
	1200	CD1	LEU B 165	44.794	1.202	20.101	1.00	39.99
	1201	CD2	LEU B 165	46.424	-0.682	20.377	1.00	39.90
5	1202	C	LEU B 165	45.218	-3.174	18.526	1.00	63.35
	1203	O	LEU B 165	46.195	-3.143	17.778	1.00	63.16
	1204	N	ASP B 166	45.053	-4.099	19.466	1.00	64.85
	1205	CA	ASP B 166	46.029	-5.161	19.678	1.00	65.80
	1206	CB	ASP B 166	45.736	-5.902	20.983	1.00	71.82
10	1207	CG	ASP B 166	46.139	-5.108	22.204	1.00	70.86
	1208	OD1	ASP B 166	45.691	-3.950	22.338	1.00	65.25
	1209	OD2	ASP B 166	46.904	-5.642	23.035	1.00	80.37
	1210	C	ASP B 166	45.977	-6.145	18.514	1.00	66.21
	1211	O	ASP B 166	46.435	-7.282	18.625	1.00	65.89
15	1212	N	ALA B 167	45.408	-5.691	17.400	1.00	66.17
	1213	CA	ALA B 167	45.280	-6.503	16.194	1.00	66.51
	1214	CB	ALA B 167	46.612	-6.539	15.449	1.00	63.12
	1215	C	ALA B 167	44.800	-7.923	16.485	1.00	67.20
	1216	O	ALA B 167	45.594	-8.860	16.545	1.00	64.87
20	1217	N	LYS B 168	43.493	-8.068	16.675	1.00	69.56
	1218	CA	LYS B 168	42.891	-9.369	16.935	1.00	70.73
	1219	CB	LYS B 168	42.391	-9.467	18.371	1.00	55.74
	1220	CG	LYS B 168	43.483	-9.612	19.384	1.00	43.98
	1221	CD	LYS B 168	42.898	-10.035	20.709	1.00	50.77
25	1222	CE	LYS B 168	43.995	-10.341	21.712	1.00	54.71
	1223	NZ	LYS B 168	44.917	-9.181	21.875	1.00	56.54
	1224	C	LYS B 168	41.723	-9.562	15.993	1.00	74.61
	1225	O	LYS B 168	41.734	-10.448	15.137	1.00	79.29
	1226	N	ILE B 169	40.709	-8.725	16.160	1.00	75.01
30	1227	CA	ILE B 169	39.541	-8.796	15.307	1.00	77.20
	1228	CB	ILE B 169	38.228	-8.822	16.137	1.00	70.32
	1229	CG2	ILE B 169	38.252	-10.003	17.095	1.00	64.44
	1230	CG1	ILE B 169	38.051	-7.519	16.922	1.00	67.21
	1231	CD1	ILE B 169	39.064	-7.306	18.014	1.00	62.39
35	1232	C	ILE B 169	39.571	-7.577	14.400	1.00	81.65
	1233	O	ILE B 169	39.866	-6.470	14.851	1.00	82.71
	1234	N	ASN B 170	39.298	-7.792	13.116	1.00	84.48
	1235	CA	ASN B 170	39.299	-6.699	12.153	1.00	86.01
	1236	CB	ASN B 170	38.780	-7.160	10.781	1.00	99.20
40	1237	CG	ASN B 170	39.291	-8.540	10.382	1.00	105.24
	1238	OD1	ASN B 170	40.415	-8.921	10.713	1.00	109.37
	1239	ND2	ASN B 170	38.466	-9.288	9.651	1.00	104.96
	1240	C	ASN B 170	38.361	-5.641	12.695	1.00	84.21

	1241	O	ASN B 170	37.397	-5.960	13.385	1.00	83.04
	1242	N	PRO B 171	38.630	-4.364	12.407	1.00	84.49
	1243	CD	PRO B 171	39.617	-3.766	11.493	1.00	86.08
	1244	CA	PRO B 171	37.708	-3.355	12.931	1.00	84.63
5	1245	CB	PRO B 171	38.340	-2.045	12.469	1.00	86.37
	1246	CG	PRO B 171	38.976	-2.436	11.164	1.00	86.68
	1247	C	PRO B 171	36.336	-3.610	12.306	1.00	82.79
	1248	O	PRO B 171	35.323	-3.051	12.726	1.00	82.76
	1249	N	GLY B 172	36.328	-4.480	11.299	1.00	80.64
10	1250	CA	GLY B 172	35.100	-4.828	10.613	1.00	81.32
	1251	C	GLY B 172	34.411	-6.036	11.219	1.00	81.29
	1252	O	GLY B 172	33.278	-6.351	10.859	1.00	83.71
	1253	N	ASP B 173	35.094	-6.722	12.130	1.00	79.07
	1254	CA	ASP B 173	34.527	-7.890	12.795	1.00	75.74
15	1255	CB	ASP B 173	35.627	-8.696	13.487	1.00	85.90
	1256	CG	ASP B 173	36.308	-9.665	12.553	1.00	90.56
	1257	OD1	ASP B 173	36.641	-9.260	11.421	1.00	93.25
	1258	OD2	ASP B 173	36.514	-10.830	12.952	1.00	92.57
	1259	C	ASP B 173	33.481	-7.464	13.822	1.00	70.25
20	1260	O	ASP B 173	32.727	-8.288	14.343	1.00	68.50
	1261	N	ILE B 174	33.444	-6.169	14.114	1.00	65.51
	1262	CA	ILE B 174	32.486	-5.628	15.064	1.00	60.45
	1263	CB	ILE B 174	32.687	-4.119	15.234	1.00	48.40
	1264	CG2	ILE B 174	31.684	-3.562	16.226	1.00	46.12
25	1265	CG1	ILE B 174	34.115	-3.851	15.702	1.00	44.86
	1266	CD1	ILE B 174	34.461	-2.387	15.797	1.00	31.07
	1267	C	ILE B 174	31.077	-5.886	14.549	1.00	58.37
	1268	O	ILE B 174	30.679	-5.344	13.524	1.00	58.27
	1269	N	THR B 175	30.327	-6.719	15.261	1.00	55.65
30	1270	CA	THR B 175	28.964	-7.043	14.869	1.00	53.67
	1271	CB	THR B 175	28.897	-8.435	14.236	1.00	57.15
	1272	OG1	THR B 175	29.168	-9.429	15.230	1.00	55.78
	1273	CG2	THR B 175	29.932	-8.560	13.145	1.00	49.80
	1274	C	THR B 175	28.084	-7.032	16.110	1.00	52.38
35	1275	O	THR B 175	28.577	-6.835	17.217	1.00	52.43
	1276	N	GLU B 176	26.784	-7.232	15.938	1.00	51.31
	1277	CA	GLU B 176	25.895	-7.261	17.089	1.00	48.46
	1278	CB	GLU B 176	24.434	-7.240	16.643	1.00	37.51
	1279	CG	GLU B 176	23.950	-5.856	16.281	1.00	45.01
40	1280	CD	GLU B 176	22.474	-5.813	15.956	1.00	45.89
	1281	OE1	GLU B 176	21.690	-6.538	16.615	1.00	42.92
	1282	OE2	GLU B 176	22.103	-5.036	15.051	1.00	34.90
	1283	C	GLU B 176	26.187	-8.519	17.893	1.00	49.50

	1284	O	GLU B 176	26.038	-8.544	19.113	1.00	49.76
	1285	N	GLU B 177	26.613	-9.563	17.192	1.00	48.42
	1286	CA	GLU B 177	26.950	-10.820	17.836	1.00	48.94
	1287	CB	GLU B 177	27.318	-11.868	16.779	1.00	63.07
5	1288	CG	GLU B 177	27.685	-13.239	17.350	1.00	72.68
	1289	CD	GLU B 177	28.766	-13.953	16.545	1.00	76.09
	1290	OE1	GLU B 177	29.081	-15.121	16.869	1.00	77.97
	1291	OE2	GLU B 177	29.309	-13.346	15.595	1.00	76.21
	1292	C	GLU B 177	28.149	-10.576	18.754	1.00	47.13
10	1293	O	GLU B 177	28.129	-10.926	19.934	1.00	43.82
	1294	N	LEU B 178	29.189	-9.960	18.199	1.00	46.13
	1295	CA	LEU B 178	30.416	-9.678	18.938	1.00	41.18
	1296	CB	LEU B 178	31.444	-9.015	18.011	1.00	31.24
	1297	CG	LEU B 178	32.881	-8.843	18.521	1.00	29.48
15	1298	CD1	LEU B 178	33.762	-8.385	17.378	1.00	32.21
	1299	CD2	LEU B 178	32.940	-7.834	19.650	1.00	38.13
	1300	C	LEU B 178	30.176	-8.805	20.166	1.00	41.26
	1301	O	LEU B 178	30.455	-9.229	21.286	1.00	44.23
	1302	N	ILE B 179	29.669	-7.591	19.954	1.00	37.47
20	1303	CA	ILE B 179	29.395	-6.664	21.053	1.00	33.95
	1304	CB	ILE B 179	28.502	-5.491	20.592	1.00	25.86
	1305	CG2	ILE B 179	28.071	-4.676	21.783	1.00	27.50
	1306	CG1	ILE B 179	29.267	-4.596	19.617	1.00	24.58
	1307	CD1	ILE B 179	28.434	-3.481	19.007	1.00	16.92
25	1308	C	ILE B 179	28.687	-7.389	22.189	1.00	36.09
	1309	O	ILE B 179	28.901	-7.093	23.367	1.00	36.52
	1310	N	GLY B 180	27.849	-8.353	21.821	1.00	37.19
	1311	CA	GLY B 180	27.108	-9.120	22.804	1.00	34.45
	1312	C	GLY B 180	27.967	-10.057	23.630	1.00	33.00
30	1313	O	GLY B 180	27.619	-10.390	24.766	1.00	32.59
	1314	N	ASN B 181	29.085	-10.491	23.060	1.00	35.65
	1315	CA	ASN B 181	29.989	-11.388	23.766	1.00	34.95
	1316	CB	ASN B 181	30.876	-12.153	22.784	1.00	30.99
	1317	CG	ASN B 181	30.086	-13.010	21.838	1.00	27.11
35	1318	OD1	ASN B 181	29.187	-13.735	22.251	1.00	30.62
	1319	ND2	ASN B 181	30.424	-12.943	20.557	1.00	34.99
	1320	C	ASN B 181	30.880	-10.617	24.724	1.00	32.99
	1321	O	ASN B 181	31.621	-11.224	25.486	1.00	27.15
	1322	N	TYR B 182	30.811	-9.288	24.684	1.00	31.98
40	1323	CA	TYR B 182	31.634	-8.456	25.552	1.00	30.09
	1324	CB	TYR B 182	32.323	-7.372	24.742	1.00	29.07
	1325	CG	TYR B 182	33.529	-7.857	23.974	1.00	30.62
	1326	CD1	TYR B 182	33.411	-8.828	22.976	1.00	31.56

	1327	CE1	TYR	B	182	34.533	-9.256	22.247	1.00	31.15
	1328	CD2	TYR	B	182	34.796	-7.325	24.229	1.00	32.17
	1329	CE2	TYR	B	182	35.921	-7.740	23.507	1.00	29.49
	1330	CZ	TYR	B	182	35.783	-8.705	22.520	1.00	30.88
5	1331	OH	TYR	B	182	36.898	-9.105	21.814	1.00	38.87
	1332	C	TYR	B	182	30.871	-7.814	26.689	1.00	30.63
	1333	O	TYR	B	182	31.455	-7.108	27.507	1.00	27.81
	1334	N	LEU	B	183	29.565	-8.055	26.736	1.00	33.68
	1335	CA	LEU	B	183	28.722	-7.510	27.795	1.00	39.37
10	1336	CB	LEU	B	183	27.281	-7.389	27.298	1.00	39.69
	1337	CG	LEU	B	183	27.086	-6.546	26.040	1.00	35.29
	1338	CD1	LEU	B	183	25.629	-6.594	25.618	1.00	30.83
	1339	CD2	LEU	B	183	27.525	-5.121	26.308	1.00	36.26
	1340	C	LEU	B	183	28.780	-8.422	29.030	1.00	40.34
15	1341	O	LEU	B	183	29.084	-9.610	28.915	1.00	39.87
	1342	N	PHE	B	184	28.490	-7.873	30.206	1.00	38.84
	1343	CA	PHE	B	184	28.532	-8.659	31.437	1.00	37.83
	1344	CB	PHE	B	184	28.026	-7.843	32.633	1.00	31.19
	1345	CG	PHE	B	184	28.751	-6.538	32.843	1.00	28.22
20	1346	CD1	PHE	B	184	30.068	-6.377	32.436	1.00	30.85
	1347	CD2	PHE	B	184	28.115	-5.474	33.481	1.00	33.99
	1348	CE1	PHE	B	184	30.736	-5.175	32.663	1.00	24.17
	1349	CE2	PHE	B	184	28.778	-4.268	33.713	1.00	21.76
	1350	CZ	PHE	B	184	30.087	-4.120	33.305	1.00	18.36
25	1351	C	PHE	B	184	27.697	-9.929	31.319	1.00	36.97
	1352	O	PHE	B	184	27.947	-10.914	32.014	1.00	32.04
	1353	N	THR	B	185	26.704	-9.903	30.441	1.00	38.47
	1354	CA	THR	B	185	25.841	-11.059	30.243	1.00	42.41
	1355	CB	THR	B	185	24.478	-10.625	29.741	1.00	34.61
30	1356	OG1	THR	B	185	24.651	-9.691	28.671	1.00	41.28
	1357	CG2	THR	B	185	23.696	-9.975	30.853	1.00	34.33
	1358	C	THR	B	185	26.423	-12.052	29.248	1.00	44.70
	1359	O	THR	B	185	25.700	-12.896	28.720	1.00	41.53
	1360	N	GLN	B	186	27.728	-11.951	29.008	1.00	48.74
35	1361	CA	GLN	B	186	28.438	-12.826	28.074	1.00	49.59
	1362	CB	GLN	B	186	29.790	-12.227	27.736	1.00	45.10
	1363	CG	GLN	B	186	30.776	-12.389	28.875	1.00	43.93
	1364	CD	GLN	B	186	32.116	-11.753	28.593	1.00	47.95
	1365	OE1	GLN	B	186	32.249	-10.530	28.593	1.00	50.02
40	1366	NE2	GLN	B	186	33.119	-12.583	28.342	1.00	38.99
	1367	C	GLN	B	186	28.677	-14.203	28.682	1.00	51.53
	1368	O	GLN	B	186	29.115	-15.130	27.996	1.00	55.42
	1369	N	HIS	B	187	28.409	-14.320	29.977	1.00	50.40

	1370	CA	HIS B 187	28.598	-15.565	30.708	1.00	49.57
	1371	CB	HIS B 187	28.773	-15.243	32.190	1.00	42.89
	1372	CG	HIS B 187	29.841	-14.223	32.442	1.00	49.91
	1373	CD2	HIS B 187	29.801	-13.022	33.068	1.00	49.67
5	1374	ND1	HIS B 187	31.127	-14.361	31.962	1.00	43.80
	1375	CE1	HIS B 187	31.833	-13.289	32.278	1.00	48.87
	1376	NE2	HIS B 187	31.053	-12.460	32.949	1.00	46.70
	1377	C	HIS B 187	27.439	-16.521	30.487	1.00	52.33
	1378	O	HIS B 187	27.636	-17.718	30.286	1.00	53.97
10	1379	N	LEU B 188	26.226	-15.992	30.514	1.00	54.52
	1380	CA	LEU B 188	25.051	-16.813	30.289	1.00	51.83
	1381	CB	LEU B 188	23.789	-15.984	30.549	1.00	44.55
	1382	CG	LEU B 188	23.659	-15.395	31.962	1.00	47.65
	1383	CD1	LEU B 188	22.452	-14.467	32.039	1.00	49.93
15	1384	CD2	LEU B 188	23.537	-16.520	32.980	1.00	56.89
	1385	C	LEU B 188	25.085	-17.310	28.838	1.00	52.44
	1386	O	LEU B 188	25.560	-16.611	27.946	1.00	53.35
	1387	N	PRO B 189	24.594	-18.532	28.590	1.00	51.33
	1388	CD	PRO B 189	23.882	-19.388	29.549	1.00	51.94
20	1389	CA	PRO B 189	24.565	-19.127	27.244	1.00	49.93
	1390	CB	PRO B 189	23.822	-20.442	27.463	1.00	51.02
	1391	CG	PRO B 189	22.944	-20.139	28.642	1.00	52.36
	1392	C	PRO B 189	23.878	-18.244	26.210	1.00	46.59
	1393	O	PRO B 189	22.834	-17.661	26.482	1.00	45.97
25	1394	N	LYS B 190	24.451	-18.166	25.016	1.00	42.50
	1395	CA	LYS B 190	23.889	-17.315	23.977	1.00	39.80
	1396	CB	LYS B 190	24.439	-17.688	22.596	1.00	36.33
	1397	CG	LYS B 190	25.879	-17.235	22.345	1.00	38.65
	1398	CD	LYS B 190	26.252	-17.384	20.871	1.00	42.37
30	1399	CE	LYS B 190	27.748	-17.183	20.632	1.00	50.39
	1400	NZ	LYS B 190	28.221	-15.806	20.958	1.00	58.82
	1401	C	LYS B 190	22.373	-17.219	23.892	1.00	39.26
	1402	O	LYS B 190	21.838	-16.115	23.940	1.00	39.95
	1403	N	ASP B 191	21.664	-18.337	23.777	1.00	40.10
35	1404	CA	ASP B 191	20.210	-18.235	23.658	1.00	39.42
	1405	CB	ASP B 191	19.606	-19.543	23.098	1.00	39.52
	1406	CG	ASP B 191	19.725	-20.721	24.060	1.00	44.32
	1407	OD1	ASP B 191	20.868	-21.170	24.306	1.00	39.96
	1408	OD2	ASP B 191	18.674	-21.200	24.565	1.00	42.53
40	1409	C	ASP B 191	19.471	-17.804	24.936	1.00	39.16
	1410	O	ASP B 191	18.250	-17.604	24.922	1.00	41.35
	1411	N	LEU B 192	20.207	-17.632	26.031	1.00	37.21
	1412	CA	LEU B 192	19.589	-17.218	27.294	1.00	34.43

	1413	CB	LEU B 192	19.877	-18.258	28.397	1.00	26.76
	1414	CG	LEU B 192	19.100	-19.585	28.315	1.00	23.82
	1415	CD1	LEU B 192	19.659	-20.569	29.310	1.00	16.92
	1416	CD2	LEU B 192	17.607	-19.345	28.582	1.00	16.92
5	1417	C	LEU B 192	20.024	-15.826	27.761	1.00	34.24
	1418	O	LEU B 192	19.508	-15.310	28.748	1.00	38.50
	1419	N	ARG B 193	20.957	-15.221	27.029	1.00	30.50
	1420	CA	ARG B 193	21.484	-13.900	27.358	1.00	29.14
	1421	CB	ARG B 193	22.587	-13.507	26.377	1.00	23.71
10	1422	CG	ARG B 193	23.838	-14.307	26.522	1.00	24.21
	1423	CD	ARG B 193	24.862	-13.896	25.494	1.00	20.84
	1424	NE	ARG B 193	26.131	-14.599	25.681	1.00	31.16
	1425	CZ	ARG B 193	27.191	-14.455	24.890	1.00	37.18
	1426	NH1	ARG B 193	27.141	-13.630	23.846	1.00	39.87
15	1427	NH2	ARG B 193	28.303	-15.131	25.147	1.00	37.17
	1428	C	ARG B 193	20.483	-12.756	27.415	1.00	28.97
	1429	O	ARG B 193	20.638	-11.853	28.225	1.00	29.31
	1430	N	ASP B 194	19.465	-12.764	26.566	1.00	24.43
	1431	CA	ASP B 194	18.520	-11.660	26.588	1.00	26.20
20	1432	CB	ASP B 194	18.180	-11.217	25.157	1.00	21.25
	1433	CG	ASP B 194	19.413	-10.763	24.361	1.00	25.14
	1434	OD1	ASP B 194	20.357	-10.207	24.973	1.00	16.92
	1435	OD2	ASP B 194	19.427	-10.948	23.119	1.00	30.59
	1436	C	ASP B 194	17.241	-11.990	27.344	1.00	24.70
25	1437	O	ASP B 194	16.638	-13.043	27.133	1.00	31.23
	1438	N	PRO B 195	16.811	-11.088	28.242	1.00	19.04
	1439	CD	PRO B 195	17.403	-9.779	28.558	1.00	16.92
	1440	CA	PRO B 195	15.593	-11.299	29.024	1.00	22.28
	1441	CB	PRO B 195	15.552	-10.077	29.935	1.00	21.56
30	1442	CG	PRO B 195	16.229	-9.044	29.139	1.00	18.86
	1443	C	PRO B 195	14.392	-11.371	28.110	1.00	24.96
	1444	O	PRO B 195	14.345	-10.680	27.101	1.00	30.51
	1445	N	ASP B 196	13.431	-12.217	28.450	1.00	22.33
	1446	CA	ASP B 196	12.237	-12.347	27.631	1.00	21.67
35	1447	CB	ASP B 196	11.826	-13.808	27.522	1.00	21.17
	1448	CG	ASP B 196	12.875	-14.636	26.849	1.00	35.32
	1449	OD1	ASP B 196	13.781	-15.133	27.550	1.00	31.80
	1450	OD2	ASP B 196	12.808	-14.767	25.609	1.00	44.56
	1451	C	ASP B 196	11.116	-11.525	28.225	1.00	22.00
40	1452	O	ASP B 196	10.049	-11.363	27.633	1.00	22.34
	1453	N	LEU B 197	11.381	-10.999	29.409	1.00	24.46
	1454	CA	LEU B 197	10.423	-10.174	30.104	1.00	22.14
	1455	CB	LEU B 197	9.336	-11.036	30.748	1.00	16.92

	1456	CG	LEU B 197	8.462	-10.340	31.797	1.00	16.92
	1457	CD1	LEU B 197	7.828	-9.106	31.228	1.00	18.26
	1458	CD2	LEU B 197	7.396	-11.274	32.273	1.00	23.97
	1459	C	LEU B 197	11.163	-9.394	31.163	1.00	24.32
5	1460	O	LEU B 197	12.064	-9.913	31.809	1.00	31.10
	1461	N	ILE B 198	10.806	-8.128	31.312	1.00	25.23
	1462	CA	ILE B 198	11.419	-7.301	32.327	1.00	23.49
	1463	CB	ILE B 198	12.252	-6.163	31.728	1.00	16.92
	1464	CG2	ILE B 198	12.760	-5.255	32.837	1.00	16.92
10	1465	CG1	ILE B 198	13.434	-6.755	30.956	1.00	19.52
	1466	CD1	ILE B 198	14.494	-5.751	30.554	1.00	16.92
	1467	C	ILE B 198	10.312	-6.750	33.205	1.00	26.00
	1468	O	ILE B 198	9.458	-5.983	32.760	1.00	23.12
	1469	N	ILE B 199	10.336	-7.191	34.457	1.00	30.16
15	1470	CA	ILE B 199	9.361	-6.808	35.457	1.00	31.89
	1471	CB	ILE B 199	9.169	-7.966	36.461	1.00	31.40
	1472	CG2	ILE B 199	8.241	-7.539	37.597	1.00	35.99
	1473	CG1	ILE B 199	8.635	-9.194	35.709	1.00	30.96
	1474	CD1	ILE B 199	8.432	-10.422	36.562	1.00	25.50
20	1475	C	ILE B 199	9.797	-5.547	36.196	1.00	30.27
	1476	O	ILE B 199	10.973	-5.382	36.511	1.00	30.43
	1477	N	ARG B 200	8.843	-4.657	36.450	1.00	29.84
	1478	CA	ARG B 200	9.102	-3.413	37.167	1.00	34.70
	1479	CB	ARG B 200	9.192	-2.235	36.190	1.00	38.24
25	1480	CG	ARG B 200	9.649	-0.923	36.828	1.00	38.39
	1481	CD	ARG B 200	11.047	-1.036	37.439	1.00	41.65
	1482	NE	ARG B 200	11.489	0.171	38.148	1.00	34.53
	1483	CZ	ARG B 200	11.935	1.290	37.572	1.00	18.77
	1484	NH1	ARG B 200	12.014	1.399	36.252	1.00	16.92
30	1485	NH2	ARG B 200	12.314	2.307	38.326	1.00	18.24
	1486	C	ARG B 200	7.949	-3.211	38.145	1.00	35.76
	1487	O	ARG B 200	6.783	-3.252	37.756	1.00	33.19
	1488	N	THR B 201	8.277	-3.001	39.414	1.00	38.28
	1489	CA	THR B 201	7.262	-2.835	40.449	1.00	37.05
35	1490	CB	THR B 201	7.586	-3.722	41.664	1.00	16.92
	1491	OG1	THR B 201	8.943	-3.503	42.070	1.00	29.17
	1492	CG2	THR B 201	7.417	-5.174	41.315	1.00	19.67
	1493	C	THR B 201	7.102	-1.405	40.940	1.00	39.68
	1494	O	THR B 201	7.833	-0.509	40.522	1.00	41.56
40	1495	N	SER B 202	6.129	-1.204	41.826	1.00	41.87
	1496	CA	SER B 202	5.859	0.101	42.426	1.00	39.34
	1497	CB	SER B 202	7.157	0.679	42.992	1.00	19.15
	1498	OG	SER B 202	6.945	1.980	43.512	1.00	39.12

	1499	C	SER B 202	5.190	1.151	41.538	1.00	40.05
	1500	O	SER B 202	4.920	2.262	41.995	1.00	47.17
	1501	N	GLY B 203	4.922	0.811	40.281	1.00	38.45
	1502	CA	GLY B 203	4.287	1.762	39.377	1.00	37.08
5	1503	C	GLY B 203	5.271	2.563	38.534	1.00	35.70
	1504	O	GLY B 203	4.886	3.461	37.787	1.00	37.31
	1505	N	GLU B 204	6.550	2.231	38.654	1.00	29.52
	1506	CA	GLU B 204	7.586	2.917	37.908	1.00	28.07
	1507	CB	GLU B 204	8.952	2.653	38.538	1.00	26.30
10	1508	CG	GLU B 204	9.236	3.482	39.779	1.00	48.79
	1509	CD	GLU B 204	8.973	4.961	39.556	1.00	50.97
	1510	OE1	GLU B 204	7.849	5.419	39.869	1.00	42.50
	1511	OE2	GLU B 204	9.877	5.663	39.055	1.00	50.61
	1512	C	GLU B 204	7.616	2.477	36.462	1.00	29.34
15	1513	O	GLU B 204	7.878	1.317	36.175	1.00	34.97
	1514	N	LEU B 205	7.354	3.408	35.552	1.00	24.91
	1515	CA	LEU B 205	7.371	3.119	34.120	1.00	25.98
	1516	CB	LEU B 205	6.104	3.666	33.470	1.00	25.92
	1517	CG	LEU B 205	4.825	3.056	34.050	1.00	23.50
20	1518	CD1	LEU B 205	3.610	3.785	33.547	1.00	16.92
	1519	CD2	LEU B 205	4.753	1.600	33.668	1.00	30.67
	1520	C	LEU B 205	8.607	3.733	33.472	1.00	28.56
	1521	O	LEU B 205	8.526	4.382	32.441	1.00	29.61
	1522	N	ARG B 206	9.758	3.533	34.093	1.00	33.33
25	1523	CA	ARG B 206	10.992	4.075	33.561	1.00	37.25
	1524	CB	ARG B 206	11.776	4.826	34.645	1.00	42.74
	1525	CG	ARG B 206	10.936	5.391	35.782	1.00	40.30
	1526	CD	ARG B 206	11.792	6.156	36.799	1.00	44.32
	1527	NE	ARG B 206	12.921	5.371	37.312	1.00	65.13
30	1528	CZ	ARG B 206	13.705	5.748	38.324	1.00	69.76
	1529	NH1	ARG B 206	13.483	6.904	38.937	1.00	76.09
	1530	NH2	ARG B 206	14.714	4.974	38.727	1.00	74.71
	1531	C	ARG B 206	11.815	2.894	33.106	1.00	42.39
	1532	O	ARG B 206	11.384	1.745	33.228	1.00	42.90
35	1533	N	LEU B 207	13.005	3.175	32.592	1.00	44.87
	1534	CA	LEU B 207	13.887	2.114	32.150	1.00	48.66
	1535	CB	LEU B 207	14.442	2.437	30.763	1.00	63.61
	1536	CG	LEU B 207	13.391	2.281	29.657	1.00	70.49
	1537	CD1	LEU B 207	13.973	2.698	28.321	1.00	76.92
40	1538	CD2	LEU B 207	12.916	0.827	29.600	1.00	75.21
	1539	C	LEU B 207	15.001	1.932	33.175	1.00	47.29
	1540	O	LEU B 207	15.499	0.821	33.372	1.00	47.01
	1541	N	SER B 208	15.373	3.027	33.833	1.00	42.15



	1542	CA	SER B 208	16.407	3.001	34.866	1.00	32.73
	1543	CB	SER B 208	15.926	2.180	36.062	1.00	33.90
	1544	OG	SER B 208	14.588	2.494	36.396	1.00	24.12
	1545	C	SER B 208	17.752	2.451	34.404	1.00	28.39
5	1546	O	SER B 208	18.480	1.841	35.193	1.00	29.45
	1547	N	ASN B 209	18.071	2.652	33.128	1.00	26.85
	1548	CA	ASN B 209	19.348	2.212	32.561	1.00	27.50
	1549	CB	ASN B 209	20.468	3.114	33.127	1.00	16.92
	1550	CG	ASN B 209	21.836	2.862	32.494	1.00	22.61
10	1551	OD1	ASN B 209	21.954	2.602	31.300	1.00	26.46
	1552	ND2	ASN B 209	22.880	2.972	33.303	1.00	20.95
	1553	C	ASN B 209	19.645	0.730	32.814	1.00	32.21
	1554	O	ASN B 209	20.801	0.317	32.892	1.00	34.11
	1555	N	PHE B 210	18.592	-0.074	32.915	1.00	34.72
15	1556	CA	PHE B 210	18.754	-1.504	33.172	1.00	30.65
	1557	CB	PHE B 210	17.651	-1.991	34.122	1.00	21.62
	1558	CG	PHE B 210	17.790	-3.433	34.537	1.00	28.42
	1559	CD1	PHE B 210	18.932	-3.875	35.195	1.00	32.07
	1560	CD2	PHE B 210	16.769	-4.344	34.283	1.00	24.66
20	1561	CE1	PHE B 210	19.057	-5.194	35.594	1.00	22.48
	1562	CE2	PHE B 210	16.884	-5.663	34.677	1.00	24.33
	1563	CZ	PHE B 210	18.032	-6.090	35.334	1.00	18.91
	1564	C	PHE B 210	18.721	-2.309	31.881	1.00	30.28
	1565	O	PHE B 210	17.778	-2.197	31.101	1.00	26.90
25	1566	N	LEU B 211	19.759	-3.117	31.673	1.00	31.38
	1567	CA	LEU B 211	19.888	-3.959	30.484	1.00	30.02
	1568	CB	LEU B 211	19.093	-5.253	30.661	1.00	19.94
	1569	CG	LEU B 211	19.715	-6.354	31.512	1.00	17.90
	1570	CD1	LEU B 211	18.863	-7.623	31.409	1.00	17.79
30	1571	CD2	LEU B 211	21.132	-6.619	31.024	1.00	28.12
	1572	C	LEU B 211	19.454	-3.287	29.183	1.00	33.52
	1573	O	LEU B 211	18.659	-3.841	28.414	1.00	35.70
	1574	N	PRO B 212	19.994	-2.094	28.902	1.00	34.82
	1575	CD	PRO B 212	21.175	-1.502	29.547	1.00	34.05
35	1576	CA	PRO B 212	19.648	-1.359	27.684	1.00	31.21
	1577	CB	PRO B 212	20.608	-0.183	27.724	1.00	30.61
	1578	CG	PRO B 212	21.801	-0.762	28.411	1.00	33.84
	1579	C	PRO B 212	19.777	-2.188	26.400	1.00	28.88
	1580	O	PRO B 212	18.862	-2.209	25.578	1.00	28.95
40	1581	N	TRP B 213	20.905	-2.878	26.241	1.00	32.89
	1582	CA	TRP B 213	21.151	-3.705	25.062	1.00	34.16
	1583	CB	TRP B 213	22.653	-3.980	24.928	1.00	36.50
	1584	CG	TRP B 213	23.024	-4.885	23.779	1.00	40.25

	1585	CD2 TRP B 213	23.654	-4.494	22.559	1.00	41.82
	1586	CE2 TRP B 213	23.825	-5.664	21.782	1.00	42.56
	1587	CE3 TRP B 213	24.096	-3.266	22.043	1.00	36.15
	1588	CD1 TRP B 213	22.837	-6.241	23.695	1.00	34.48
5	1589	NE1 TRP B 213	23.317	-6.713	22.500	1.00	35.36
	1590	CZ2 TRP B 213	24.421	-5.640	20.516	1.00	41.79
	1591	CZ3 TRP B 213	24.687	-3.244	20.783	1.00	44.66
	1592	CH2 TRP B 213	24.845	-4.426	20.035	1.00	41.35
	1593	C TRP B 213	20.375	-5.034	25.026	1.00	31.31
10	1594	O TRP B 213	19.551	-5.252	24.140	1.00	28.47
	1595	N GLN B 214	20.644	-5.922	25.978	1.00	29.42
	1596	CA GLN B 214	19.975	-7.220	26.027	1.00	27.98
	1597	CB GLN B 214	20.420	-7.989	27.277	1.00	29.16
	1598	CG GLN B 214	21.926	-8.184	27.438	1.00	30.26
15	1599	CD GLN B 214	22.631	-7.032	28.150	1.00	35.27
	1600	OE1 GLN B 214	23.720	-7.208	28.699	1.00	35.10
	1601	NE2 GLN B 214	22.021	-5.852	28.137	1.00	36.97
	1602	C GLN B 214	18.442	-7.114	26.018	1.00	26.22
	1603	O GLN B 214	17.747	-7.935	25.414	1.00	26.19
20	1604	N GLY B 215	17.918	-6.101	26.695	1.00	24.50
	1605	CA GLY B 215	16.480	-5.932	26.755	1.00	20.34
	1606	C GLY B 215	15.870	-5.269	25.536	1.00	20.33
	1607	O GLY B 215	14.680	-4.978	25.537	1.00	19.80
	1608	N ALA B 216	16.671	-5.045	24.495	1.00	16.97
25	1609	CA ALA B 216	16.207	-4.397	23.265	1.00	17.93
	1610	CB ALA B 216	17.162	-4.710	22.109	1.00	17.20
	1611	C ALA B 216	14.773	-4.758	22.875	1.00	20.59
	1612	O ALA B 216	13.970	-3.865	22.602	1.00	23.60
	1613	N TYR B 217	14.437	-6.049	22.854	1.00	24.42
30	1614	CA TYR B 217	13.073	-6.462	22.494	1.00	18.63
	1615	CB TYR B 217	13.070	-7.402	21.282	1.00	16.92
	1616	CG TYR B 217	13.921	-6.990	20.092	1.00	16.92
	1617	CD1 TYR B 217	15.315	-7.115	20.127	1.00	16.92
	1618	CE1 TYR B 217	16.092	-6.810	19.007	1.00	16.92
35	1619	CD2 TYR B 217	13.328	-6.538	18.901	1.00	16.92
	1620	CE2 TYR B 217	14.098	-6.230	17.779	1.00	16.92
	1621	CZ TYR B 217	15.476	-6.371	17.840	1.00	16.92
	1622	OH TYR B 217	16.247	-6.095	16.735	1.00	16.92
	1623	C TYR B 217	12.326	-7.173	23.629	1.00	16.92
40	1624	O TYR B 217	11.433	-7.982	23.380	1.00	16.92
	1625	N SER B 218	12.673	-6.874	24.873	1.00	16.92
	1626	CA SER B 218	12.011	-7.527	25.989	1.00	16.92
	1627	CB SER B 218	12.814	-7.308	27.268	1.00	23.90

	1628	OG	SER B 218	14.181	-7.591	27.042	1.00	36.44
	1629	C	SER B 218	10.582	-7.052	26.212	1.00	16.92
	1630	O	SER B 218	10.243	-5.890	25.965	1.00	16.92
	1631	N	GLU B 219	9.737	-7.967	26.666	1.00	16.92
5	1632	CA	GLU B 219	8.363	-7.621	26.978	1.00	24.28
	1633	CB	GLU B 219	7.544	-8.878	27.249	1.00	24.60
	1634	CG	GLU B 219	7.232	-9.715	26.023	1.00	31.57
	1635	CD	GLU B 219	5.970	-9.255	25.321	1.00	37.84
	1636	OE1	GLU B 219	4.889	-9.294	25.955	1.00	42.71
10	1637	OE2	GLU B 219	6.057	-8.857	24.141	1.00	36.71
	1638	C	GLU B 219	8.527	-6.841	28.265	1.00	30.17
	1639	O	GLU B 219	9.576	-6.911	28.897	1.00	36.16
	1640	N	LEU B 220	7.515	-6.089	28.660	1.00	29.51
	1641	CA	LEU B 220	7.618	-5.337	29.896	1.00	24.66
15	1642	CB	LEU B 220	7.876	-3.861	29.623	1.00	22.54
	1643	CG	LEU B 220	9.059	-3.555	28.710	1.00	17.48
	1644	CD1	LEU B 220	9.104	-2.066	28.464	1.00	23.19
	1645	CD2	LEU B 220	10.356	-4.050	29.325	1.00	16.92
	1646	C	LEU B 220	6.319	-5.494	30.634	1.00	25.51
20	1647	O	LEU B 220	5.241	-5.344	30.062	1.00	27.73
	1648	N	TYR B 221	6.432	-5.830	31.909	1.00	23.31
	1649	CA	TYR B 221	5.272	-6.006	32.767	1.00	21.83
	1650	CB	TYR B 221	5.222	-7.442	33.304	1.00	17.51
	1651	CG	TYR B 221	4.169	-7.655	34.360	1.00	20.23
25	1652	CD1	TYR B 221	2.815	-7.627	34.035	1.00	25.68
	1653	CE1	TYR B 221	1.828	-7.778	35.020	1.00	30.87
	1654	CD2	TYR B 221	4.524	-7.842	35.694	1.00	26.61
	1655	CE2	TYR B 221	3.547	-7.991	36.689	1.00	32.18
	1656	CZ	TYR B 221	2.201	-7.957	36.342	1.00	35.05
30	1657	OH	TYR B 221	1.237	-8.088	37.316	1.00	38.11
	1658	C	TYR B 221	5.432	-5.008	33.915	1.00	22.41
	1659	O	TYR B 221	6.468	-4.973	34.577	1.00	23.28
	1660	N	PHE B 222	4.422	-4.179	34.138	1.00	24.60
	1661	CA	PHE B 222	4.510	-3.207	35.214	1.00	25.33
35	1662	CB	PHE B 222	4.484	-1.775	34.654	1.00	22.58
	1663	CG	PHE B 222	5.662	-1.442	33.767	1.00	25.69
	1664	CD1	PHE B 222	5.584	-1.605	32.389	1.00	26.52
	1665	CD2	PHE B 222	6.850	-0.972	34.316	1.00	30.15
	1666	CE1	PHE B 222	6.669	-1.301	31.572	1.00	25.08
40	1667	CE2	PHE B 222	7.940	-0.667	33.505	1.00	36.11
	1668	CZ	PHE B 222	7.847	-0.832	32.131	1.00	30.23
	1669	C	PHE B 222	3.377	-3.418	36.209	1.00	25.48
	1670	O	PHE B 222	2.215	-3.533	35.830	1.00	24.81

	1671	N	THR B 223	3.729	-3.485	37.486	1.00	27.43
	1672	CA	THR B 223	2.747	-3.695	38.529	1.00	29.24
	1673	CB	THR B 223	2.922	-5.072	39.179	1.00	30.96
	1674	OG1	THR B 223	1.913	-5.255	40.173	1.00	38.54
5	1675	CG2	THR B 223	4.290	-5.188	39.834	1.00	18.62
	1676	C	THR B 223	2.913	-2.643	39.591	1.00	31.84
	1677	O	THR B 223	3.992	-2.094	39.757	1.00	30.89
	1678	N	ASP B 224	1.842	-2.359	40.315	1.00	36.42
	1679	CA	ASP B 224	1.895	-1.365	41.377	1.00	40.14
10	1680	CB	ASP B 224	0.494	-0.818	41.648	1.00	41.56
	1681	CG	ASP B 224	0.062	0.206	40.624	1.00	46.72
	1682	OD1	ASP B 224	-1.144	0.529	40.590	1.00	43.47
	1683	OD2	ASP B 224	0.928	0.693	39.864	1.00	54.57
	1684	C	ASP B 224	2.480	-1.939	42.667	1.00	40.48
15	1685	O	ASP B 224	3.280	-1.285	43.341	1.00	42.72
	1686	N	THR B 225	2.085	-3.163	43.002	1.00	37.47
	1687	CA	THR B 225	2.566	-3.806	44.217	1.00	37.52
	1688	CB	THR B 225	2.344	-5.347	44.183	1.00	32.35
	1689	OG1	THR B 225	2.884	-5.882	42.971	1.00	45.94
20	1690	CG2	THR B 225	0.853	-5.686	44.282	1.00	27.82
	1691	C	THR B 225	4.045	-3.520	44.459	1.00	36.64
	1692	O	THR B 225	4.853	-3.545	43.525	1.00	32.74
	1693	N	LEU B 226	4.374	-3.221	45.718	1.00	40.20
	1694	CA	LEU B 226	5.742	-2.934	46.126	1.00	37.95
25	1695	CB	LEU B 226	5.768	-2.291	47.511	1.00	27.85
	1696	CG	LEU B 226	5.116	-0.918	47.627	1.00	16.92
	1697	CD1	LEU B 226	5.462	-0.129	46.383	1.00	20.23
	1698	CD2	LEU B 226	3.612	-1.053	47.765	1.00	16.92
	1699	C	LEU B 226	6.536	-4.225	46.145	1.00	34.39
30	1700	O	LEU B 226	6.008	-5.281	46.476	1.00	33.65
	1701	N	TRP B 227	7.815	-4.129	45.807	1.00	27.74
	1702	CA	TRP B 227	8.661	-5.302	45.736	1.00	26.44
	1703	CB	TRP B 227	10.104	-4.903	45.490	1.00	16.92
	1704	CG	TRP B 227	10.987	-6.092	45.465	1.00	16.92
35	1705	CD2	TRP B 227	10.954	-7.160	44.513	1.00	24.25
	1706	CE2	TRP B 227	11.975	-8.066	44.869	1.00	21.82
	1707	CE3	TRP B 227	10.167	-7.437	43.388	1.00	27.14
	1708	CD1	TRP B 227	11.990	-6.386	46.338	1.00	16.92
	1709	NE1	TRP B 227	12.589	-7.570	45.989	1.00	18.37
40	1710	CZ2	TRP B 227	12.231	-9.229	44.140	1.00	17.65
	1711	CZ3	TRP B 227	10.422	-8.590	42.665	1.00	22.73
	1712	CH2	TRP B 227	11.447	-9.473	43.046	1.00	19.73
	1713	C	TRP B 227	8.613	-6.284	46.898	1.00	29.41

	1714	O	TRP	B	227	8.387	-7.475	46.683	1.00	29.54
	1715	N	PRO	B	228	8.852	-5.817	48.140	1.00	34.10
	1716	CD	PRO	B	228	9.315	-4.485	48.571	1.00	32.12
	1717	CA	PRO	B	228	8.816	-6.738	49.281	1.00	33.56
5	1718	CB	PRO	B	228	9.021	-5.818	50.469	1.00	30.46
	1719	CG	PRO	B	228	9.943	-4.792	49.913	1.00	31.06
	1720	C	PRO	B	228	7.511	-7.501	49.359	1.00	36.50
	1721	O	PRO	B	228	7.412	-8.499	50.067	1.00	39.78
	1722	N	ASP	B	229	6.513	-7.023	48.620	1.00	38.84
10	1723	CA	ASP	B	229	5.195	-7.645	48.581	1.00	37.34
	1724	CB	ASP	B	229	4.107	-6.564	48.528	1.00	34.82
	1725	CG	ASP	B	229	3.782	-5.992	49.888	1.00	34.97
	1726	OD1	ASP	B	229	3.018	-5.009	49.953	1.00	49.11
	1727	OD2	ASP	B	229	4.275	-6.527	50.897	1.00	48.81
15	1728	C	ASP	B	229	5.042	-8.564	47.370	1.00	35.86
	1729	O	ASP	B	229	3.979	-9.139	47.164	1.00	38.47
	1730	N	PHE	B	230	6.100	-8.703	46.575	1.00	31.52
	1731	CA	PHE	B	230	6.047	-9.533	45.371	1.00	29.58
	1732	CB	PHE	B	230	7.152	-9.127	44.382	1.00	30.24
20	1733	CG	PHE	B	230	6.750	-9.240	42.922	1.00	39.74
	1734	CD1	PHE	B	230	5.791	-8.388	42.380	1.00	35.52
	1735	CD2	PHE	B	230	7.357	-10.171	42.082	1.00	36.37
	1736	CE1	PHE	B	230	5.447	-8.456	41.021	1.00	28.22
	1737	CE2	PHE	B	230	7.021	-10.247	40.727	1.00	28.28
25	1738	CZ	PHE	B	230	6.066	-9.386	40.199	1.00	28.51
	1739	C	PHE	B	230	6.168	-11.020	45.695	1.00	31.09
	1740	O	PHE	B	230	7.265	-11.582	45.722	1.00	31.82
	1741	N	ASP	B	231	5.017	-11.642	45.927	1.00	30.72
	1742	CA	ASP	B	231	4.908	-13.056	46.265	1.00	32.63
30	1743	CB	ASP	B	231	3.586	-13.288	47.001	1.00	35.43
	1744	CG	ASP	B	231	2.387	-12.714	46.244	1.00	41.36
	1745	OD1	ASP	B	231	1.259	-12.730	46.792	1.00	51.61
	1746	OD2	ASP	B	231	2.573	-12.247	45.093	1.00	31.99
	1747	C	ASP	B	231	4.963	-13.930	45.017	1.00	36.99
35	1748	O	ASP	B	231	5.143	-13.432	43.906	1.00	37.67
	1749	N	GLU	B	232	4.811	-15.238	45.215	1.00	40.17
	1750	CA	GLU	B	232	4.825	-16.192	44.115	1.00	36.69
	1751	CB	GLU	B	232	4.744	-17.624	44.656	1.00	27.12
	1752	CG	GLU	B	232	4.652	-18.694	43.577	1.00	35.46
40	1753	CD	GLU	B	232	4.506	-20.106	44.129	1.00	35.04
	1754	OE1	GLU	B	232	3.511	-20.390	44.825	1.00	37.13
	1755	OE2	GLU	B	232	5.385	-20.945	43.863	1.00	31.43
	1756	C	GLU	B	232	3.638	-15.907	43.198	1.00	35.17

	1757	O	GLU B 232	3.753	-15.974	41.978	1.00	34.55
	1758	N	ALA B 233	2.497	-15.574	43.793	1.00	34.03
	1759	CA	ALA B 233	1.292	-15.277	43.030	1.00	35.23
	1760	CB	ALA B 233	0.184	-14.858	43.974	1.00	30.01
5	1761	C	ALA B 233	1.542	-14.182	41.994	1.00	39.77
	1762	O	ALA B 233	1.216	-14.335	40.816	1.00	45.65
	1763	N	ALA B 234	2.121	-13.074	42.439	1.00	37.20
	1764	CA	ALA B 234	2.418	-11.958	41.557	1.00	36.19
	1765	CB	ALA B 234	3.066	-10.832	42.350	1.00	38.99
10	1766	C	ALA B 234	3.329	-12.392	40.407	1.00	37.57
	1767	O	ALA B 234	3.145	-11.962	39.268	1.00	37.82
	1768	N	LEU B 235	4.315	-13.237	40.704	1.00	34.88
	1769	CA	LEU B 235	5.233	-13.710	39.681	1.00	31.18
	1770	CB	LEU B 235	6.294	-14.628	40.281	1.00	16.92
15	1771	CG	LEU B 235	7.644	-14.796	39.563	1.00	16.92
	1772	CD1	LEU B 235	8.168	-16.195	39.818	1.00	17.38
	1773	CD2	LEU B 235	7.510	-14.576	38.078	1.00	23.73
	1774	C	LEU B 235	4.408	-14.489	38.676	1.00	35.86
	1775	O	LEU B 235	4.602	-14.367	37.471	1.00	38.82
20	1776	N	GLN B 236	3.481	-15.299	39.173	1.00	37.65
	1777	CA	GLN B 236	2.630	-16.080	38.287	1.00	38.39
	1778	CB	GLN B 236	1.690	-16.963	39.112	1.00	50.00
	1779	CG	GLN B 236	2.377	-18.163	39.760	1.00	52.97
	1780	CD	GLN B 236	1.458	-18.947	40.687	1.00	59.21
25	1781	OE1	GLN B 236	1.768	-20.076	41.071	1.00	62.28
	1782	NE2	GLN B 236	0.328	-18.348	41.058	1.00	61.76
	1783	C	GLN B 236	1.841	-15.122	37.394	1.00	39.03
	1784	O	GLN B 236	1.685	-15.359	36.194	1.00	38.78
	1785	N	GLU B 237	1.353	-14.038	37.992	1.00	39.68
30	1786	CA	GLU B 237	0.611	-13.014	37.261	1.00	35.56
	1787	CB	GLU B 237	0.211	-11.869	38.190	1.00	41.41
	1788	CG	GLU B 237	-1.083	-12.099	38.938	1.00	56.97
	1789	CD	GLU B 237	-2.300	-11.897	38.057	1.00	67.71
	1790	OE1	GLU B 237	-2.376	-12.546	36.993	1.00	76.95
35	1791	OE2	GLU B 237	-3.180	-11.090	38.428	1.00	81.30
	1792	C	GLU B 237	1.498	-12.467	36.157	1.00	29.79
	1793	O	GLU B 237	1.112	-12.454	34.997	1.00	26.60
	1794	N	ALA B 238	2.688	-12.006	36.526	1.00	29.71
	1795	CA	ALA B 238	3.625	-11.481	35.548	1.00	30.48
40	1796	CB	ALA B 238	4.960	-11.174	36.212	1.00	17.71
	1797	C	ALA B 238	3.824	-12.509	34.447	1.00	32.85
	1798	O	ALA B 238	3.821	-12.171	33.266	1.00	39.01
	1799	N	ILE B 239	3.987	-13.769	34.840	1.00	34.48

	1800	CA	ILE B 239	4.209	-14.844	33.882	1.00	32.58
	1801	CB	ILE B 239	4.667	-16.122	34.585	1.00	20.63
	1802	CG2	ILE B 239	4.624	-17.300	33.613	1.00	31.10
	1803	CG1	ILE B 239	6.085	-15.920	35.115	1.00	16.92
5	1804	CD1	ILE B 239	6.735	-17.180	35.625	1.00	28.23
	1805	C	ILE B 239	3.004	-15.159	33.022	1.00	30.58
	1806	O	ILE B 239	3.148	-15.532	31.863	1.00	27.47
	1807	N	LEU B 240	1.815	-15.041	33.587	1.00	30.48
	1808	CA	LEU B 240	0.620	-15.292	32.805	1.00	34.89
10	1809	CB	LEU B 240	-0.616	-15.333	33.701	1.00	48.13
	1810	CG	LEU B 240	-0.916	-16.644	34.422	1.00	43.96
	1811	CD1	LEU B 240	-2.158	-16.473	35.263	1.00	40.59
	1812	CD2	LEU B 240	-1.123	-17.752	33.410	1.00	43.57
	1813	C	LEU B 240	0.483	-14.161	31.789	1.00	31.63
15	1814	O	LEU B 240	0.454	-14.392	30.581	1.00	33.47
	1815	N	ALA B 241	0.417	-12.934	32.293	1.00	33.00
	1816	CA	ALA B 241	0.283	-11.754	31.448	1.00	35.65
	1817	CB	ALA B 241	0.095	-10.510	32.314	1.00	36.36
	1818	C	ALA B 241	1.488	-11.570	30.547	1.00	40.07
20	1819	O	ALA B 241	1.686	-10.494	30.002	1.00	43.62
	1820	N	TYR B 242	2.287	-12.617	30.390	1.00	46.16
	1821	CA	TYR B 242	3.482	-12.539	29.560	1.00	49.44
	1822	CB	TYR B 242	4.282	-13.835	29.674	1.00	42.71
	1823	CG	TYR B 242	5.537	-13.870	28.843	1.00	37.89
25	1824	CD1	TYR B 242	6.327	-12.738	28.680	1.00	38.49
	1825	CE1	TYR B 242	7.499	-12.786	27.932	1.00	37.07
	1826	CD2	TYR B 242	5.950	-15.051	28.242	1.00	33.74
	1827	CE2	TYR B 242	7.115	-15.115	27.501	1.00	31.74
	1828	CZ	TYR B 242	7.885	-13.986	27.346	1.00	33.16
30	1829	OH	TYR B 242	9.044	-14.074	26.609	1.00	32.83
	1830	C	TYR B 242	3.153	-12.230	28.106	1.00	56.18
	1831	O	TYR B 242	2.797	-11.093	27.788	1.00	77.34
	1832	N	ASN B 243	3.270	-13.212	27.217	1.00	62.00
	1833	CA	ASN B 243	2.970	-12.947	25.812	1.00	65.83
35	1834	CB	ASN B 243	3.531	-14.053	24.911	1.00	65.24
	1835	CG	ASN B 243	4.301	-13.500	23.715	1.00	65.31
	1836	OD1	ASN B 243	5.303	-12.807	23.873	1.00	63.84
	1837	ND2	ASN B 243	3.831	-13.806	22.513	1.00	65.91
	1838	C	ASN B 243	1.456	-12.828	25.643	1.00	69.21
40	1839	O	ASN B 243	0.694	-13.666	26.142	1.00	69.74
	1840	N	ARG B 244	1.033	-11.764	24.957	1.00	68.62
	1841	CA	ARG B 244	-0.385	-11.484	24.723	1.00	71.05
	1842	CB	ARG B 244	-0.991	-10.800	25.955	1.00	71.10

	1843	CG	ARG B 244		-2.481	-10.523	25.847	1.00	72.04
	1844	CD	ARG B 244		-3.318	-11.770	26.111	1.00	73.39
	1845	NE	ARG B 244		-3.582	-11.987	27.538	1.00	72.71
	1846	CZ	ARG B 244		-2.727	-12.523	28.408	1.00	71.35
5	1847	NH1	ARG B 244		-1.517	-12.921	28.020	1.00	69.95
	1848	NH2	ARG B 244		-3.092	-12.661	29.680	1.00	70.30
	1849	C	ARG B 244		-0.581	-10.586	23.491	1.00	73.21
	1850	OT	ARG B 244		-1.352	-10.983	22.588	1.00	73.64
	1851	OXT	ARG B 244		0.031	-9.492	23.446	1.00	73.64
10	1852	C1	FPP C 1		4.195	-0.508	11.603	1.00	88.17
	1853	O1	FPP C 1		2.980	-0.490	12.373	1.00	93.81
	1854	C2	FPP C 1		4.310	0.697	10.721	1.00	84.31
	1855	C3	FPP C 1		5.442	1.322	10.336	1.00	82.06
	1856	C4	FPP C 1		6.843	0.843	10.782	1.00	83.48
15	1857	C5	FPP C 1		5.291	2.516	9.451	1.00	81.22
	1858	C6	FPP C 1		4.740	3.746	10.219	1.00	81.08
	1859	C7	FPP C 1		5.081	5.117	9.616	1.00	80.55
	1860	C8	FPP C 1		4.280	6.164	9.255	1.00	78.44
	1861	C10	FPP C 1		2.743	6.118	9.420	1.00	78.25
20	1862	C9	FPP C 1		4.953	7.413	8.666	1.00	77.35
	1863	C11	FPP C 1		5.702	7.123	7.337	1.00	74.94
	1864	C12	FPP C 1		6.909	7.995	7.015	1.00	74.41
	1865	C13	FPP C 1		6.934	9.266	6.513	1.00	73.49
	1866	C14	FPP C 1		8.184	10.059	6.220	1.00	74.43
25	1867	C15	FPP C 1		5.701	10.077	6.170	1.00	73.47
	1868	PA	FPP C 1		1.996	-1.762	12.404	1.00	96.03
	1869	O1A	FPP C 1		1.608	-2.214	10.958	1.00	94.67
	1870	O2A	FPP C 1		2.846	-2.721	13.261	1.00	95.64
	1871	O3A	FPP C 1		0.576	-1.582	12.923	1.00	97.67
30	1872	PB	FPP C 1		-0.074	-2.809	13.626	1.00	100.77
	1873	O1B	FPP C 1		0.495	-3.100	15.024	1.00	102.75
	1874	O2B	FPP C 1		0.181	-4.000	12.737	1.00	103.25
	1875	O3B	FPP C 1		-1.564	-2.764	13.949	1.00	101.13
	1852	C1	FPP C 2		16.059	0.426	45.536	1.00	88.17
35	1853	O1	FPP C 2		14.629	0.380	45.687	1.00	93.81
	1854	C2	FPP C 2		16.720	-0.770	46.150	1.00	84.31
	1855	C3	FPP C 2		17.858	-1.371	45.746	1.00	82.06
	1856	C4	FPP C 2		18.670	-0.870	44.529	1.00	83.48
	1857	C5	FPP C 2		18.313	-2.560	46.527	1.00	81.22
40	1858	C6	FPP C 2		17.428	-3.806	46.261	1.00	81.08
	1859	C7	FPP C 2		18.096	-5.166	46.514	1.00	80.55
	1860	C8	FPP C 2		17.712	-6.225	47.289	1.00	78.44
	1861	C10	FPP C 2		16.404	-6.208	48.114	1.00	78.25



	1862	C9	FPP	C	2	18.629	-7.457	47.326	1.00	77.35
	1863	C11	FPP	C	2	20.036	-7.142	47.905	1.00	74.94
	1864	C12	FPP	C	2	21.199	-7.990	47.403	1.00	74.41
	1865	C13	FPP	C	2	21.554	-9.256	47.774	1.00	73.49
5	1866	C14	FPP	C	2	22.731	-10.024	47.224	1.00	74.43
	1867	C15	FPP	C	2	20.816	-10.087	48.804	1.00	73.47
	1868	PA	FPP	C	2	13.814	1.633	46.280	1.00	96.03
	1869	O1A	FPP	C	2	14.399	2.089	47.657	1.00	94.67
	1870	O2A	FPP	C	2	13.930	2.601	45.086	1.00	95.64
10	1871	O3A	FPP	C	2	12.383	1.423	46.754	1.00	97.67
	1872	PB	FPP	C	2	11.413	2.632	46.613	1.00	100.77
	1873	O1B	FPP	C	2	10.986	2.923	45.165	1.00	102.75
	1874	O2B	FPP	C	2	12.142	3.835	47.158	1.00	103.25
	1875	O3B	FPP	C	2	10.046	2.557	47.285	1.00	101.13
15	1876	OH2	WAT	W	1	4.773	7.298	32.511	1.00	36.80
	1877	OH2	WAT	W	2	6.323	0.871	14.427	1.00	36.80
	1878	OH2	WAT	W	3	15.515	-0.599	23.674	1.00	36.80
	1879	OH2	WAT	W	4	-7.863	3.523	18.482	1.00	36.80
	1880	OH2	WAT	W	5	16.858	9.374	28.786	1.00	36.80
20	1881	OH2	WAT	W	6	11.507	-3.595	14.868	1.00	36.80
	1882	OH2	WAT	W	7	34.098	13.685	24.109	1.00	36.80
	1883	OH2	WAT	W	8	-6.504	15.936	17.044	1.00	36.80
	1884	OH2	WAT	W	9	16.680	15.674	27.816	1.00	36.80
	1885	OH2	WAT	W	10	16.423	23.057	25.423	1.00	36.80
25	1886	OH2	WAT	W	11	-0.276	12.147	0.194	1.00	36.80
	1887	OH2	WAT	W	12	41.369	13.097	17.334	1.00	36.80
	1888	OH2	WAT	W	13	22.635	10.116	22.907	1.00	36.80
	1889	OH2	WAT	W	14	15.672	1.557	26.009	1.00	36.80
	1890	OH2	WAT	W	15	19.186	15.106	27.885	1.00	36.80
30	1891	OH2	WAT	W	16	39.396	4.075	29.930	1.00	36.80
	1892	OH2	WAT	W	17	23.260	21.078	25.999	1.00	36.80
	1893	OH2	WAT	W	18	10.020	-9.291	1.405	1.00	36.80
	1894	OH2	WAT	W	19	23.088	-10.033	21.137	1.00	36.80
	1895	OH2	WAT	W	20	7.776	-6.623	10.879	1.00	36.80
35	1896	OH2	WAT	W	21	19.914	-3.586	15.083	1.00	36.80
	1897	OH2	WAT	W	22	-12.008	5.707	9.673	1.00	36.80
	1898	OH2	WAT	W	23	8.883	29.025	9.092	1.00	36.80
	1899	OH2	WAT	W	24	24.894	18.337	19.301	1.00	36.80
	1900	OH2	WAT	W	25	8.252	24.015	19.421	1.00	36.80
40	1901	OH2	WAT	W	26	-9.407	8.770	13.621	1.00	36.80
	1902	OH2	WAT	W	27	46.239	3.613	19.856	1.00	36.80
	1903	OH2	WAT	W	28	-1.747	5.460	-3.436	1.00	36.80
	1904	OH2	WAT	W	29	37.326	11.576	17.425	1.00	36.80

	1905	OH2	WAT	W	30	14.148	-10.191	16.523	1.00	36.80
	1906	OH2	WAT	W	31	15.836	20.107	8.725	1.00	36.80
	1907	OH2	WAT	W	32	-4.798	11.641	14.018	1.00	36.80
	1908	OH2	WAT	W	33	-7.822	7.982	31.296	1.00	36.80
5	1909	OH2	WAT	W	34	3.598	15.873	33.954	1.00	33.31
	1910	OH2	WAT	W	35	10.074	21.605	27.336	1.00	33.31
	1911	OH2	WAT	W	36	18.840	22.270	14.224	1.00	33.31
	1912	OH2	WAT	W	37	-1.792	24.266	11.374	1.00	33.31
	1913	OH2	WAT	W	38	-8.931	8.878	19.966	1.00	33.31
10	1914	OH2	WAT	W	39	-3.553	21.551	14.907	1.00	33.31
	1915	OH2	WAT	W	40	8.399	-0.175	13.515	1.00	33.31
	1916	OH2	WAT	W	41	-6.204	12.470	11.990	1.00	33.31
	1917	OH2	WAT	W	42	4.589	8.276	34.603	1.00	33.31
	1918	OH2	WAT	W	43	28.648	16.280	19.235	1.00	33.31
15	1919	OH2	WAT	W	44	18.590	15.236	-2.478	1.00	33.31
	1920	OH2	WAT	W	45	-9.057	0.909	19.891	1.00	33.31
	1921	OH2	WAT	W	46	-4.172	-4.775	22.498	1.00	33.31
	1922	OH2	WAT	W	47	2.411	6.885	32.413	1.00	33.31
	1923	OH2	WAT	W	48	12.792	13.554	-5.547	1.00	33.31
20	1924	OH2	WAT	W	49	-4.512	-6.634	11.993	1.00	33.31
	1925	OH2	WAT	W	50	-1.349	8.211	-3.909	1.00	33.31
	1926	OH2	WAT	W	51	13.234	14.853	39.074	1.00	33.31
	1927	OH2	WAT	W	52	37.819	4.036	7.107	1.00	33.31
	1928	OH2	WAT	W	53	-3.499	3.773	29.867	1.00	33.31
25	1929	OH2	WAT	W	54	2.292	20.765	40.034	1.00	33.31
	1930	OH2	WAT	W	55	15.806	-0.857	-1.454	1.00	33.31
	1931	OH2	WAT	W	56	3.305	-4.239	15.620	1.00	36.80
	1876	OH2	WAT	X	1	3.683	-7.531	28.746	1.00	36.80
	1877	OH2	WAT	X	2	16.001	-0.936	41.994	1.00	36.80
30	1878	OH2	WAT	X	3	17.436	0.631	29.046	1.00	36.80
	1879	OH2	WAT	X	4	2.416	-3.880	47.608	1.00	36.80
	1880	OH2	WAT	X	5	15.507	-9.355	24.152	1.00	36.80
	1881	OH2	WAT	X	6	19.704	3.621	38.454	1.00	36.80
	1882	OH2	WAT	X	7	32.005	-13.312	17.093	1.00	36.80
35	1883	OH2	WAT	X	8	4.613	-16.254	47.826	1.00	36.80
	1884	OH2	WAT	X	9	16.091	-15.650	24.990	1.00	36.80
	1885	OH2	WAT	X	10	17.517	-23.017	26.986	1.00	36.80
	1886	OH2	WAT	X	11	19.882	-12.220	57.189	1.00	36.80
	1887	OH2	WAT	X	12	41.898	-12.537	17.893	1.00	36.80
40	1888	OH2	WAT	X	13	23.698	-9.945	25.171	1.00	36.80
	1889	OH2	WAT	X	14	16.151	-1.540	27.107	1.00	36.80
	1890	OH2	WAT	X	15	18.001	-15.036	23.383	1.00	36.80
	1891	OH2	WAT	X	16	32.358	-3.652	9.291	1.00	36.80

	1892	OH2 WAT X	17	22.480	-20.917	22.300	1.00	36.80
	1893	OH2 WAT X	18	26.786	9.394	49.961	1.00	36.80
	1894	OH2 WAT X	19	24.764	10.222	26.384	1.00	36.80
	1895	OH2 WAT X	20	19.198	6.611	43.913	1.00	36.80
5	1896	OH2 WAT X	21	26.159	3.765	33.066	1.00	36.80
	1897	OH2 WAT X	22	4.678	-6.071	57.076	1.00	36.80
	1898	OH2 WAT X	23	21.861	-28.995	44.438	1.00	36.80
	1899	OH2 WAT X	24	27.866	-18.095	26.551	1.00	36.80
	1900	OH2 WAT X	25	14.858	-24.079	36.759	1.00	36.80
10	1901	OH2 WAT X	26	4.325	-9.116	52.350	1.00	36.80
	1902	OH2 WAT X	27	43.966	-2.985	12.943	1.00	36.80
	1903	OH2 WAT X	28	20.854	-5.533	60.983	1.00	36.80
	1904	OH2 WAT X	29	38.644	-11.092	20.340	1.00	36.80
	1905	OH2 WAT X	30	20.619	10.252	35.552	1.00	36.80
15	1906	OH2 WAT X	31	27.367	-19.948	40.456	1.00	36.80
	1907	OH2 WAT X	32	7.746	-11.905	49.162	1.00	36.80
	1908	OH2 WAT X	33	-5.421	-8.437	37.514	1.00	36.80
	1909	OH2 WAT X	34	2.031	-16.137	28.299	1.00	33.31
	1910	OH2 WAT X	35	11.326	-21.697	29.436	1.00	33.31
20	1911	OH2 WAT X	36	26.349	-22.099	34.269	1.00	33.31
	1912	OH2 WAT X	37	11.987	-24.451	49.302	1.00	33.31
	1913	OH2 WAT X	38	0.761	-9.265	47.080	1.00	33.31
	1914	OH2 WAT X	39	8.361	-21.797	47.640	1.00	33.31
	1915	OH2 WAT X	40	18.174	0.155	41.426	1.00	33.31
25	1916	OH2 WAT X	41	7.919	-12.744	51.620	1.00	33.31
	1917	OH2 WAT X	42	2.259	-8.529	27.215	1.00	33.31
	1918	OH2 WAT X	43	30.809	-15.968	24.283	1.00	33.31
	1919	OH2 WAT X	44	36.386	-14.940	47.555	1.00	33.31
	1920	OH2 WAT X	45	0.555	-1.299	47.259	1.00	33.31
30	1921	OH2 WAT X	46	2.656	4.453	42.213	1.00	33.31
	1922	OH2 WAT X	47	1.885	-7.161	30.291	1.00	33.31
	1923	OH2 WAT X	48	33.715	-13.341	53.569	1.00	33.31
	1924	OH2 WAT X	49	8.875	6.387	50.669	1.00	33.31
	1925	OH2 WAT X	50	21.512	-8.272	61.092	1.00	33.31
35	1926	OH2 WAT X	51	6.385	-14.980	18.308	1.00	33.31
	1927	OH2 WAT X	52	45.290	-3.463	28.162	1.00	33.31
	1928	OH2 WAT X	53	-1.227	-4.138	35.973	1.00	33.31
	1929	OH2 WAT X	54	-2.672	-21.100	24.317	1.00	33.31
	1930	OH2 WAT X	55	33.258	1.090	48.566	1.00	33.31
40	1931	OH2 WAT X	56	12.796	4.108	42.960	1.00	36.80

END

Table IC

## Atomic coordinates of UPPS in complex with IPP

CRYST1 59.428 118.168 175.973 90.00 90.00 90.00							
	ATOM	RESIDUE		X	Y	Z	Occ B
5	1	CB GLN A 18		7.946	25.118	75.253	1.00 80.17
	2	CG GLN A 18		8.344	25.155	76.710	1.00 83.70
	3	CD GLN A 18		7.166	25.025	77.641	1.00 85.97
	4	OE1 GLN A 18		6.296	24.165	77.449	1.00 88.60
10	5	NE2 GLN A 18		7.131	25.869	78.670	1.00 86.19
	6	C GLN A 18		8.855	24.342	73.075	1.00 71.58
	7	O GLN A 18		7.697	24.074	72.743	1.00 71.79
	8	N GLN A 18		9.569	26.528	74.025	1.00 72.89
	9	CA GLN A 18		9.157	25.128	74.330	1.00 72.72
15	10	N VAL A 19		9.929	23.964	72.392	1.00 76.37
	11	CA VAL A 19		9.836	23.216	71.156	1.00 74.76
	12	CB VAL A 19		10.081	24.140	69.983	1.00 77.30
	13	CG1 VAL A 19		8.898	25.079	69.823	1.00 76.99
	14	CG2 VAL A 19		11.372	24.915	70.222	1.00 74.13
20	15	C VAL A 19		10.822	22.055	71.076	1.00 72.83
	16	O VAL A 19		11.780	21.982	71.841	1.00 73.33
	17	N PRO A 20		10.592	21.131	70.132	1.00 45.38
	18	CD PRO A 20		9.422	21.115	69.233	1.00 63.68
	19	CA PRO A 20		11.437	19.951	69.912	1.00 42.31
25	20	CB PRO A 20		10.557	19.077	69.022	1.00 62.36
	21	CG PRO A 20		9.821	20.101	68.208	1.00 63.80
	22	C PRO A 20		12.790	20.266	69.270	1.00 39.14
	23	O PRO A 20		12.862	20.855	68.195	1.00 36.95
	24	N ALA A 21		13.864	19.872	69.932	1.00 43.53
30	25	CA ALA A 21		15.203	20.117	69.408	1.00 43.37
	26	CB ALA A 21		16.249	19.644	70.409	1.00 19.22
	27	C ALA A 21		15.430	19.423	68.067	1.00 43.25
	28	O ALA A 21		16.207	19.899	67.238	1.00 41.42
	29	N HIS A 22		14.748	18.298	67.860	1.00 50.77
35	30	CA HIS A 22		14.898	17.536	66.631	1.00 49.24
	31	CB HIS A 22		15.805	16.347	66.896	1.00 40.18
	32	CG HIS A 22		16.130	15.547	65.676	1.00 38.94
	33	CD2 HIS A 22		15.467	15.386	64.509	1.00 37.84
	34	ND1 HIS A 22		17.279	14.792	65.570	1.00 40.51
40	35	CE1 HIS A 22		17.314	14.206	64.388	1.00 40.05
	36	NE2 HIS A 22		16.225	14.551	63.725	1.00 40.19
	37	C HIS A 22		13.591	17.041	66.038	1.00 49.35
	38	O HIS A 22		12.929	16.204	66.630	1.00 49.93

	39	N	ILE A	23	13.229	17.556	64.865	1.00	50.60
	40	CA	ILE A	23	12.012	17.127	64.185	1.00	52.08
	41	CB	ILE A	23	11.116	18.303	63.770	1.00	52.30
	42	CG2	ILE A	23	9.907	17.785	63.017	1.00	49.04
5	43	CG1	ILE A	23	10.606	19.039	64.996	1.00	52.99
	44	CD1	ILE A	23	9.575	18.258	65.745	1.00	55.11
	45	C	ILE A	23	12.372	16.371	62.914	1.00	53.34
	46	O	ILE A	23	13.278	16.763	62.186	1.00	52.81
	47	N	GLY A	24	11.664	15.280	62.655	1.00	55.59
10	48	CA	GLY A	24	11.916	14.510	61.454	1.00	55.68
	49	C	GLY A	24	10.636	14.558	60.652	1.00	57.28
	50	O	GLY A	24	9.561	14.279	61.188	1.00	58.15
	51	N	ILE A	25	10.723	14.925	59.379	1.00	60.87
	52	CA	ILE A	25	9.518	14.997	58.574	1.00	60.55
15	53	CB	ILE A	25	9.274	16.407	58.016	1.00	44.36
	54	CG2	ILE A	25	7.783	16.649	57.880	1.00	43.36
	55	CG1	ILE A	25	9.863	17.464	58.946	1.00	43.88
	56	CD1	ILE A	25	9.805	18.870	58.385	1.00	40.84
	57	C	ILE A	25	9.628	14.080	57.388	1.00	61.16
20	58	O	ILE A	25	10.688	13.955	56.781	1.00	61.90
	59	N	ILE A	26	8.526	13.430	57.062	1.00	50.76
	60	CA	ILE A	26	8.491	12.557	55.912	1.00	51.38
	61	CB	ILE A	26	7.771	11.250	56.229	1.00	39.40
	62	CG2	ILE A	26	7.530	10.469	54.944	1.00	36.96
25	63	CG1	ILE A	26	8.590	10.437	57.231	1.00	38.89
	64	CD1	ILE A	26	7.963	9.106	57.576	1.00	36.95
	65	C	ILE A	26	7.669	13.332	54.905	1.00	52.89
	66	O	ILE A	26	6.455	13.472	55.089	1.00	52.47
	67	N	MET A	27	8.333	13.838	53.861	1.00	56.05
30	68	CA	MET A	27	7.696	14.642	52.808	1.00	57.51
	69	CB	MET A	27	8.733	15.596	52.181	1.00	43.28
	70	CG	MET A	27	9.433	16.489	53.193	1.00	37.98
	71	SD	MET A	27	10.718	17.550	52.514	1.00	33.89
	72	CE	MET A	27	12.040	16.489	52.414	1.00	32.98
35	73	C	MET A	27	6.998	13.821	51.708	1.00	61.12
	74	O	MET A	27	7.577	13.539	50.653	1.00	61.44
	75	N	ASP A	28	5.738	13.469	51.968	1.00	78.26
	76	CA	ASP A	28	4.906	12.680	51.056	1.00	81.87
	77	CB	ASP A	28	4.483	11.376	51.743	1.00	106.31
40	78	CG	ASP A	28	3.741	10.431	50.809	1.00	108.55
	79	OD1	ASP A	28	4.298	10.095	49.740	1.00	109.62
	80	OD2	ASP A	28	2.609	10.016	51.146	1.00	109.84
	81	C	ASP A	28	3.655	13.455	50.635	1.00	83.95

	82	O	ASP	A	28	3.234	14.385	51.319	1.00	83.92
	83	N	GLY	A	29	3.059	13.053	49.515	1.00	106.68
	84	CA	GLY	A	29	1.862	13.715	49.020	1.00	107.99
	85	C	GLY	A	29	2.204	14.690	47.911	1.00	109.08
5	86	O	GLY	A	29	1.356	15.050	47.089	1.00	110.54
	87	N	ASN	A	30	3.467	15.109	47.906	1.00	49.18
	88	CA	ASN	A	30	4.021	16.044	46.933	1.00	49.76
	89	CB	ASN	A	30	5.550	15.954	47.000	1.00	59.70
	90	CG	ASN	A	30	6.243	17.124	46.348	1.00	58.94
10	91	OD1	ASN	A	30	7.404	17.402	46.641	1.00	57.39
	92	ND2	ASN	A	30	5.546	17.811	45.452	1.00	60.12
	93	C	ASN	A	30	3.505	15.720	45.525	1.00	51.86
	94	O	ASN	A	30	3.456	16.575	44.637	1.00	51.26
	95	N	GLY	A	31	3.121	14.469	45.322	1.00	95.59
15	96	CA	GLY	A	31	2.597	14.087	44.033	1.00	98.36
	97	C	GLY	A	31	1.105	14.334	44.044	1.00	100.46
	98	O	GLY	A	31	0.622	15.299	43.451	1.00	100.95
	99	N	ARG	A	32	0.384	13.460	44.745	1.00	100.88
	100	CA	ARG	A	32	-1.068	13.529	44.859	1.00	102.40
20	101	CB	ARG	A	32	-1.524	12.829	46.138	1.00	88.53
	102	CG	ARG	A	32	-2.962	12.357	46.121	1.00	88.65
	103	CD	ARG	A	32	-3.289	11.704	47.441	1.00	89.95
	104	NE	ARG	A	32	-3.128	12.661	48.534	1.00	92.42
	105	CZ	ARG	A	32	-3.101	12.339	49.826	1.00	93.94
25	106	NH1	ARG	A	32	-3.221	11.072	50.204	1.00	93.86
	107	NH2	ARG	A	32	-2.954	13.288	50.746	1.00	94.90
	108	C	ARG	A	32	-1.536	14.972	44.871	1.00	103.65
	109	O	ARG	A	32	-2.621	15.288	44.375	1.00	103.26
	110	N	TRP	A	33	-0.710	15.845	45.439	1.00	95.39
30	111	CA	TRP	A	33	-1.044	17.255	45.501	1.00	97.04
	112	CB	TRP	A	33	-0.002	18.031	46.298	1.00	86.98
	113	CG	TRP	A	33	-0.284	19.509	46.337	1.00	87.76
	114	CD2	TRP	A	33	0.489	20.547	45.720	1.00	87.70
	115	CE2	TRP	A	33	-0.144	21.772	46.017	1.00	87.59
35	116	CE3	TRP	A	33	1.655	20.560	44.943	1.00	87.55
	117	CD1	TRP	A	33	-1.329	20.130	46.962	1.00	87.37
	118	NE1	TRP	A	33	-1.250	21.489	46.774	1.00	87.39
	119	CZ2	TRP	A	33	0.353	22.999	45.568	1.00	87.37
	120	CZ3	TRP	A	33	2.145	21.780	44.497	1.00	86.53
40	121	CH2	TRP	A	33	1.497	22.981	44.812	1.00	86.99
	122	C	TRP	A	33	-1.129	17.841	44.104	1.00	98.03
	123	O	TRP	A	33	-2.222	17.953	43.544	1.00	98.44
	124	N	ALA	A	34	0.025	18.209	43.546	1.00	103.06

	125	CA	ALA	A	34	0.086	18.809	42.212	1.00103.60
	126	CB	ALA	A	34	1.553	19.001	41.778	1.00 43.07
	127	C	ALA	A	34	-0.692	18.001	41.163	1.00104.15
	128	O	ALA	A	34	-0.767	18.388	39.998	1.00104.13
5	129	N	LYS	A	35	-1.278	16.884	41.585	1.00102.73
	130	CA	LYS	A	35	-2.070	16.049	40.689	1.00104.36
	131	CB	LYS	A	35	-2.305	14.670	41.327	1.00103.46
	132	CG	LYS	A	35	-2.952	13.616	40.416	1.00103.78
	133	CD	LYS	A	35	-4.481	13.720	40.345	1.00104.86
10	134	CE	LYS	A	35	-5.060	12.605	39.472	1.00104.77
	135	NZ	LYS	A	35	-6.547	12.587	39.430	1.00103.24
	136	C	LYS	A	35	-3.409	16.750	40.409	1.00104.89
	137	O	LYS	A	35	-3.633	17.247	39.303	1.00104.89
	138	N	LYS	A	36	-4.283	16.799	41.415	1.00108.67
15	139	CA	LYS	A	36	-5.596	17.433	41.288	1.00108.81
	140	CB	LYS	A	36	-6.275	17.496	42.656	1.00116.28
	141	CG	LYS	A	36	-7.584	18.276	42.663	1.00116.03
	142	CD	LYS	A	36	-7.654	19.234	43.851	1.00115.08
	143	CE	LYS	A	36	-6.594	20.332	43.760	1.00114.82
20	144	NZ	LYS	A	36	-6.626	21.277	44.921	1.00113.37
	145	C	LYS	A	36	-5.547	18.844	40.694	1.00108.73
	146	O	LYS	A	36	-6.529	19.321	40.115	1.00108.16
	147	N	ARG	A	37	-4.407	19.510	40.850	1.00111.25
	148	CA	ARG	A	37	-4.226	20.863	40.334	1.00111.49
25	149	CB	ARG	A	37	-2.984	21.503	40.954	1.00 99.74
	150	CG	ARG	A	37	-3.031	21.668	42.457	1.00100.08
	151	CD	ARG	A	37	-4.044	22.718	42.877	1.00100.41
	152	NE	ARG	A	37	-3.537	23.542	43.974	1.00100.65
	153	CZ	ARG	A	37	-3.282	23.099	45.203	1.00100.42
30	154	NH1	ARG	A	37	-3.489	21.825	45.522	1.00100.28
	155	NH2	ARG	A	37	-2.800	23.938	46.110	1.00100.50
	156	C	ARG	A	37	-4.071	20.885	38.817	1.00111.43
	157	O	ARG	A	37	-3.974	21.957	38.222	1.00111.99
	158	N	MET	A	38	-4.049	19.707	38.198	1.00 98.41
35	159	CA	MET	A	38	-3.875	19.595	36.749	1.00 97.99
	160	CB	MET	A	38	-4.941	20.407	36.004	1.00115.32
	161	CG	MET	A	38	-6.343	19.822	36.074	1.00116.27
	162	SD	MET	A	38	-6.439	18.168	35.357	1.00117.85
	163	CE	MET	A	38	-6.633	18.546	33.608	1.00116.66
40	164	C	MET	A	38	-2.483	20.107	36.393	1.00 97.09
	165	O	MET	A	38	-2.304	20.916	35.478	1.00 96.60
	166	N	GLN	A	39	-1.499	19.623	37.137	1.00 91.07
	167	CA	GLN	A	39	-0.117	20.021	36.928	1.00 90.66

	168	CB	GLN	A	39	0.318	20.955	38.059	1.00	92.12
	169	CG	GLN	A	39	-0.117	22.368	37.829	1.00	91.01
	170	CD	GLN	A	39	0.473	22.901	36.551	1.00	90.64
	171	OE1	GLN	A	39	1.638	23.305	36.511	1.00	90.38
5	172	NE2	GLN	A	39	-0.317	22.877	35.484	1.00	89.76
	173	C	GLN	A	39	0.848	18.836	36.821	1.00	90.86
	174	O	GLN	A	39	0.525	17.710	37.221	1.00	90.62
	175	N	PRO	A	40	2.045	19.076	36.262	1.00	106.45
	176	CD	PRO	A	40	2.499	20.328	35.630	1.00	72.93
10	177	CA	PRO	A	40	3.051	18.026	36.109	1.00	106.75
	178	CB	PRO	A	40	4.011	18.626	35.090	1.00	73.27
	179	CG	PRO	A	40	3.981	20.077	35.443	1.00	73.16
	180	C	PRO	A	40	3.737	17.709	37.434	1.00	107.09
	181	O	PRO	A	40	3.962	18.599	38.258	1.00	106.50
15	182	N	ARG	A	41	4.058	16.437	37.640	1.00	100.27
	183	CA	ARG	A	41	4.725	16.024	38.862	1.00	100.09
	184	CB	ARG	A	41	5.176	14.571	38.754	1.00	110.99
	185	CG	ARG	A	41	4.096	13.631	38.289	1.00	111.15
	186	CD	ARG	A	41	2.975	13.533	39.298	1.00	111.80
20	187	NE	ARG	A	41	1.922	12.624	38.847	1.00	112.39
	188	CZ	ARG	A	41	2.111	11.345	38.524	1.00	112.83
	189	NH1	ARG	A	41	3.323	10.805	38.599	1.00	112.44
	190	NH2	ARG	A	41	1.083	10.601	38.130	1.00	112.36
	191	C	ARG	A	41	5.940	16.921	39.069	1.00	99.99
25	192	O	ARG	A	41	6.215	17.356	40.185	1.00	100.63
	193	N	VAL	A	42	6.659	17.206	37.986	1.00	93.73
	194	CA	VAL	A	42	7.847	18.048	38.072	1.00	93.74
	195	CB	VAL	A	42	8.355	18.480	36.684	1.00	99.03
	196	CG1	VAL	A	42	9.616	19.301	36.839	1.00	98.65
30	197	CG2	VAL	A	42	8.631	17.265	35.821	1.00	99.84
	198	C	VAL	A	42	7.527	19.298	38.869	1.00	93.42
	199	O	VAL	A	42	8.127	19.553	39.908	1.00	93.37
	200	N	PHE	A	43	6.573	20.074	38.375	1.00	110.29
	201	CA	PHE	A	43	6.163	21.300	39.046	1.00	110.29
35	202	CB	PHE	A	43	5.004	21.943	38.268	1.00	136.60
	203	CG	PHE	A	43	4.281	23.027	39.021	1.00	137.78
	204	CD1	PHE	A	43	4.967	24.130	39.519	1.00	138.53
	205	CD2	PHE	A	43	2.904	22.940	39.233	1.00	137.52
	206	CE1	PHE	A	43	4.293	25.131	40.219	1.00	138.89
40	207	CE2	PHE	A	43	2.221	23.932	39.929	1.00	137.63
	208	CZ	PHE	A	43	2.915	25.030	40.424	1.00	138.21
	209	C	PHE	A	43	5.757	21.014	40.493	1.00	109.11
	210	O	PHE	A	43	5.906	21.870	41.368	1.00	108.34



	211	N	GLY A	44	5.250	19.806	40.735	1.00	84.30
	212	CA	GLY A	44	4.834	19.423	42.076	1.00	83.06
	213	C	GLY A	44	6.001	19.390	43.042	1.00	82.12
	214	O	GLY A	44	5.981	20.042	44.085	1.00	81.72
5	215	N	HIS A	45	7.025	18.619	42.698	1.00	92.58
	216	CA	HIS A	45	8.207	18.530	43.539	1.00	92.23
	217	CB	HIS A	45	9.121	17.388	43.057	1.00	89.47
	218	CG	HIS A	45	8.646	16.023	43.467	1.00	89.70
	219	CD2	HIS A	45	7.864	15.119	42.828	1.00	90.25
10	220	ND1	HIS A	45	8.925	15.478	44.704	1.00	89.71
	221	CE1	HIS A	45	8.334	14.300	44.808	1.00	89.80
	222	NE2	HIS A	45	7.683	14.059	43.684	1.00	90.18
	223	C	HIS A	45	8.916	19.882	43.505	1.00	91.27
	224	O	HIS A	45	9.828	20.149	44.296	1.00	91.42
15	225	N	LYS A	46	8.487	20.734	42.577	1.00	82.42
	226	CA	LYS A	46	9.034	22.081	42.465	1.00	81.87
	227	CB	LYS A	46	8.683	22.710	41.114	1.00	97.17
	228	CG	LYS A	46	9.491	22.162	39.947	1.00	99.47
	229	CD	LYS A	46	9.162	22.876	38.643	1.00	99.67
20	230	CE	LYS A	46	10.094	22.419	37.536	1.00	99.93
	231	NZ	LYS A	46	9.782	23.075	36.241	1.00	100.68
	232	C	LYS A	46	8.343	22.847	43.578	1.00	80.96
	233	O	LYS A	46	8.927	23.727	44.207	1.00	80.53
	234	N	ALA A	47	7.085	22.485	43.813	1.00	76.83
25	235	CA	ALA A	47	6.276	23.094	44.858	1.00	75.35
	236	CB	ALA A	47	4.819	23.105	44.452	1.00	69.13
	237	C	ALA A	47	6.466	22.241	46.094	1.00	75.37
	238	O	ALA A	47	5.505	21.722	46.665	1.00	76.47
	239	N	GLY A	48	7.724	22.088	46.489	1.00	75.42
30	240	CA	GLY A	48	8.044	21.284	47.651	1.00	74.30
	241	C	GLY A	48	9.323	21.784	48.278	1.00	74.36
	242	O	GLY A	48	9.384	21.985	49.491	1.00	74.58
	243	N	MET A	49	10.355	21.975	47.458	1.00	81.06
	244	CA	MET A	49	11.628	22.480	47.963	1.00	81.70
35	245	CB	MET A	49	12.641	22.627	46.825	1.00	87.38
	246	CG	MET A	49	13.136	21.307	46.243	1.00	87.33
	247	SD	MET A	49	14.010	21.505	44.663	1.00	87.62
	248	CE	MET A	49	12.610	21.420	43.554	1.00	85.01
	249	C	MET A	49	11.320	23.833	48.586	1.00	81.21
40	250	O	MET A	49	11.946	24.240	49.564	1.00	81.58
	251	N	GLU A	50	10.337	24.517	48.007	1.00	77.92
	252	CA	GLU A	50	9.900	25.810	48.506	1.00	77.34
	253	CB	GLU A	50	8.822	26.402	47.588	1.00	95.37

	254	CG	GLU	A	50	9.050	27.860	47.157	1.00	95.61
	255	CD	GLU	A	50	9.139	28.834	48.326	1.00	96.16
	256	OE1	GLU	A	50	8.198	28.884	49.148	1.00	95.48
	257	OE2	GLU	A	50	10.154	29.556	48.417	1.00	96.34
5	258	C	GLU	A	50	9.306	25.500	49.873	1.00	76.40
	259	O	GLU	A	50	9.684	26.094	50.883	1.00	76.44
	260	N	ALA	A	51	8.377	24.551	49.896	1.00	70.94
	261	CA	ALA	A	51	7.741	24.135	51.142	1.00	69.92
	262	CB	ALA	A	51	6.856	22.914	50.889	1.00	99.69
10	263	C	ALA	A	51	8.798	23.817	52.207	1.00	68.95
	264	O	ALA	A	51	8.601	24.073	53.393	1.00	68.42
	265	N	LEU	A	52	9.914	23.242	51.775	1.00	66.05
	266	CA	LEU	A	52	10.998	22.922	52.689	1.00	65.82
	267	CB	LEU	A	52	12.066	22.062	51.993	1.00	68.86
15	268	CG	LEU	A	52	13.451	21.922	52.648	1.00	67.64
	269	CD1	LEU	A	52	13.322	21.671	54.148	1.00	67.79
	270	CD2	LEU	A	52	14.210	20.788	51.977	1.00	65.11
	271	C	LEU	A	52	11.601	24.242	53.116	1.00	65.19
	272	O	LEU	A	52	11.896	24.446	54.288	1.00	64.48
20	273	N	GLN	A	53	11.759	25.132	52.140	1.00	76.33
	274	CA	GLN	A	53	12.325	26.459	52.347	1.00	75.19
	275	CB	GLN	A	53	12.367	27.216	51.022	1.00	69.00
	276	CG	GLN	A	53	13.340	28.356	51.018	1.00	68.46
	277	CD	GLN	A	53	14.740	27.863	51.257	1.00	68.74
25	278	OE1	GLN	A	53	15.006	27.198	52.256	1.00	69.27
	279	NE2	GLN	A	53	15.647	28.175	50.339	1.00	67.93
	280	C	GLN	A	53	11.519	27.265	53.355	1.00	74.92
	281	O	GLN	A	53	12.068	28.045	54.126	1.00	74.08
	282	N	THR	A	54	10.209	27.081	53.334	1.00	84.09
30	283	CA	THR	A	54	9.340	27.782	54.258	1.00	84.86
	284	CB	THR	A	54	7.870	27.659	53.820	1.00	67.41
	285	OG1	THR	A	54	7.669	28.444	52.639	1.00	68.01
	286	CG2	THR	A	54	6.922	28.124	54.928	1.00	66.49
	287	C	THR	A	54	9.493	27.214	55.665	1.00	85.32
35	288	O	THR	A	54	9.546	27.970	56.638	1.00	86.21
	289	N	VAL	A	55	9.579	25.884	55.764	1.00	69.54
	290	CA	VAL	A	55	9.710	25.189	57.051	1.00	67.41
	291	CB	VAL	A	55	9.164	23.745	56.973	1.00	69.10
	292	CG1	VAL	A	55	9.287	23.091	58.325	1.00	68.82
40	293	CG2	VAL	A	55	7.705	23.744	56.534	1.00	68.80
	294	C	VAL	A	55	11.128	25.141	57.625	1.00	67.02
	295	O	VAL	A	55	11.327	25.472	58.791	1.00	67.32
	296	N	THR	A	56	12.111	24.722	56.832	1.00	58.40

	297	CA	THR	A	56	13.480	24.689	57.341	1.00	59.09
	298	CB	THR	A	56	14.520	24.231	56.257	1.00	61.50
	299	OG1	THR	A	56	15.859	24.425	56.750	1.00	60.24
	300	CG2	THR	A	56	14.351	25.021	54.981	1.00	64.31
5	301	C	THR	A	56	13.827	26.103	57.802	1.00	59.69
	302	O	THR	A	56	14.827	26.327	58.500	1.00	60.34
	303	N	LYS	A	57	12.973	27.046	57.405	1.00	74.50
	304	CA	LYS	A	57	13.118	28.466	57.726	1.00	74.27
	305	CB	LYS	A	57	12.374	29.300	56.672	1.00	59.08
10	306	CG	LYS	A	57	12.783	30.751	56.603	1.00	59.25
	307	CD	LYS	A	57	12.913	31.221	55.158	1.00	60.46
	308	CE	LYS	A	57	11.557	31.349	54.476	1.00	62.59
	309	NZ	LYS	A	57	11.681	31.790	53.056	1.00	60.91
	310	C	LYS	A	57	12.520	28.701	59.101	1.00	74.12
15	311	O	LYS	A	57	13.228	29.020	60.062	1.00	74.74
	312	N	ALA	A	58	11.204	28.526	59.171	1.00	63.23
	313	CA	ALA	A	58	10.456	28.684	60.405	1.00	63.11
	314	CB	ALA	A	58	9.019	28.284	60.182	1.00	34.72
	315	C	ALA	A	58	11.089	27.785	61.452	1.00	63.84
20	316	O	ALA	A	58	11.256	28.172	62.612	1.00	63.83
	317	N	ALA	A	59	11.434	26.575	61.028	1.00	82.06
	318	CA	ALA	A	59	12.068	25.615	61.907	1.00	81.68
	319	CB	ALA	A	59	12.589	24.453	61.100	1.00	82.06
	320	C	ALA	A	59	13.219	26.302	62.635	1.00	82.43
25	321	O	ALA	A	59	13.247	26.358	63.864	1.00	82.77
	322	N	ASN	A	60	14.160	26.837	61.865	1.00	89.28
	323	CA	ASN	A	60	15.319	27.521	62.425	1.00	89.34
	324	CB	ASN	A	60	16.229	28.003	61.292	1.00	67.34
	325	CG	ASN	A	60	17.591	28.441	61.788	1.00	67.19
30	326	OD1	ASN	A	60	18.176	27.796	62.651	1.00	67.36
	327	ND2	ASN	A	60	18.113	29.530	61.232	1.00	67.97
	328	C	ASN	A	60	14.888	28.702	63.289	1.00	89.22
	329	O	ASN	A	60	15.512	29.008	64.305	1.00	89.44
	330	N	LYS	A	61	13.805	29.352	62.880	1.00	65.39
35	331	CA	LYS	A	61	13.277	30.507	63.597	1.00	65.03
	332	CB	LYS	A	61	12.132	31.127	62.786	1.00	97.09
	333	CG	LYS	A	61	11.459	32.356	63.412	1.00	98.41
	334	CD	LYS	A	61	10.527	33.060	62.407	1.00	98.42
	335	CE	LYS	A	61	9.436	32.130	61.884	1.00	98.05
40	336	NZ	LYS	A	61	8.681	32.724	60.750	1.00	97.33
	337	C	LYS	A	61	12.795	30.167	65.004	1.00	63.12
	338	O	LYS	A	61	13.407	30.563	65.993	1.00	61.87
	339	N	LEU	A	62	11.692	29.429	65.076	1.00	64.11

	340	CA	LEU	A	62	11.083	29.024	66.340	1.00	61.44
	341	CB	LEU	A	62	9.944	28.056	66.059	1.00	69.48
	342	CG	LEU	A	62	8.665	28.748	65.619	1.00	69.94
	343	CD1	LEU	A	62	7.889	27.836	64.693	1.00	69.75
5	344	CD2	LEU	A	62	7.854	29.131	66.856	1.00	68.18
	345	C	LEU	A	62	11.994	28.425	67.406	1.00	60.15
	346	O	LEU	A	62	11.608	28.349	68.573	1.00	58.71
	347	N	GLY	A	63	13.190	27.991	67.019	1.00	61.68
	348	CA	GLY	A	63	14.104	27.423	67.997	1.00	59.91
10	349	C	GLY	A	63	14.637	26.045	67.660	1.00	59.47
	350	O	GLY	A	63	15.771	25.723	68.012	1.00	59.31
	351	N	VAL	A	64	13.824	25.234	66.982	1.00	47.50
	352	CA	VAL	A	64	14.201	23.873	66.588	1.00	45.51
	353	CB	VAL	A	64	13.335	23.389	65.416	1.00	51.13
15	354	CG1	VAL	A	64	13.641	21.942	65.125	1.00	51.54
	355	CG2	VAL	A	64	11.857	23.563	65.744	1.00	49.05
	356	C	VAL	A	64	15.671	23.768	66.179	1.00	44.45
	357	O	VAL	A	64	16.091	24.389	65.209	1.00	43.84
	358	N	LYS	A	65	16.452	22.983	66.914	1.00	59.01
20	359	CA	LYS	A	65	17.865	22.839	66.590	1.00	59.09
	360	CB	LYS	A	65	18.631	22.183	67.740	1.00	53.91
	361	CG	LYS	A	65	19.048	23.142	68.846	1.00	54.76
	362	CD	LYS	A	65	20.320	22.658	69.551	1.00	56.55
	363	CE	LYS	A	65	20.844	23.668	70.582	1.00	56.86
25	364	NZ	LYS	A	65	21.257	24.993	70.004	1.00	54.91
	365	C	LYS	A	65	18.154	22.074	65.304	1.00	59.50
	366	O	LYS	A	65	19.032	22.465	64.547	1.00	60.94
	367	N	VAL	A	66	17.432	20.986	65.050	1.00	47.31
	368	CA	VAL	A	66	17.670	20.197	63.838	1.00	46.46
30	369	CB	VAL	A	66	18.763	19.107	64.057	1.00	69.80
	370	CG1	VAL	A	66	18.384	18.222	65.215	1.00	68.87
	371	CG2	VAL	A	66	18.928	18.254	62.805	1.00	67.78
	372	C	VAL	A	66	16.422	19.501	63.368	1.00	44.59
	373	O	VAL	A	66	15.518	19.256	64.153	1.00	43.25
35	374	N	ILE	A	67	16.374	19.208	62.074	1.00	54.98
	375	CA	ILE	A	67	15.245	18.509	61.484	1.00	55.14
	376	CB	ILE	A	67	14.199	19.447	60.841	1.00	55.30
	377	CG2	ILE	A	67	13.718	20.459	61.843	1.00	57.20
	378	CG1	ILE	A	67	14.790	20.156	59.639	1.00	54.89
40	379	CD1	ILE	A	67	13.759	20.916	58.888	1.00	53.68
	380	C	ILE	A	67	15.746	17.590	60.395	1.00	55.13
	381	O	ILE	A	67	16.686	17.930	59.657	1.00	53.23
	382	N	THR	A	68	15.117	16.420	60.304	1.00	48.41

	383	CA	THR	A	68	15.480	15.449	59.294	1.00	47.13
	384	CB	THR	A	68	15.928	14.150	59.936	1.00	48.21
	385	OG1	THR	A	68	16.994	14.427	60.849	1.00	47.66
	386	CG2	THR	A	68	16.444	13.207	58.887	1.00	50.16
5	387	C	THR	A	68	14.299	15.224	58.365	1.00	46.51
	388	O	THR	A	68	13.194	14.868	58.792	1.00	44.30
	389	N	VAL	A	69	14.560	15.478	57.086	1.00	41.74
	390	CA	VAL	A	69	13.575	15.358	56.014	1.00	43.69
	391	CB	VAL	A	69	13.657	16.564	55.062	1.00	58.55
10	392	CG1	VAL	A	69	13.219	17.831	55.789	1.00	57.65
	393	CG2	VAL	A	69	15.089	16.705	54.524	1.00	58.16
	394	C	VAL	A	69	13.773	14.097	55.190	1.00	44.57
	395	O	VAL	A	69	14.863	13.837	54.673	1.00	43.05
	396	N	TYR	A	70	12.707	13.318	55.068	1.00	59.78
15	397	CA	TYR	A	70	12.760	12.075	54.325	1.00	62.67
	398	CB	TYR	A	70	11.929	11.009	55.031	1.00	52.64
	399	CG	TYR	A	70	12.143	9.625	54.494	1.00	49.53
	400	CD1	TYR	A	70	13.301	9.310	53.786	1.00	48.16
	401	CE1	TYR	A	70	13.526	8.026	53.316	1.00	47.14
20	402	CD2	TYR	A	70	11.208	8.619	54.722	1.00	48.32
	403	CE2	TYR	A	70	11.424	7.329	54.260	1.00	48.99
	404	CZ	TYR	A	70	12.587	7.041	53.557	1.00	48.59
	405	OH	TYR	A	70	12.816	5.770	53.100	1.00	48.72
	406	C	TYR	A	70	12.208	12.353	52.954	1.00	66.44
25	407	O	TYR	A	70	11.023	12.625	52.796	1.00	65.91
	408	N	ALA	A	71	13.077	12.270	51.959	1.00	68.56
	409	CA	ALA	A	71	12.692	12.566	50.594	1.00	74.30
	410	CB	ALA	A	71	13.886	13.176	49.878	1.00	72.73
	411	C	ALA	A	71	12.111	11.423	49.755	1.00	78.56
30	412	O	ALA	A	71	12.851	10.771	49.016	1.00	78.80
	413	N	PHE	A	72	10.796	11.197	49.859	1.00	83.41
	414	CA	PHE	A	72	10.088	10.161	49.080	1.00	89.46
	415	CB	PHE	A	72	11.012	8.973	48.765	1.00	140.39
	416	CG	PHE	A	72	10.397	7.944	47.849	1.00	144.03
35	417	CD1	PHE	A	72	9.767	8.329	46.669	1.00	145.48
	418	CD2	PHE	A	72	10.457	6.588	48.163	1.00	144.94
	419	CE1	PHE	A	72	9.204	7.378	45.815	1.00	146.82
	420	CE2	PHE	A	72	9.897	5.628	47.314	1.00	146.70
	421	CZ	PHE	A	72	9.270	6.026	46.138	1.00	147.70
40	422	C	PHE	A	72	8.817	9.643	49.753	1.00	92.23
	423	O	PHE	A	72	7.868	10.397	49.967	1.00	92.28
	424	N	SER	A	73	8.809	8.343	50.050	1.00	140.18
	425	CA	SER	A	73	7.697	7.659	50.704	1.00	143.09

	426	CB	SER A	73	7.333	8.400	51.987	1.00120.39
	427	OG	SER A	73	8.499	8.670	52.748	1.00120.18
	428	C	SER A	73	6.448	7.467	49.837	1.00145.30
	429	O	SER A	73	5.332	7.741	50.276	1.00145.74
5	430	N	THR A	74	6.642	6.983	48.613	1.00161.50
	431	CA	THR A	74	5.544	6.735	47.677	1.00163.44
	432	CB	THR A	74	4.495	5.764	48.297	1.00143.68
	433	OG1	THR A	74	5.170	4.625	48.844	1.00143.22
	434	CG2	THR A	74	3.518	5.267	47.238	1.00143.83
10	435	C	THR A	74	4.857	8.034	47.233	1.00164.62
	436	O	THR A	74	5.346	9.129	47.523	1.00164.97
	437	N	GLU A	75	3.738	7.887	46.520	1.00167.70
	438	CA	GLU A	75	2.920	8.983	45.978	1.00168.57
	439	CB	GLU A	75	3.099	10.281	46.783	1.00113.85
15	440	CG	GLU A	75	2.167	10.413	47.988	1.00112.90
	441	CD	GLU A	75	0.722	10.670	47.599	1.00112.00
	442	OE1	GLU A	75	-0.130	10.790	48.504	1.00110.81
	443	OE2	GLU A	75	0.437	10.753	46.389	1.00111.35
	444	C	GLU A	75	3.199	9.251	44.499	1.00169.23
20	445	O	GLU A	75	2.777	10.272	43.953	1.00168.89
	446	N	ASN A	76	3.909	8.331	43.853	1.00157.50
	447	CA	ASN A	76	4.220	8.466	42.433	1.00158.07
	448	CB	ASN A	76	5.667	8.052	42.148	1.00124.17
	449	CG	ASN A	76	6.677	8.942	42.841	1.00123.19
25	450	OD1	ASN A	76	6.695	10.157	42.643	1.00121.77
	451	ND2	ASN A	76	7.528	8.339	43.657	1.00122.49
	452	C	ASN A	76	3.265	7.577	41.651	1.00158.97
	453	O	ASN A	76	3.361	7.462	40.427	1.00159.05
	454	N	TRP A	77	2.348	6.947	42.380	1.00169.16
30	455	CA	TRP A	77	1.347	6.066	41.791	1.00169.99
	456	CB	TRP A	77	0.583	6.809	40.693	1.00167.20
	457	CG	TRP A	77	-0.286	7.902	41.215	1.00169.26
	458	CD2	TRP A	77	0.095	9.260	41.438	1.00169.83
	459	CE2	TRP A	77	-1.030	9.928	41.965	1.00170.05
35	460	CE3	TRP A	77	1.280	9.979	41.243	1.00169.57
	461	CD1	TRP A	77	-1.590	7.799	41.605	1.00169.57
	462	NE1	TRP A	77	-2.045	9.013	42.057	1.00169.91
	463	CZ2	TRP A	77	-1.005	11.282	42.301	1.00170.18
	464	CZ3	TRP A	77	1.305	11.323	41.577	1.00169.40
40	465	CH2	TRP A	77	0.169	11.961	42.099	1.00169.90
	466	C	TRP A	77	1.914	4.769	41.225	1.00169.29
	467	O	TRP A	77	1.659	3.684	41.755	1.00169.41
	468	N	THR A	78	2.682	4.880	40.147	1.00115.73

	469	CA	THR	A	78	3.248	3.700	39.519	1.00114.21
	470	CB	THR	A	78	2.400	3.268	38.303	1.00109.37
	471	OG1	THR	A	78	2.277	4.369	37.392	1.00108.51
	472	CG2	THR	A	78	1.015	2.815	38.750	1.00109.06
5	473	C	THR	A	78	4.681	3.891	39.051	1.00113.51
	474	O	THR	A	78	5.342	4.872	39.388	1.00113.25
	475	N	ARG	A	79	5.142	2.922	38.268	1.00125.73
	476	CA	ARG	A	79	6.480	2.924	37.702	1.00124.36
	477	CB	ARG	A	79	6.630	4.068	36.696	1.00100.13
10	478	CG	ARG	A	79	6.029	3.801	35.325	1.00 99.59
	479	CD	ARG	A	79	4.510	3.914	35.335	1.00 99.41
	480	NE	ARG	A	79	3.943	3.589	34.028	1.00 99.30
	481	CZ	ARG	A	79	4.263	4.207	32.894	1.00 99.40
	482	NH1	ARG	A	79	5.151	5.196	32.901	1.00 98.32
15	483	NH2	ARG	A	79	3.694	3.832	31.753	1.00 98.96
	484	C	ARG	A	79	7.620	2.998	38.708	1.00123.56
	485	O	ARG	A	79	7.632	3.843	39.604	1.00122.92
	486	N	PRO	A	80	8.595	2.089	38.568	1.00135.20
	487	CD	PRO	A	80	8.454	0.857	37.775	1.00 91.42
20	488	CA	PRO	A	80	9.776	2.009	39.432	1.00134.63
	489	CB	PRO	A	80	10.338	0.621	39.122	1.00 91.34
	490	CG	PRO	A	80	9.135	-0.148	38.653	1.00 91.06
	491	C	PRO	A	80	10.759	3.114	39.047	1.00134.17
	492	O	PRO	A	80	11.628	3.495	39.835	1.00133.81
25	493	N	ASP	A	81	10.603	3.620	37.825	1.00124.52
	494	CA	ASP	A	81	11.466	4.668	37.288	1.00123.80
	495	CB	ASP	A	81	11.398	4.658	35.755	1.00124.36
	496	CG	ASP	A	81	9.979	4.739	35.231	1.00124.61
	497	OD1	ASP	A	81	9.792	4.730	33.997	1.00124.69
30	498	OD2	ASP	A	81	9.047	4.814	36.052	1.00124.42
	499	C	ASP	A	81	11.179	6.076	37.817	1.00122.94
	500	O	ASP	A	81	12.101	6.769	38.251	1.00122.42
	501	N	GLN	A	82	9.917	6.503	37.781	1.00103.22
	502	CA	GLN	A	82	9.552	7.835	38.271	1.00103.09
35	503	CB	GLN	A	82	8.034	8.030	38.224	1.00102.55
	504	CG	GLN	A	82	7.388	7.617	36.920	1.00100.84
	505	CD	GLN	A	82	5.871	7.635	36.992	1.00 99.45
	506	OE1	GLN	A	82	5.274	7.098	37.929	1.00 99.09
	507	NE2	GLN	A	82	5.239	8.242	35.995	1.00 98.90
40	508	C	GLN	A	82	10.033	7.992	39.716	1.00104.06
	509	O	GLN	A	82	10.541	9.049	40.107	1.00104.24
	510	N	GLU	A	83	9.867	6.927	40.499	1.00127.58
	511	CA	GLU	A	83	10.270	6.908	41.904	1.00127.87

	512	CB	GLU A	83	10.440	5.463	42.398	1.00122.12
	513	CG	GLU A	83	9.184	4.609	42.327	1.00122.02
	514	CD	GLU A	83	9.364	3.252	42.983	1.00122.35
	515	OE1	GLU A	83	9.748	3.215	44.173	1.00122.36
5	516	OE2	GLU A	83	9.115	2.225	42.314	1.00121.82
	517	C	GLU A	83	11.578	7.655	42.115	1.00127.94
	518	O	GLU A	83	11.587	8.847	42.417	1.00127.58
	519	N	VAL A	84	12.681	6.935	41.947	1.00125.17
	520	CA	VAL A	84	14.013	7.496	42.121	1.00125.01
10	521	CB	VAL A	84	15.079	6.366	42.105	1.00112.12
	522	CG1	VAL A	84	16.316	6.789	42.884	1.00112.24
	523	CG2	VAL A	84	14.493	5.092	42.690	1.00112.22
	524	C	VAL A	84	14.320	8.511	41.010	1.00124.71
	525	O	VAL A	84	15.377	8.450	40.378	1.00124.65
15	526	N	LYS A	85	13.395	9.443	40.780	1.00113.93
	527	CA	LYS A	85	13.567	10.460	39.743	1.00113.27
	528	CB	LYS A	85	12.601	10.196	38.584	1.00111.88
	529	CG	LYS A	85	12.617	11.251	37.477	1.00111.13
	530	CD	LYS A	85	13.891	11.195	36.649	1.00110.38
20	531	CE	LYS A	85	13.819	12.144	35.464	1.00108.46
	532	NZ	LYS A	85	14.993	11.971	34.569	1.00106.72
	533	C	LYS A	85	13.346	11.875	40.265	1.00113.10
	534	O	LYS A	85	14.304	12.596	40.549	1.00112.69
	535	N	PHE A	86	12.078	12.267	40.380	1.00115.23
25	536	CA	PHE A	86	11.719	13.601	40.853	1.00114.38
	537	CB	PHE A	86	10.197	13.741	41.011	1.00145.14
	538	CG	PHE A	86	9.417	13.511	39.745	1.00146.80
	539	CD1	PHE A	86	8.997	12.231	39.392	1.00147.19
	540	CD2	PHE A	86	9.089	14.577	38.912	1.00147.37
30	541	CE1	PHE A	86	8.257	12.016	38.226	1.00147.74
	542	CE2	PHE A	86	8.353	14.373	37.746	1.00147.59
	543	CZ	PHE A	86	7.936	13.090	37.402	1.00148.12
	544	C	PHE A	86	12.372	13.903	42.195	1.00112.83
	545	O	PHE A	86	12.296	15.029	42.692	1.00112.68
35	546	N	ILE A	87	13.008	12.897	42.783	1.00102.29
	547	CA	ILE A	87	13.651	13.063	44.076	1.00100.37
	548	CB	ILE A	87	13.168	11.948	45.059	1.00 82.82
	549	CG2	ILE A	87	13.916	10.646	44.798	1.00 82.63
	550	CG1	ILE A	87	13.349	12.401	46.508	1.00 82.54
40	551	CD1	ILE A	87	14.790	12.546	46.949	1.00 82.39
	552	C	ILE A	87	15.179	13.053	43.935	1.00 99.43
	553	O	ILE A	87	15.890	13.645	44.748	1.00 99.59
	554	N	MET A	88	15.680	12.402	42.889	1.00 92.97



	555	CA	MET	A	88	17.120	12.329	42.667	1.00	91.11
	556	CB	MET	A	88	17.449	11.174	41.729	1.00	86.60
	557	CG	MET	A	88	17.169	9.824	42.350	1.00	86.35
	558	SD	MET	A	88	17.899	9.667	43.995	1.00	84.59
5	559	CE	MET	A	88	19.624	9.507	43.566	1.00	84.86
	560	C	MET	A	88	17.730	13.617	42.136	1.00	90.01
	561	O	MET	A	88	18.940	13.822	42.232	1.00	88.88
	562	N	ASN	A	89	16.903	14.480	41.561	1.00	104.78
	563	CA	ASN	A	89	17.410	15.750	41.070	1.00	104.87
10	564	CB	ASN	A	89	16.839	16.082	39.689	1.00	87.23
	565	CG	ASN	A	89	17.897	16.004	38.592	1.00	87.62
	566	OD1	ASN	A	89	18.388	14.922	38.265	1.00	86.84
	567	ND2	ASN	A	89	18.265	17.156	38.035	1.00	87.72
	568	C	ASN	A	89	17.061	16.833	42.083	1.00	105.04
15	569	O	ASN	A	89	17.406	18.005	41.916	1.00	104.79
	570	N	LEU	A	90	16.379	16.418	43.145	1.00	128.36
	571	CA	LEU	A	90	15.992	17.317	44.222	1.00	127.84
	572	CB	LEU	A	90	15.315	16.512	45.350	1.00	66.10
	573	CG	LEU	A	90	15.098	17.105	46.753	1.00	65.85
20	574	CD1	LEU	A	90	14.041	16.301	47.498	1.00	65.18
	575	CD2	LEU	A	90	16.407	17.106	47.534	1.00	65.04
	576	C	LEU	A	90	17.230	18.054	44.743	1.00	127.97
	577	O	LEU	A	90	17.257	19.283	44.783	1.00	128.37
	578	N	PRO	A	91	18.278	17.308	45.129	1.00	109.94
25	579	CD	PRO	A	91	18.358	15.838	45.126	1.00	94.03
	580	CA	PRO	A	91	19.524	17.875	45.650	1.00	109.40
	581	CB	PRO	A	91	20.425	16.656	45.767	1.00	93.11
	582	CG	PRO	A	91	19.468	15.584	46.104	1.00	93.72
	583	C	PRO	A	91	20.146	18.958	44.782	1.00	109.63
30	584	O	PRO	A	91	20.902	19.796	45.278	1.00	110.18
	585	N	VAL	A	92	19.839	18.934	43.489	1.00	75.43
	586	CA	VAL	A	92	20.385	19.932	42.573	1.00	74.80
	587	CB	VAL	A	92	20.681	19.329	41.187	1.00	87.82
	588	CG1	VAL	A	92	21.515	20.307	40.369	1.00	87.19
35	589	CG2	VAL	A	92	21.400	18.000	41.339	1.00	88.11
	590	C	VAL	A	92	19.427	21.105	42.393	1.00	73.85
	591	O	VAL	A	92	19.839	22.263	42.449	1.00	72.31
	592	N	GLU	A	93	18.149	20.799	42.179	1.00	106.54
	593	CA	GLU	A	93	17.138	21.837	41.995	1.00	107.87
40	594	CB	GLU	A	93	15.812	21.237	41.514	1.00	91.08
	595	CG	GLU	A	93	15.005	22.155	40.596	1.00	91.12
	596	CD	GLU	A	93	13.787	21.464	39.986	1.00	92.42
	597	OE1	GLU	A	93	13.882	20.259	39.652	1.00	93.59

	598	OE2	GLU	A	93	12.737	22.126	39.826	1.00	92.19
	599	C	GLU	A	93	16.937	22.536	43.328	1.00	108.68
	600	O	GLU	A	93	16.034	23.358	43.485	1.00	108.62
	601	N	PHE	A	94	17.779	22.183	44.293	1.00	105.29
5	602	CA	PHE	A	94	17.725	22.796	45.606	1.00	104.35
	603	CB	PHE	A	94	17.850	21.747	46.713	1.00	76.81
	604	CG	PHE	A	94	17.169	22.142	47.999	1.00	76.33
	605	CD1	PHE	A	94	15.781	22.291	48.048	1.00	76.16
	606	CD2	PHE	A	94	17.910	22.389	49.153	1.00	74.78
10	607	CE1	PHE	A	94	15.144	22.679	49.223	1.00	75.31
	608	CE2	PHE	A	94	17.280	22.778	50.331	1.00	73.59
	609	CZ	PHE	A	94	15.895	22.924	50.364	1.00	74.31
	610	C	PHE	A	94	18.915	23.737	45.649	1.00	104.38
	611	O	PHE	A	94	18.787	24.896	46.038	1.00	104.76
15	612	N	TYR	A	95	20.072	23.236	45.224	1.00	82.09
	613	CA	TYR	A	95	21.279	24.052	45.209	1.00	81.85
	614	CB	TYR	A	95	22.494	23.240	44.762	1.00	111.52
	615	CG	TYR	A	95	23.808	23.931	45.064	1.00	112.46
	616	CD1	TYR	A	95	24.575	23.559	46.168	1.00	112.65
20	617	CE1	TYR	A	95	25.765	24.208	46.471	1.00	113.39
	618	CD2	TYR	A	95	24.268	24.976	44.267	1.00	112.48
	619	CE2	TYR	A	95	25.458	25.634	44.563	1.00	113.53
	620	CZ	TYR	A	95	26.201	25.244	45.665	1.00	113.91
	621	OH	TYR	A	95	27.385	25.882	45.958	1.00	113.52
25	622	C	TYR	A	95	21.094	25.227	44.258	1.00	81.59
	623	O	TYR	A	95	21.463	26.356	44.578	1.00	81.88
	624	N	ASP	A	96	20.534	24.963	43.082	1.00	74.79
	625	CA	ASP	A	96	20.316	26.037	42.128	1.00	74.33
	626	CB	ASP	A	96	19.315	25.621	41.032	1.00	95.08
30	627	CG	ASP	A	96	19.907	24.643	40.018	1.00	95.76
	628	OD1	ASP	A	96	21.097	24.790	39.668	1.00	95.20
	629	OD2	ASP	A	96	19.175	23.739	39.555	1.00	95.10
	630	C	ASP	A	96	19.765	27.250	42.878	1.00	73.49
	631	O	ASP	A	96	20.432	28.278	43.002	1.00	72.28
35	632	N	ASN	A	97	18.560	27.105	43.417	1.00	96.37
	633	CA	ASN	A	97	17.914	28.210	44.111	1.00	95.56
	634	CB	ASN	A	97	16.953	28.902	43.129	1.00	104.54
	635	CG	ASN	A	97	16.296	27.920	42.148	1.00	104.98
	636	OD1	ASN	A	97	16.978	27.177	41.441	1.00	104.13
40	637	ND2	ASN	A	97	14.968	27.927	42.101	1.00	105.62
	638	C	ASN	A	97	17.182	27.877	45.421	1.00	93.84
	639	O	ASN	A	97	15.952	27.860	45.457	1.00	93.36
	640	N	TYR	A	98	17.944	27.636	46.489	1.00	67.33

	641	CA	TYR A	98	17.397	27.325	47.818	1.00	64.16
	642	CB	TYR A	98	16.630	26.003	47.792	1.00	79.35
	643	CG	TYR A	98	15.207	26.142	47.321	1.00	80.45
	644	CD1	TYR A	98	14.739	25.409	46.240	1.00	80.98
5	645	CE1	TYR A	98	13.431	25.556	45.787	1.00	81.40
	646	CD2	TYR A	98	14.331	27.025	47.945	1.00	80.03
	647	CE2	TYR A	98	13.020	27.176	47.501	1.00	80.71
	648	CZ	TYR A	98	12.577	26.440	46.420	1.00	81.85
	649	OH	TYR A	98	11.288	26.590	45.961	1.00	83.00
10	650	C	TYR A	98	18.490	27.255	48.889	1.00	61.91
	651	O	TYR A	98	18.369	27.850	49.954	1.00	61.10
	652	N	VAL A	99	19.558	26.525	48.599	1.00	67.38
	653	CA	VAL A	99	20.662	26.401	49.534	1.00	66.08
	654	CB	VAL A	99	21.701	25.351	49.033	1.00	66.14
15	655	CG1	VAL A	99	23.024	25.480	49.789	1.00	64.79
	656	CG2	VAL A	99	21.138	23.954	49.231	1.00	65.78
	657	C	VAL A	99	21.348	27.747	49.802	1.00	65.56
	658	O	VAL A	99	21.954	27.943	50.858	1.00	66.27
	659	N	PRO A	100	21.268	28.700	48.859	1.00	65.97
20	660	CD	PRO A	100	20.708	28.730	47.499	1.00	64.74
	661	CA	PRO A	100	21.937	29.966	49.168	1.00	65.09
	662	CB	PRO A	100	21.892	30.705	47.838	1.00	63.82
	663	CG	PRO A	100	20.614	30.212	47.235	1.00	63.76
	664	C	PRO A	100	21.221	30.714	50.293	1.00	64.62
25	665	O	PRO A	100	21.856	31.172	51.248	1.00	62.57
	666	N	GLU A	101	19.900	30.827	50.175	1.00	68.29
	667	CA	GLU A	101	19.109	31.500	51.194	1.00	68.70
	668	CB	GLU A	101	17.622	31.503	50.824	1.00	73.17
	669	CG	GLU A	101	16.795	32.555	51.570	1.00	72.83
30	670	CD	GLU A	101	15.297	32.238	51.614	1.00	72.47
	671	OE1	GLU A	101	14.731	31.826	50.576	1.00	72.69
	672	OE2	GLU A	101	14.680	32.412	52.691	1.00	72.65
	673	C	GLU A	101	19.311	30.736	52.502	1.00	69.44
	674	O	GLU A	101	19.631	31.323	53.532	1.00	71.27
35	675	N	LEU A	102	19.126	29.421	52.460	1.00	66.14
	676	CA	LEU A	102	19.312	28.608	53.655	1.00	65.87
	677	CB	LEU A	102	19.224	27.117	53.312	1.00	82.81
	678	CG	LEU A	102	17.850	26.441	53.384	1.00	84.46
	679	CD1	LEU A	102	17.894	25.105	52.661	1.00	85.14
40	680	CD2	LEU A	102	17.449	26.244	54.838	1.00	83.94
	681	C	LEU A	102	20.658	28.915	54.310	1.00	65.74
	682	O	LEU A	102	20.789	28.842	55.532	1.00	65.65
	683	N	HIS A	103	21.658	29.260	53.505	1.00	68.24

	684	CA	HIS A 103	22.965	29.587	54.058	1.00	68.04
	685	CB	HIS A 103	24.034	29.559	52.983	1.00	68.97
	686	CG	HIS A 103	25.407	29.807	53.512	1.00	70.22
	687	CD2	HIS A 103	26.321	30.758	53.212	1.00	71.41
5	688	ND1	HIS A 103	25.983	29.015	54.481	1.00	70.78
	689	CE1	HIS A 103	27.193	29.467	54.753	1.00	72.26
	690	NE2	HIS A 103	27.424	30.525	53.997	1.00	72.11
	691	C	HIS A 103	22.913	30.981	54.653	1.00	68.36
	692	O	HIS A 103	23.689	31.330	55.538	1.00	68.09
10	693	N	ALA A 104	21.986	31.778	54.144	1.00	86.77
	694	CA	ALA A 104	21.800	33.140	54.607	1.00	86.04
	695	CB	ALA A 104	21.223	33.984	53.483	1.00	71.18
	696	C	ALA A 104	20.867	33.143	55.817	1.00	85.42
	697	O	ALA A 104	20.108	34.086	56.045	1.00	86.66
15	698	N	ASN A 105	20.923	32.061	56.579	1.00	57.79
	699	CA	ASN A 105	20.116	31.918	57.781	1.00	55.08
	700	CB	ASN A 105	18.759	31.305	57.450	1.00	68.95
	701	CG	ASN A 105	17.722	32.353	57.096	1.00	69.83
	702	OD1	ASN A 105	16.980	32.833	57.957	1.00	69.95
20	703	ND2	ASN A 105	17.677	32.728	55.827	1.00	68.58
	704	C	ASN A 105	20.900	31.027	58.726	1.00	53.23
	705	O	ASN A 105	20.351	30.409	59.644	1.00	51.84
	706	N	ASN A 106	22.203	30.973	58.472	1.00	66.42
	707	CA	ASN A 106	23.113	30.182	59.271	1.00	65.39
25	708	CB	ASN A 106	23.144	30.737	60.688	1.00	50.54
	709	CG	ASN A 106	24.382	30.317	61.439	1.00	51.95
	710	OD1	ASN A 106	24.379	30.196	62.673	1.00	50.50
	711	ND2	ASN A 106	25.466	30.103	60.696	1.00	51.43
	712	C	ASN A 106	22.693	28.706	59.305	1.00	64.44
30	713	O	ASN A 106	23.062	27.972	60.225	1.00	64.11
	714	N	VAL A 107	21.929	28.270	58.304	1.00	62.70
	715	CA	VAL A 107	21.458	26.886	58.244	1.00	61.91
	716	CB	VAL A 107	20.177	26.755	57.423	1.00	45.28
	717	CG1	VAL A 107	19.846	25.278	57.216	1.00	44.48
35	718	CG2	VAL A 107	19.037	27.476	58.134	1.00	44.90
	719	C	VAL A 107	22.456	25.925	57.650	1.00	61.32
	720	O	VAL A 107	22.876	26.080	56.510	1.00	60.88
	721	N	LYS A 108	22.823	24.921	58.428	1.00	59.03
	722	CA	LYS A 108	23.762	23.939	57.945	1.00	60.75
40	723	CB	LYS A 108	24.606	23.361	59.082	1.00	48.27
	724	CG	LYS A 108	25.668	22.380	58.584	1.00	45.59
	725	CD	LYS A 108	26.930	22.362	59.436	1.00	42.19
	726	CE	LYS A 108	26.663	21.902	60.832	1.00	40.45

	727	NZ	LYS A 108	27.933	21.381	61.392	1.00	40.56
	728	C	LYS A 108	22.964	22.842	57.280	1.00	62.55
	729	O	LYS A 108	21.847	22.532	57.696	1.00	62.25
	730	N	ILE A 109	23.548	22.258	56.241	1.00	63.15
5	731	CA	ILE A 109	22.901	21.209	55.480	1.00	64.39
	732	CB	ILE A 109	22.766	21.633	54.019	1.00	61.39
	733	CG2	ILE A 109	22.142	20.511	53.204	1.00	61.36
	734	CG1	ILE A 109	21.941	22.921	53.939	1.00	62.99
	735	CD1	ILE A 109	21.865	23.534	52.550	1.00	64.37
10	736	C	ILE A 109	23.722	19.942	55.529	1.00	64.81
	737	O	ILE A 109	24.930	19.987	55.306	1.00	64.56
	738	N	GLN A 110	23.069	18.821	55.832	1.00	61.92
	739	CA	GLN A 110	23.743	17.524	55.874	1.00	63.70
	740	CB	GLN A 110	24.274	17.225	57.283	1.00	64.74
15	741	CG	GLN A 110	25.553	17.989	57.581	1.00	65.42
	742	CD	GLN A 110	26.177	17.634	58.907	1.00	67.02
	743	OE1	GLN A 110	25.534	17.723	59.954	1.00	68.13
	744	NE2	GLN A 110	27.447	17.238	58.875	1.00	64.55
	745	C	GLN A 110	22.870	16.373	55.357	1.00	63.93
20	746	O	GLN A 110	21.698	16.223	55.735	1.00	63.57
	747	N	MET A 111	23.469	15.567	54.481	1.00	70.88
	748	CA	MET A 111	22.794	14.437	53.852	1.00	71.45
	749	CB	MET A 111	23.359	14.221	52.440	1.00	90.85
	750	CG	MET A 111	23.877	15.493	51.757	1.00	92.69
25	751	SD	MET A 111	22.648	16.821	51.587	1.00	94.81
	752	CE	MET A 111	23.664	18.140	50.918	1.00	94.19
	753	C	MET A 111	22.931	13.138	54.643	1.00	70.23
	754	O	MET A 111	23.995	12.842	55.193	1.00	69.63
	755	N	ILE A 112	21.856	12.357	54.682	1.00	52.02
30	756	CA	ILE A 112	21.866	11.087	55.388	1.00	51.86
	757	CB	ILE A 112	21.021	11.184	56.673	1.00	43.65
	758	CG2	ILE A 112	19.545	10.953	56.385	1.00	43.05
	759	CG1	ILE A 112	21.485	10.131	57.660	1.00	43.76
	760	CD1	ILE A 112	20.993	10.368	59.061	1.00	45.10
35	761	C	ILE A 112	21.363	9.948	54.491	1.00	52.76
	762	O	ILE A 112	20.244	9.984	53.996	1.00	53.77
	763	N	GLY A 113	22.207	8.948	54.260	1.00	50.86
	764	CA	GLY A 113	21.812	7.833	53.417	1.00	51.82
	765	C	GLY A 113	22.968	7.184	52.672	1.00	52.95
40	766	O	GLY A 113	24.115	7.273	53.098	1.00	51.02
	767	N	GLU A 114	22.662	6.504	51.571	1.00	61.56
	768	CA	GLU A 114	23.694	5.865	50.767	1.00	64.78
	769	CB	GLU A 114	23.177	4.584	50.110	1.00	105.16

	770	CG	GLU A 114	23.581	3.303	50.840	1.00108.67
	771	CD	GLU A 114	22.762	3.035	52.093	1.00110.31
	772	OE1	GLU A 114	23.207	2.207	52.918	1.00109.52
	773	OE2	GLU A 114	21.673	3.636	52.249	1.00111.56
5	774	C	GLU A 114	24.092	6.861	49.706	1.00 65.85
	775	O	GLU A 114	23.273	7.284	48.900	1.00 65.40
	776	N	THR A 115	25.360	7.236	49.714	1.00 71.62
	777	CA	THR A 115	25.866	8.222	48.776	1.00 73.72
	778	CB	THR A 115	26.786	9.199	49.503	1.00 86.49
10	779	OG1	THR A 115	27.911	8.482	50.027	1.00 87.69
	780	CG2	THR A 115	26.042	9.867	50.656	1.00 86.39
	781	C	THR A 115	26.629	7.599	47.618	1.00 74.60
	782	O	THR A 115	26.708	8.177	46.536	1.00 73.55
	783	N	ASP A 116	27.182	6.415	47.855	1.00 95.32
15	784	CA	ASP A 116	27.961	5.696	46.850	1.00 97.46
	785	CB	ASP A 116	28.632	4.480	47.498	1.00107.89
	786	CG	ASP A 116	29.260	4.806	48.847	1.00109.36
	787	OD1	ASP A 116	29.832	3.889	49.478	1.00109.95
	788	OD2	ASP A 116	29.176	5.977	49.281	1.00108.66
20	789	C	ASP A 116	27.100	5.241	45.666	1.00 97.97
	790	O	ASP A 116	27.571	5.164	44.530	1.00 97.37
	791	N	ARG A 117	25.837	4.939	45.945	1.00104.25
	792	CA	ARG A 117	24.898	4.489	44.922	1.00105.55
	793	CB	ARG A 117	23.867	3.538	45.550	1.00116.04
25	794	CG	ARG A 117	24.432	2.230	46.106	1.00117.82
	795	CD	ARG A 117	24.634	1.204	45.003	1.00118.34
	796	NE	ARG A 117	24.982	-0.128	45.505	1.00119.32
	797	CZ	ARG A 117	26.167	-0.465	46.012	1.00120.88
	798	NH1	ARG A 117	27.138	0.436	46.093	1.00121.11
30	799	NH2	ARG A 117	26.387	-1.709	46.433	1.00121.66
	800	C	ARG A 117	24.172	5.687	44.296	1.00104.47
	801	O	ARG A 117	23.033	5.566	43.838	1.00104.68
	802	N	LEU A 118	24.835	6.838	44.270	1.00 74.35
	803	CA	LEU A 118	24.228	8.052	43.726	1.00 72.87
35	804	CB	LEU A 118	24.291	9.181	44.763	1.00110.14
	805	CG	LEU A 118	23.458	9.140	46.046	1.00111.44
	806	CD1	LEU A 118	23.873	10.295	46.944	1.00110.85
	807	CD2	LEU A 118	21.977	9.233	45.710	1.00111.93
	808	C	LEU A 118	24.840	8.575	42.429	1.00 69.74
40	809	O	LEU A 118	26.017	8.364	42.151	1.00 68.60
	810	N	PRO A 119	24.036	9.285	41.627	1.00 77.21
	811	CD	PRO A 119	22.608	9.547	41.875	1.00 38.10
	812	CA	PRO A 119	24.464	9.868	40.351	1.00 76.11

	813	CB	PRO A 119	23.275	10.722	39.953	1.00	36.32
	814	CG	PRO A 119	22.120	9.955	40.517	1.00	36.96
	815	C	PRO A 119	25.681	10.731	40.621	1.00	76.10
	816	O	PRO A 119	25.975	11.025	41.771	1.00	77.08
5	817	N	LYS A 120	26.394	11.141	39.584	1.00	73.54
	818	CA	LYS A 120	27.553	11.989	39.813	1.00	73.53
	819	CB	LYS A 120	28.475	11.998	38.595	1.00	77.02
	820	CG	LYS A 120	29.886	12.450	38.917	1.00	76.00
	821	CD	LYS A 120	30.664	12.820	37.670	1.00	75.01
10	822	CE	LYS A 120	30.217	14.158	37.124	1.00	74.67
	823	NZ	LYS A 120	30.845	14.418	35.807	1.00	73.90
	824	C	LYS A 120	26.995	13.389	40.063	1.00	74.96
	825	O	LYS A 120	27.321	14.038	41.057	1.00	75.96
	826	N	GLN A 121	26.137	13.837	39.153	1.00	95.99
15	827	CA	GLN A 121	25.499	15.146	39.253	1.00	96.22
	828	CB	GLN A 121	24.257	15.199	38.343	1.00	118.01
	829	CG	GLN A 121	23.363	16.432	38.550	1.00	119.87
	830	CD	GLN A 121	21.948	16.257	38.005	1.00	120.22
	831	OE1	GLN A 121	21.203	15.380	38.443	1.00	120.50
20	832	NE2	GLN A 121	21.573	17.102	37.051	1.00	119.65
	833	C	GLN A 121	25.068	15.412	40.688	1.00	94.96
	834	O	GLN A 121	25.486	16.384	41.314	1.00	95.10
	835	N	THR A 122	24.230	14.526	41.206	1.00	72.28
	836	CA	THR A 122	23.709	14.679	42.547	1.00	70.99
25	837	CB	THR A 122	22.593	13.652	42.823	1.00	74.92
	838	OG1	THR A 122	21.535	13.822	41.866	1.00	74.12
	839	CG2	THR A 122	22.033	13.844	44.230	1.00	74.49
	840	C	THR A 122	24.752	14.586	43.651	1.00	68.97
	841	O	THR A 122	24.668	15.309	44.635	1.00	68.88
30	842	N	PHE A 123	25.737	13.709	43.497	1.00	68.02
	843	CA	PHE A 123	26.746	13.568	44.538	1.00	67.10
	844	CB	PHE A 123	27.649	12.370	44.297	1.00	58.71
	845	CG	PHE A 123	28.722	12.230	45.327	1.00	55.47
	846	CD1	PHE A 123	28.405	11.854	46.621	1.00	53.69
35	847	CD2	PHE A 123	30.046	12.518	45.014	1.00	55.49
	848	CE1	PHE A 123	29.387	11.766	47.588	1.00	54.44
	849	CE2	PHE A 123	31.038	12.433	45.973	1.00	54.03
	850	CZ	PHE A 123	30.710	12.056	47.263	1.00	54.36
	851	C	PHE A 123	27.621	14.789	44.688	1.00	67.57
40	852	O	PHE A 123	28.497	14.831	45.550	1.00	68.16
	853	N	GLU A 124	27.405	15.786	43.848	1.00	75.95
	854	CA	GLU A 124	28.200	16.991	43.956	1.00	76.79
	855	CB	GLU A 124	28.843	17.307	42.598	1.00	80.65

	856	CG	GLU A 124	29.798	16.182	42.148	1.00	82.59
	857	CD	GLU A 124	30.518	16.439	40.826	1.00	83.92
	858	OE1	GLU A 124	31.407	15.627	40.485	1.00	83.64
	859	OE2	GLU A 124	30.205	17.429	40.128	1.00	83.54
5	860	C	GLU A 124	27.302	18.108	44.473	1.00	75.88
	861	O	GLU A 124	27.696	18.880	45.339	1.00	75.13
	862	N	ALA A 125	26.071	18.152	43.981	1.00	84.09
	863	CA	ALA A 125	25.117	19.164	44.415	1.00	84.39
	864	CB	ALA A 125	23.796	18.993	43.665	1.00	66.98
10	865	C	ALA A 125	24.875	19.059	45.917	1.00	84.54
	866	O	ALA A 125	24.202	19.908	46.508	1.00	85.62
	867	N	LEU A 126	25.418	18.010	46.529	1.00	65.31
	868	CA	LEU A 126	25.241	17.792	47.956	1.00	64.25
	869	CB	LEU A 126	24.767	16.365	48.242	1.00	70.77
15	870	CG	LEU A 126	23.383	15.898	47.772	1.00	70.91
	871	CD1	LEU A 126	23.216	14.443	48.171	1.00	70.54
	872	CD2	LEU A 126	22.272	16.747	48.381	1.00	69.72
	873	C	LEU A 126	26.540	18.031	48.675	1.00	63.55
	874	O	LEU A 126	26.579	18.752	49.663	1.00	63.93
20	875	N	THR A 127	27.604	17.407	48.192	1.00	65.05
	876	CA	THR A 127	28.904	17.600	48.809	1.00	65.26
	877	CB	THR A 127	30.015	16.941	47.971	1.00	66.39
	878	OG1	THR A 127	29.973	15.525	48.165	1.00	65.75
	879	CG2	THR A 127	31.378	17.464	48.374	1.00	64.17
25	880	C	THR A 127	29.134	19.106	48.905	1.00	66.15
	881	O	THR A 127	29.770	19.601	49.834	1.00	66.20
	882	N	LYS A 128	28.595	19.832	47.934	1.00	77.97
	883	CA	LYS A 128	28.711	21.279	47.920	1.00	78.25
	884	CB	LYS A 128	28.249	21.833	46.568	1.00	105.04
30	885	CG	LYS A 128	29.271	21.637	45.443	1.00	107.69
	886	CD	LYS A 128	28.658	21.819	44.049	1.00	110.08
	887	CE	LYS A 128	28.078	23.211	43.828	1.00	111.01
	888	NZ	LYS A 128	27.460	23.338	42.477	1.00	110.08
	889	C	LYS A 128	27.849	21.824	49.051	1.00	77.57
35	890	O	LYS A 128	28.377	22.358	50.029	1.00	78.91
	891	N	ALA A 129	26.531	21.674	48.926	1.00	50.63
	892	CA	ALA A 129	25.594	22.138	49.957	1.00	49.27
	893	CB	ALA A 129	24.233	21.473	49.767	1.00	52.30
	894	C	ALA A 129	26.121	21.857	51.370	1.00	48.39
40	895	O	ALA A 129	25.630	22.413	52.349	1.00	47.09
	896	N	GLU A 130	27.108	20.970	51.460	1.00	69.05
	897	CA	GLU A 130	27.735	20.632	52.726	1.00	69.85
	898	CB	GLU A 130	28.345	19.234	52.671	1.00	73.70



	899	CG	GLU A 130	27.359	18.104	52.909	1.00	75.38
	900	CD	GLU A 130	27.995	16.739	52.728	1.00	77.65
	901	OE1	GLU A 130	29.126	16.541	53.227	1.00	77.51
	902	OE2	GLU A 130	27.363	15.864	52.092	1.00	79.19
5	903	C	GLU A 130	28.838	21.644	52.926	1.00	69.66
	904	O	GLU A 130	28.725	22.547	53.749	1.00	70.62
	905	N	GLU A 131	29.905	21.486	52.154	1.00	72.50
	906	CA	GLU A 131	31.044	22.394	52.216	1.00	72.74
	907	CB	GLU A 131	31.884	22.260	50.935	1.00	86.15
10	908	CG	GLU A 131	32.712	20.968	50.857	1.00	88.08
	909	CD	GLU A 131	33.296	20.702	49.470	1.00	87.78
	910	OE1	GLU A 131	34.089	19.748	49.327	1.00	88.78
	911	OE2	GLU A 131	32.957	21.437	48.521	1.00	88.68
	912	C	GLU A 131	30.606	23.852	52.420	1.00	71.58
15	913	O	GLU A 131	31.262	24.605	53.130	1.00	70.81
	914	N	LEU A 132	29.500	24.247	51.797	1.00	72.44
	915	CA	LEU A 132	29.009	25.605	51.953	1.00	69.35
	916	CB	LEU A 132	27.799	25.857	51.052	1.00	51.80
	917	CG	LEU A 132	27.078	27.187	51.325	1.00	51.99
20	918	CD1	LEU A 132	27.998	28.349	50.978	1.00	51.32
	919	CD2	LEU A 132	25.780	27.277	50.524	1.00	51.24
	920	C	LEU A 132	28.619	25.822	53.411	1.00	69.71
	921	O	LEU A 132	29.401	26.362	54.194	1.00	72.99
	922	N	THR A 133	27.412	25.397	53.780	1.00	58.08
25	923	CA	THR A 133	26.936	25.548	55.157	1.00	54.72
	924	CB	THR A 133	25.530	24.960	55.340	1.00	50.26
	925	OG1	THR A 133	25.593	23.531	55.219	1.00	51.51
	926	CG2	THR A 133	24.587	25.524	54.308	1.00	49.40
	927	C	THR A 133	27.850	24.828	56.148	1.00	52.98
30	928	O	THR A 133	27.551	24.757	57.339	1.00	53.40
	929	N	LYS A 134	28.957	24.291	55.650	1.00	43.95
	930	CA	LYS A 134	29.902	23.570	56.483	1.00	42.50
	931	CB	LYS A 134	31.218	23.368	55.740	1.00	39.55
	932	CG	LYS A 134	32.367	22.935	56.632	1.00	39.17
35	933	CD	LYS A 134	33.672	22.921	55.853	1.00	42.39
	934	CE	LYS A 134	34.882	22.871	56.795	1.00	43.17
	935	NZ	LYS A 134	34.950	24.052	57.749	1.00	37.72
	936	C	LYS A 134	30.207	24.233	57.808	1.00	43.79
	937	O	LYS A 134	30.712	23.584	58.716	1.00	46.26
40	938	N	ASN A 135	29.918	25.524	57.928	1.00	44.43
	939	CA	ASN A 135	30.227	26.225	59.160	1.00	42.56
	940	CB	ASN A 135	31.268	27.301	58.896	1.00	50.79
	941	CG	ASN A 135	32.648	26.733	58.755	1.00	50.28

	942	OD1	ASN	A	135	33.134	26.051	59.651	1.00	52.78
	943	ND2	ASN	A	135	33.291	27.003	57.631	1.00	49.32
	944	C	ASN	A	135	29.058	26.823	59.880	1.00	42.96
	945	O	ASN	A	135	29.145	27.063	61.064	1.00	41.37
5	946	N	ASN	A	136	27.961	27.075	59.186	1.00	60.18
	947	CA	ASN	A	136	26.794	27.637	59.856	1.00	63.99
	948	CB	ASN	A	136	25.567	27.505	58.967	1.00	69.42
	949	CG	ASN	A	136	25.764	28.162	57.631	1.00	73.86
	950	OD1	ASN	A	136	24.803	28.412	56.901	1.00	78.59
10	951	ND2	ASN	A	136	27.024	28.443	57.290	1.00	71.93
	952	C	ASN	A	136	26.549	26.948	61.204	1.00	64.95
	953	O	ASN	A	136	26.948	25.800	61.411	1.00	67.14
	954	N	THR	A	137	25.891	27.648	62.118	1.00	53.61
	955	CA	THR	A	137	25.655	27.100	63.434	1.00	51.59
15	956	CB	THR	A	137	26.435	27.868	64.489	1.00	43.42
	957	OG1	THR	A	137	25.937	29.207	64.552	1.00	40.10
	958	CG2	THR	A	137	27.912	27.894	64.147	1.00	41.95
	959	C	THR	A	137	24.205	27.176	63.806	1.00	52.09
	960	O	THR	A	137	23.856	27.074	64.975	1.00	53.76
20	961	N	GLY	A	138	23.350	27.374	62.820	1.00	37.97
	962	CA	GLY	A	138	21.935	27.450	63.126	1.00	35.38
	963	C	GLY	A	138	21.327	26.064	63.058	1.00	36.39
	964	O	GLY	A	138	22.015	25.053	63.282	1.00	35.12
	965	N	LEU	A	139	20.035	26.017	62.748	1.00	41.92
25	966	CA	LEU	A	139	19.333	24.759	62.625	1.00	41.72
	967	CB	LEU	A	139	17.885	25.000	62.251	1.00	37.32
	968	CG	LEU	A	139	17.294	23.959	61.326	1.00	37.20
	969	CD1	LEU	A	139	15.830	23.689	61.650	1.00	35.94
	970	CD2	LEU	A	139	17.462	24.473	59.919	1.00	38.23
30	971	C	LEU	A	139	20.026	23.953	61.557	1.00	43.39
	972	O	LEU	A	139	20.548	24.512	60.598	1.00	43.90
	973	N	ILE	A	140	20.044	22.637	61.742	1.00	58.59
	974	CA	ILE	A	140	20.685	21.724	60.806	1.00	59.15
	975	CB	ILE	A	140	21.486	20.659	61.546	1.00	47.83
35	976	CG2	ILE	A	140	22.252	19.823	60.547	1.00	47.48
	977	CG1	ILE	A	140	22.456	21.303	62.519	1.00	45.36
	978	CD1	ILE	A	140	23.565	20.356	62.945	1.00	45.55
	979	C	ILE	A	140	19.679	20.990	59.919	1.00	59.47
	980	O	ILE	A	140	18.889	20.194	60.415	1.00	60.20
40	981	N	LEU	A	141	19.700	21.237	58.612	1.00	49.92
	982	CA	LEU	A	141	18.761	20.536	57.747	1.00	51.76
	983	CB	LEU	A	141	18.451	21.297	56.467	1.00	48.53
	984	CG	LEU	A	141	17.368	20.547	55.683	1.00	46.53

	985	CD1	LEU	A	141	16.302	20.076	56.641	1.00	44.35
	986	CD2	LEU	A	141	16.734	21.436	54.636	1.00	47.51
	987	C	LEU	A	141	19.330	19.204	57.366	1.00	54.28
	988	O	LEU	A	141	20.393	19.132	56.748	1.00	54.11
5	989	N	ASN	A	142	18.606	18.152	57.737	1.00	68.18
	990	CA	ASN	A	142	19.029	16.792	57.460	1.00	68.84
	991	CB	ASN	A	142	18.807	15.932	58.701	1.00	62.25
	992	CG	ASN	A	142	20.051	15.173	59.099	1.00	64.68
	993	OD1	ASN	A	142	21.109	15.761	59.313	1.00	64.14
10	994	ND2	ASN	A	142	19.935	13.854	59.195	1.00	64.75
	995	C	ASN	A	142	18.322	16.184	56.248	1.00	68.52
	996	O	ASN	A	142	17.130	15.869	56.301	1.00	68.03
	997	N	PHE	A	143	19.077	16.038	55.157	1.00	61.73
	998	CA	PHE	A	143	18.580	15.464	53.908	1.00	62.22
15	999	CB	PHE	A	143	19.317	16.059	52.714	1.00	61.02
	1000	CG	PHE	A	143	18.679	17.289	52.162	1.00	61.64
	1001	CD1	PHE	A	143	19.451	18.418	51.868	1.00	61.00
	1002	CD2	PHE	A	143	17.311	17.327	51.931	1.00	60.15
	1003	CE1	PHE	A	143	18.866	19.572	51.354	1.00	59.35
20	1004	CE2	PHE	A	143	16.715	18.474	51.417	1.00	60.25
	1005	CZ	PHE	A	143	17.494	19.601	51.128	1.00	61.12
	1006	C	PHE	A	143	18.789	13.961	53.888	1.00	61.89
	1007	O	PHE	A	143	19.905	13.475	54.037	1.00	62.39
	1008	N	ALA	A	144	17.710	13.224	53.693	1.00	49.90
25	1009	CA	ALA	A	144	17.799	11.786	53.645	1.00	49.55
	1010	CB	ALA	A	144	16.723	11.182	54.524	1.00	92.76
	1011	C	ALA	A	144	17.626	11.331	52.202	1.00	49.68
	1012	O	ALA	A	144	16.539	11.447	51.642	1.00	49.05
	1013	N	LEU	A	145	18.704	10.834	51.601	1.00	57.94
30	1014	CA	LEU	A	145	18.686	10.344	50.219	1.00	57.96
	1015	CB	LEU	A	145	19.591	11.185	49.332	1.00	79.55
	1016	CG	LEU	A	145	19.205	12.637	49.132	1.00	81.27
	1017	CD1	LEU	A	145	20.209	13.239	48.180	1.00	82.54
	1018	CD2	LEU	A	145	17.788	12.751	48.579	1.00	81.27
35	1019	C	LEU	A	145	19.183	8.908	50.178	1.00	57.03
	1020	O	LEU	A	145	20.241	8.597	50.738	1.00	56.02
	1021	N	ASN	A	146	18.448	8.038	49.491	1.00	47.95
	1022	CA	ASN	A	146	18.850	6.640	49.439	1.00	44.04
	1023	CB	ASN	A	146	20.138	6.449	48.644	1.00	82.72
40	1024	CG	ASN	A	146	19.978	6.810	47.191	1.00	86.25
	1025	OD1	ASN	A	146	20.761	6.377	46.348	1.00	88.63
	1026	ND2	ASN	A	146	18.966	7.617	46.885	1.00	88.55
	1027	C	ASN	A	146	19.098	6.285	50.888	1.00	39.69

	1028	O	ASN A 146	20.195	5.874	51.280	1.00	34.78
	1029	N	TYR A 147	18.062	6.502	51.684	1.00	45.65
	1030	CA	TYR A 147	18.124	6.220	53.088	1.00	42.54
	1031	CB	TYR A 147	17.802	7.451	53.915	1.00	44.10
5	1032	CG	TYR A 147	17.617	7.102	55.371	1.00	41.51
	1033	CD1	TYR A 147	18.718	6.907	56.200	1.00	40.40
	1034	CE1	TYR A 147	18.556	6.515	57.507	1.00	39.78
	1035	CD2	TYR A 147	16.343	6.894	55.900	1.00	38.78
	1036	CE2	TYR A 147	16.175	6.504	57.205	1.00	38.27
10	1037	CZ	TYR A 147	17.286	6.320	58.007	1.00	40.14
	1038	OH	TYR A 147	17.130	5.986	59.331	1.00	40.48
	1039	C	TYR A 147	17.104	5.185	53.414	1.00	40.18
	1040	O	TYR A 147	15.963	5.268	52.984	1.00	41.31
	1041	N	GLY A 148	17.519	4.221	54.215	1.00	30.96
15	1042	CA	GLY A 148	16.612	3.172	54.615	1.00	25.83
	1043	C	GLY A 148	16.986	2.669	55.982	1.00	22.68
	1044	O	GLY A 148	18.117	2.244	56.209	1.00	19.72
	1045	N	GLY A 149	16.028	2.729	56.894	1.00	23.36
	1046	CA	GLY A 149	16.276	2.263	58.233	1.00	21.82
20	1047	C	GLY A 149	17.062	0.971	58.244	1.00	23.42
	1048	O	GLY A 149	18.261	0.945	58.511	1.00	23.33
	1049	N	ARG A 150	16.393	-0.120	57.931	1.00	26.63
	1050	CA	ARG A 150	17.067	-1.392	57.961	1.00	28.33
	1051	CB	ARG A 150	16.178	-2.452	57.328	1.00	30.57
25	1052	CG	ARG A 150	14.928	-2.732	58.121	1.00	29.95
	1053	CD	ARG A 150	14.090	-3.730	57.397	1.00	31.28
	1054	NE	ARG A 150	12.931	-4.125	58.183	1.00	35.12
	1055	CZ	ARG A 150	11.986	-4.950	57.747	1.00	34.81
	1056	NH1	ARG A 150	12.062	-5.463	56.523	1.00	30.05
30	1057	NH2	ARG A 150	10.978	-5.274	58.545	1.00	32.55
	1058	C	ARG A 150	18.419	-1.336	57.292	1.00	29.09
	1059	O	ARG A 150	19.355	-1.970	57.747	1.00	30.88
	1060	N	ALA A 151	18.535	-0.572	56.216	1.00	31.88
	1061	CA	ALA A 151	19.825	-0.475	55.543	1.00	33.10
35	1062	CB	ALA A 151	19.742	0.438	54.348	1.00	25.20
	1063	C	ALA A 151	20.808	0.084	56.549	1.00	33.39
	1064	O	ALA A 151	21.753	-0.595	56.941	1.00	30.97
	1065	N	GLU A 152	20.565	1.321	56.972	1.00	35.58
	1066	CA	GLU A 152	21.409	1.995	57.958	1.00	35.53
40	1067	CB	GLU A 152	20.619	3.096	58.668	1.00	33.72
	1068	CG	GLU A 152	21.449	4.084	59.459	1.00	33.67
	1069	CD	GLU A 152	20.586	5.141	60.155	1.00	35.80
	1070	OE1	GLU A 152	19.365	5.158	59.945	1.00	35.63

	1071	OE2	GLU A 152	21.119	5.961	60.922	1.00	33.07
	1072	C	GLU A 152	21.922	1.002	58.993	1.00	34.85
	1073	O	GLU A 152	23.119	0.732	59.043	1.00	36.40
	1074	N	ILE A 153	21.019	0.443	59.799	1.00	32.57
5	1075	CA	ILE A 153	21.414	-0.498	60.846	1.00	32.51
	1076	CB	ILE A 153	20.182	-1.128	61.538	1.00	24.50
	1077	CG2	ILE A 153	20.609	-1.939	62.726	1.00	20.87
	1078	CG1	ILE A 153	19.221	-0.039	62.007	1.00	24.46
	1079	CD1	ILE A 153	17.847	-0.577	62.380	1.00	19.80
10	1080	C	ILE A 153	22.296	-1.602	60.279	1.00	33.63
	1081	O	ILE A 153	23.155	-2.150	60.963	1.00	32.70
	1082	N	THR A 154	22.098	-1.931	59.016	1.00	35.83
	1083	CA	THR A 154	22.914	-2.971	58.425	1.00	41.14
	1084	CB	THR A 154	22.322	-3.465	57.116	1.00	37.45
15	1085	OG1	THR A 154	21.037	-4.022	57.371	1.00	36.05
	1086	CG2	THR A 154	23.206	-4.530	56.514	1.00	39.31
	1087	C	THR A 154	24.309	-2.430	58.166	1.00	43.73
	1088	O	THR A 154	25.298	-3.100	58.438	1.00	43.89
	1089	N	GLN A 155	24.373	-1.213	57.636	1.00	42.14
20	1090	CA	GLN A 155	25.640	-0.566	57.350	1.00	45.62
	1091	CB	GLN A 155	25.390	0.827	56.768	1.00	76.02
	1092	CG	GLN A 155	26.644	1.667	56.578	1.00	81.62
	1093	CD	GLN A 155	26.994	2.480	57.810	1.00	82.79
	1094	OE1	GLN A 155	28.105	3.004	57.933	1.00	83.15
25	1095	NE2	GLN A 155	26.040	2.599	58.726	1.00	82.73
	1096	C	GLN A 155	26.433	-0.474	58.649	1.00	46.41
	1097	O	GLN A 155	27.615	-0.819	58.709	1.00	45.18
	1098	N	ALA A 156	25.767	-0.017	59.699	1.00	54.15
	1099	CA	ALA A 156	26.410	0.106	60.989	1.00	55.23
30	1100	CB	ALA A 156	25.468	0.707	61.969	1.00	29.84
	1101	C	ALA A 156	26.828	-1.269	61.451	1.00	57.51
	1102	O	ALA A 156	27.998	-1.503	61.726	1.00	59.16
	1103	N	LEU A 157	25.867	-2.181	61.541	1.00	50.07
	1104	CA	LEU A 157	26.175	-3.532	61.970	1.00	51.33
35	1105	CB	LEU A 157	25.100	-4.509	61.519	1.00	62.02
	1106	CG	LEU A 157	25.643	-5.939	61.389	1.00	63.68
	1107	CD1	LEU A 157	26.290	-6.380	62.694	1.00	66.21
	1108	CD2	LEU A 157	24.523	-6.883	61.007	1.00	64.36
	1109	C	LEU A 157	27.488	-3.932	61.332	1.00	52.70
40	1110	O	LEU A 157	28.411	-4.366	62.012	1.00	52.30
	1111	N	LYS A 158	27.553	-3.768	60.015	1.00	67.21
	1112	CA	LYS A 158	28.727	-4.102	59.217	1.00	67.40
	1113	CB	LYS A 158	28.580	-3.494	57.829	1.00	55.19

	1114	CG	LYS A 158	28.859	-4.430	56.676	1.00	54.11
	1115	CD	LYS A 158	28.669	-3.678	55.369	1.00	52.46
	1116	CE	LYS A 158	28.770	-4.597	54.175	1.00	52.26
	1117	NZ	LYS A 158	28.228	-3.947	52.951	1.00	52.15
5	1118	C	LYS A 158	30.020	-3.592	59.838	1.00	68.32
	1119	O	LYS A 158	30.753	-4.344	60.482	1.00	68.80
	1120	N	LEU A 159	30.297	-2.310	59.625	1.00	80.36
	1121	CA	LEU A 159	31.500	-1.682	60.150	1.00	78.90
	1122	CB	LEU A 159	31.297	-0.176	60.258	1.00	36.32
10	1123	CG	LEU A 159	30.965	0.378	58.877	1.00	34.91
	1124	CD1	LEU A 159	30.559	1.847	58.932	1.00	33.48
	1125	CD2	LEU A 159	32.181	0.167	58.004	1.00	35.51
	1126	C	LEU A 159	31.875	-2.239	61.503	1.00	78.99
	1127	O	LEU A 159	33.037	-2.555	61.740	1.00	79.12
15	1128	N	ILE A 160	30.886	-2.376	62.381	1.00	60.80
	1129	CA	ILE A 160	31.141	-2.887	63.715	1.00	60.63
	1130	CB	ILE A 160	29.867	-2.984	64.541	1.00	42.72
	1131	CG2	ILE A 160	30.183	-3.602	65.894	1.00	40.34
	1132	CG1	ILE A 160	29.252	-1.592	64.682	1.00	40.87
20	1133	CD1	ILE A 160	28.236	-1.436	65.795	1.00	40.24
	1134	C	ILE A 160	31.799	-4.247	63.721	1.00	63.26
	1135	O	ILE A 160	32.814	-4.444	64.385	1.00	64.68
	1136	N	SER A 161	31.227	-5.192	62.986	1.00	61.04
	1137	CA	SER A 161	31.789	-6.532	62.942	1.00	62.20
25	1138	CB	SER A 161	30.726	-7.538	62.490	1.00	60.75
	1139	OG	SER A 161	30.196	-7.173	61.231	1.00	61.83
	1140	C	SER A 161	33.029	-6.599	62.050	1.00	63.53
	1141	O	SER A 161	33.513	-7.678	61.733	1.00	64.04
	1142	N	GLN A 162	33.531	-5.446	61.621	1.00	70.57
30	1143	CA	GLN A 162	34.762	-5.430	60.836	1.00	72.95
	1144	CB	GLN A 162	34.714	-4.386	59.714	1.00	86.39
	1145	CG	GLN A 162	35.842	-4.540	58.670	1.00	88.49
	1146	CD	GLN A 162	35.848	-5.905	57.950	1.00	90.31
	1147	OE1	GLN A 162	36.000	-6.960	58.576	1.00	91.24
35	1148	NE2	GLN A 162	35.691	-5.877	56.627	1.00	88.78
	1149	C	GLN A 162	35.805	-5.050	61.885	1.00	74.13
	1150	O	GLN A 162	36.852	-5.688	62.001	1.00	73.43
	1151	N	ASP A 163	35.476	-4.017	62.662	1.00	87.35
	1152	CA	ASP A 163	36.312	-3.536	63.756	1.00	88.17
40	1153	CB	ASP A 163	35.640	-2.360	64.466	1.00	67.85
	1154	CG	ASP A 163	35.667	-1.095	63.649	1.00	68.28
	1155	OD1	ASP A 163	35.890	-1.195	62.427	1.00	67.62
	1156	OD2	ASP A 163	35.459	-0.004	64.223	1.00	68.07

	1157	C	ASP A 163	36.457	-4.681	64.745	1.00	89.53
	1158	O	ASP A 163	37.478	-4.813	65.413	1.00	90.95
	1159	N	VAL A 164	35.414	-5.499	64.843	1.00	78.28
	1160	CA	VAL A 164	35.428	-6.646	65.742	1.00	78.53
5	1161	CB	VAL A 164	34.051	-7.337	65.785	1.00	63.02
	1162	CG1	VAL A 164	34.088	-8.510	66.758	1.00	62.71
	1163	CG2	VAL A 164	32.994	-6.343	66.211	1.00	63.75
	1164	C	VAL A 164	36.481	-7.639	65.248	1.00	78.78
	1165	O	VAL A 164	36.988	-8.467	66.006	1.00	78.76
10	1166	N	LEU A 165	36.798	-7.549	63.962	1.00	101.75
	1167	CA	LEU A 165	37.810	-8.408	63.374	1.00	101.52
	1168	CB	LEU A 165	37.652	-8.465	61.856	1.00	55.10
	1169	CG	LEU A 165	36.645	-9.493	61.342	1.00	52.60
	1170	CD1	LEU A 165	36.727	-9.549	59.812	1.00	51.28
15	1171	CD2	LEU A 165	36.939	-10.867	61.963	1.00	50.90
	1172	C	LEU A 165	39.149	-7.795	63.724	1.00	102.44
	1173	O	LEU A 165	40.065	-8.476	64.184	1.00	102.07
	1174	N	ASP A 166	39.240	-6.489	63.512	1.00	76.01
	1175	CA	ASP A 166	40.450	-5.743	63.798	1.00	76.03
20	1176	CB	ASP A 166	40.370	-4.379	63.114	1.00	66.22
	1177	CG	ASP A 166	39.924	-4.491	61.654	1.00	66.29
	1178	OD1	ASP A 166	39.819	-5.644	61.151	1.00	65.56
	1179	OD2	ASP A 166	39.679	-3.435	61.012	1.00	65.50
	1180	C	ASP A 166	40.606	-5.611	65.311	1.00	76.86
25	1181	O	ASP A 166	41.195	-4.651	65.813	1.00	76.81
	1182	N	ALA A 167	40.067	-6.612	66.010	1.00	94.70
	1183	CA	ALA A 167	40.085	-6.732	67.469	1.00	96.07
	1184	CB	ALA A 167	41.322	-7.509	67.908	1.00	63.15
	1185	C	ALA A 167	39.993	-5.420	68.238	1.00	96.93
30	1186	O	ALA A 167	40.364	-5.357	69.414	1.00	97.39
	1187	N	LYS A 168	39.480	-4.385	67.575	1.00	121.13
	1188	CA	LYS A 168	39.329	-3.067	68.182	1.00	121.34
	1189	CB	LYS A 168	39.176	-1.996	67.101	1.00	73.03
	1190	CG	LYS A 168	40.336	-1.907	66.131	1.00	75.20
35	1191	CD	LYS A 168	40.175	-0.714	65.180	1.00	75.99
	1192	CE	LYS A 168	41.462	-0.448	64.379	1.00	77.45
	1193	NZ	LYS A 168	41.422	0.809	63.564	1.00	77.88
	1194	C	LYS A 168	38.120	-3.005	69.112	1.00	122.08
	1195	O	LYS A 168	37.939	-2.024	69.832	1.00	122.94
40	1196	N	ILE A 169	37.287	-4.043	69.082	1.00	65.77
	1197	CA	ILE A 169	36.094	-4.107	69.920	1.00	64.78
	1198	CB	ILE A 169	34.895	-3.425	69.220	1.00	84.86
	1199	CG2	ILE A 169	33.660	-3.532	70.081	1.00	85.34

	1200	CG1	ILE A 169	35.196	-1.954	68.938	1.00	85.60
	1201	CD1	ILE A 169	35.849	-1.709	67.605	1.00	88.07
	1202	C	ILE A 169	35.714	-5.561	70.213	1.00	63.79
	1203	O	ILE A 169	35.846	-6.423	69.348	1.00	63.19
5	1204	N	ASN A 170	35.239	-5.830	71.428	1.00	60.51
	1205	CA	ASN A 170	34.823	-7.186	71.817	1.00	60.73
	1206	CB	ASN A 170	35.308	-7.519	73.239	1.00	93.50
	1207	CG	ASN A 170	36.777	-7.908	73.288	1.00	95.03
	1208	OD1	ASN A 170	37.278	-8.622	72.419	1.00	96.41
10	1209	ND2	ASN A 170	37.468	-7.455	74.325	1.00	94.45
	1210	C	ASN A 170	33.298	-7.392	71.750	1.00	61.11
	1211	O	ASN A 170	32.530	-6.437	71.607	1.00	60.69
	1212	N	PRO A 171	32.842	-8.653	71.850	1.00	112.62
	1213	CD	PRO A 171	33.572	-9.887	72.187	1.00	109.80
15	1214	CA	PRO A 171	31.400	-8.906	71.796	1.00	112.24
	1215	CB	PRO A 171	31.300	-10.405	72.084	1.00	109.42
	1216	CG	PRO A 171	32.520	-10.677	72.922	1.00	110.03
	1217	C	PRO A 171	30.646	-8.056	72.817	1.00	110.67
	1218	O	PRO A 171	29.782	-7.263	72.451	1.00	111.40
20	1219	N	GLY A 172	30.984	-8.220	74.093	1.00	71.03
	1220	CA	GLY A 172	30.339	-7.450	75.145	1.00	66.18
	1221	C	GLY A 172	30.734	-5.978	75.122	1.00	63.03
	1222	O	GLY A 172	30.400	-5.209	76.029	1.00	62.01
	1223	N	ASP A 173	31.461	-5.584	74.084	1.00	51.73
25	1224	CA	ASP A 173	31.879	-4.202	73.942	1.00	49.09
	1225	CB	ASP A 173	33.210	-4.146	73.194	1.00	94.86
	1226	CG	ASP A 173	33.742	-2.732	73.044	1.00	99.00
	1227	OD1	ASP A 173	33.015	-1.864	72.502	1.00	101.48
	1228	OD2	ASP A 173	34.897	-2.494	73.461	1.00	100.69
30	1229	C	ASP A 173	30.793	-3.461	73.157	1.00	45.66
	1230	O	ASP A 173	30.590	-2.258	73.306	1.00	43.70
	1231	N	ILE A 174	30.097	-4.197	72.306	1.00	66.57
	1232	CA	ILE A 174	29.035	-3.618	71.516	1.00	63.27
	1233	CB	ILE A 174	28.653	-4.536	70.364	1.00	47.32
35	1234	CG2	ILE A 174	27.359	-4.070	69.738	1.00	43.95
	1235	CG1	ILE A 174	29.778	-4.548	69.333	1.00	46.82
	1236	CD1	ILE A 174	29.596	-5.579	68.244	1.00	47.02
	1237	C	ILE A 174	27.829	-3.391	72.398	1.00	60.97
	1238	O	ILE A 174	27.384	-4.287	73.121	1.00	59.95
40	1239	N	THR A 175	27.304	-2.180	72.331	1.00	45.44
	1240	CA	THR A 175	26.154	-1.811	73.126	1.00	43.76
	1241	CB	THR A 175	26.600	-1.230	74.440	1.00	37.79
	1242	OG1	THR A 175	27.565	-0.210	74.179	1.00	37.68



	1243	CG2	THR	A	175	27.217	-2.293	75.302	1.00	34.58
	1244	C	THR	A	175	25.334	-0.769	72.401	1.00	42.00
	1245	O	THR	A	175	25.796	-0.179	71.438	1.00	43.43
	1246	N	GLU	A	176	24.120	-0.534	72.880	1.00	26.48
5	1247	CA	GLU	A	176	23.257	0.439	72.245	1.00	27.13
	1248	CB	GLU	A	176	21.991	0.659	73.076	1.00	39.71
	1249	CG	GLU	A	176	20.886	-0.337	72.768	1.00	41.29
	1250	CD	GLU	A	176	19.843	-0.452	73.868	1.00	41.35
	1251	OE1	GLU	A	176	19.367	0.597	74.359	1.00	38.96
10	1252	OE2	GLU	A	176	19.494	-1.599	74.227	1.00	40.23
	1253	C	GLU	A	176	23.976	1.752	72.015	1.00	27.65
	1254	O	GLU	A	176	23.873	2.341	70.934	1.00	28.15
	1255	N	GLU	A	177	24.727	2.212	73.010	1.00	36.25
	1256	CA	GLU	A	177	25.428	3.477	72.847	1.00	38.11
15	1257	CB	GLU	A	177	26.223	3.862	74.096	1.00	74.89
	1258	CG	GLU	A	177	26.736	5.302	74.007	1.00	80.42
	1259	CD	GLU	A	177	27.922	5.586	74.911	1.00	83.92
	1260	OE1	GLU	A	177	28.916	4.829	74.841	1.00	85.62
	1261	OE2	GLU	A	177	27.865	6.575	75.677	1.00	84.97
20	1262	C	GLU	A	177	26.373	3.313	71.684	1.00	36.69
	1263	O	GLU	A	177	26.515	4.200	70.846	1.00	35.68
	1264	N	LEU	A	178	27.012	2.157	71.629	1.00	38.10
	1265	CA	LEU	A	178	27.945	1.892	70.556	1.00	37.84
	1266	CB	LEU	A	178	28.592	0.517	70.769	1.00	40.70
25	1267	CG	LEU	A	178	29.703	0.063	69.825	1.00	40.68
	1268	CD1	LEU	A	178	30.500	1.254	69.349	1.00	40.04
	1269	CD2	LEU	A	178	30.589	-0.953	70.544	1.00	42.36
	1270	C	LEU	A	178	27.239	1.985	69.193	1.00	38.87
	1271	O	LEU	A	178	27.585	2.849	68.368	1.00	37.36
30	1272	N	ILE	A	179	26.240	1.125	68.965	1.00	37.15
	1273	CA	ILE	A	179	25.522	1.127	67.697	1.00	35.50
	1274	CB	ILE	A	179	24.250	0.291	67.758	1.00	31.43
	1275	CG2	ILE	A	179	23.637	0.233	66.365	1.00	31.86
	1276	CG1	ILE	A	179	24.551	-1.121	68.265	1.00	29.02
35	1277	CD1	ILE	A	179	25.101	-2.060	67.228	1.00	30.26
	1278	C	ILE	A	179	25.129	2.556	67.354	1.00	36.09
	1279	O	ILE	A	179	25.065	2.943	66.177	1.00	34.96
	1280	N	GLY	A	180	24.876	3.334	68.400	1.00	37.28
	1281	CA	GLY	A	180	24.493	4.721	68.218	1.00	39.91
40	1282	C	GLY	A	180	25.492	5.510	67.392	1.00	40.71
	1283	O	GLY	A	180	25.112	6.244	66.479	1.00	41.45
	1284	N	ASN	A	181	26.774	5.350	67.707	1.00	45.98
	1285	CA	ASN	A	181	27.833	6.057	67.000	1.00	46.45

	1286	CB	ASN	A	181	29.161	5.907	67.747	1.00	45.81
	1287	CG	ASN	A	181	29.082	6.387	69.177	1.00	46.04
	1288	OD1	ASN	A	181	28.605	7.489	69.446	1.00	46.69
	1289	ND2	ASN	A	181	29.560	5.566	70.106	1.00	43.29
5	1290	C	ASN	A	181	28.021	5.583	65.565	1.00	47.23
	1291	O	ASN	A	181	28.492	6.332	64.714	1.00	48.29
	1292	N	TYR	A	182	27.658	4.340	65.286	1.00	43.54
	1293	CA	TYR	A	182	27.850	3.838	63.942	1.00	41.55
	1294	CB	TYR	A	182	28.119	2.336	63.956	1.00	46.19
10	1295	CG	TYR	A	182	29.496	1.931	64.458	1.00	48.01
	1296	CD1	TYR	A	182	29.880	2.149	65.789	1.00	48.48
	1297	CE1	TYR	A	182	31.123	1.704	66.266	1.00	46.44
	1298	CD2	TYR	A	182	30.398	1.263	63.616	1.00	47.00
	1299	CE2	TYR	A	182	31.641	0.816	64.088	1.00	46.87
15	1300	CZ	TYR	A	182	31.994	1.038	65.412	1.00	46.91
	1301	OH	TYR	A	182	33.211	0.584	65.874	1.00	48.89
	1302	C	TYR	A	182	26.696	4.128	63.013	1.00	41.45
	1303	O	TYR	A	182	26.769	3.790	61.832	1.00	39.57
	1304	N	LEU	A	183	25.635	4.749	63.519	1.00	45.79
20	1305	CA	LEU	A	183	24.494	5.051	62.658	1.00	47.78
	1306	CB	LEU	A	183	23.218	5.203	63.490	1.00	39.84
	1307	CG	LEU	A	183	22.754	3.944	64.233	1.00	36.79
	1308	CD1	LEU	A	183	21.519	4.267	65.018	1.00	36.60
	1309	CD2	LEU	A	183	22.457	2.828	63.260	1.00	36.31
25	1310	C	LEU	A	183	24.753	6.308	61.841	1.00	48.51
	1311	O	LEU	A	183	25.705	7.019	62.099	1.00	50.48
	1312	N	PHE	A	184	23.912	6.578	60.853	1.00	48.19
	1313	CA	PHE	A	184	24.091	7.747	59.994	1.00	49.49
	1314	CB	PHE	A	184	23.081	7.725	58.849	1.00	44.20
30	1315	CG	PHE	A	184	23.347	6.671	57.820	1.00	44.57
	1316	CD1	PHE	A	184	22.477	6.497	56.760	1.00	44.44
	1317	CD2	PHE	A	184	24.448	5.837	57.922	1.00	44.74
	1318	CE1	PHE	A	184	22.696	5.506	55.821	1.00	44.26
	1319	CE2	PHE	A	184	24.676	4.841	56.988	1.00	43.37
35	1320	CZ	PHE	A	184	23.798	4.675	55.935	1.00	44.96
	1321	C	PHE	A	184	23.972	9.063	60.729	1.00	51.09
	1322	O	PHE	A	184	24.696	10.014	60.430	1.00	50.84
	1323	N	THR	A	185	23.046	9.115	61.678	1.00	46.98
	1324	CA	THR	A	185	22.827	10.308	62.487	1.00	50.50
40	1325	CB	THR	A	185	21.630	10.113	63.422	1.00	44.57
	1326	OG1	THR	A	185	21.765	8.854	64.084	1.00	42.04
	1327	CG2	THR	A	185	20.330	10.138	62.662	1.00	44.51
	1328	C	THR	A	185	24.050	10.649	63.370	1.00	54.78

	1329	O	THR A 185	24.046	11.661	64.087	1.00	54.81
	1330	N	GLN A 186	25.079	9.799	63.323	1.00	56.18
	1331	CA	GLN A 186	26.291	9.988	64.115	1.00	60.77
	1332	CB	GLN A 186	27.387	9.029	63.654	1.00	92.96
5	1333	CG	GLN A 186	27.942	9.355	62.282	1.00	96.28
	1334	CD	GLN A 186	29.106	8.469	61.894	1.00	98.93
	1335	OE1	GLN A 186	28.952	7.260	61.722	1.00	100.11
	1336	NE2	GLN A 186	30.284	9.068	61.756	1.00	100.05
	1337	C	GLN A 186	26.816	11.404	64.002	1.00	63.76
10	1338	O	GLN A 186	27.168	12.022	65.005	1.00	64.46
	1339	N	HIS A 187	26.867	11.905	62.769	1.00	63.31
	1340	CA	HIS A 187	27.360	13.246	62.470	1.00	64.48
	1341	CB	HIS A 187	27.415	13.451	60.957	1.00	75.76
	1342	CG	HIS A 187	28.288	12.465	60.246	1.00	76.39
15	1343	CD2	HIS A 187	28.006	11.552	59.286	1.00	77.37
	1344	ND1	HIS A 187	29.636	12.341	60.507	1.00	76.18
	1345	CE1	HIS A 187	30.146	11.394	59.738	1.00	77.18
	1346	NE2	HIS A 187	29.178	10.899	58.988	1.00	76.82
	1347	C	HIS A 187	26.502	14.333	63.091	1.00	65.00
20	1348	O	HIS A 187	26.121	15.287	62.418	1.00	65.43
	1349	N	LEU A 188	26.201	14.182	64.374	1.00	63.51
	1350	CA	LEU A 188	25.383	15.142	65.101	1.00	64.86
	1351	CB	LEU A 188	23.888	14.904	64.818	1.00	67.36
	1352	CG	LEU A 188	23.177	15.455	63.567	1.00	68.27
25	1353	CD1	LEU A 188	23.581	14.720	62.288	1.00	67.48
	1354	CD2	LEU A 188	21.674	15.303	63.785	1.00	68.32
	1355	C	LEU A 188	25.649	15.042	66.607	1.00	66.30
	1356	O	LEU A 188	26.180	14.047	67.097	1.00	66.36
	1357	N	PRO A 189	25.279	16.078	67.363	1.00	100.45
30	1358	CD	PRO A 189	24.497	17.262	66.975	1.00	88.10
	1359	CA	PRO A 189	25.505	16.047	68.810	1.00	100.81
	1360	CB	PRO A 189	24.948	17.390	69.266	1.00	87.78
	1361	CG	PRO A 189	23.841	17.634	68.273	1.00	88.99
	1362	C	PRO A 189	24.804	14.869	69.480	1.00	100.89
35	1363	O	PRO A 189	23.607	14.653	69.274	1.00	100.89
	1364	N	LYS A 190	25.549	14.118	70.287	1.00	73.62
	1365	CA	LYS A 190	24.995	12.961	70.983	1.00	73.72
	1366	CB	LYS A 190	26.045	12.324	71.901	1.00	91.61
	1367	CG	LYS A 190	27.125	11.528	71.183	1.00	95.52
40	1368	CD	LYS A 190	27.938	10.688	72.165	1.00	96.56
	1369	CE	LYS A 190	29.027	9.877	71.460	1.00	96.04
	1370	NZ	LYS A 190	29.800	9.013	72.413	1.00	96.75
	1371	C	LYS A 190	23.741	13.242	71.809	1.00	72.54

	1372	O	LYS A 190	23.292	12.376	72.553	1.00	72.29
	1373	N	ASP A 191	23.169	14.436	71.686	1.00	84.70
	1374	CA	ASP A 191	21.975	14.773	72.459	1.00	83.52
	1375	CB	ASP A 191	22.312	15.829	73.526	1.00	118.93
5	1376	CG	ASP A 191	23.039	17.042	72.955	1.00	121.92
	1377	OD1	ASP A 191	24.050	16.861	72.242	1.00	122.89
	1378	OD2	ASP A 191	22.608	18.182	73.229	1.00	122.16
	1379	C	ASP A 191	20.831	15.253	71.584	1.00	80.20
	1380	O	ASP A 191	19.785	15.671	72.084	1.00	79.39
10	1381	N	LEU A 192	21.040	15.182	70.273	1.00	72.77
	1382	CA	LEU A 192	20.038	15.597	69.294	1.00	69.38
	1383	CB	LEU A 192	20.429	16.939	68.684	1.00	72.72
	1384	CG	LEU A 192	20.070	18.160	69.520	1.00	72.64
	1385	CD1	LEU A 192	21.228	19.131	69.548	1.00	74.95
15	1386	CD2	LEU A 192	18.831	18.805	68.945	1.00	72.23
	1387	C	LEU A 192	19.898	14.553	68.191	1.00	66.49
	1388	O	LEU A 192	19.062	14.686	67.299	1.00	65.42
	1389	N	ARG A 193	20.731	13.518	68.267	1.00	50.93
	1390	CA	ARG A 193	20.728	12.428	67.297	1.00	46.98
20	1391	CB	ARG A 193	21.658	11.312	67.794	1.00	49.52
	1392	CG	ARG A 193	23.152	11.689	67.813	1.00	49.10
	1393	CD	ARG A 193	24.032	10.612	68.489	1.00	47.28
	1394	NE	ARG A 193	25.452	10.736	68.150	1.00	47.28
	1395	CZ	ARG A 193	26.392	9.851	68.479	1.00	48.04
25	1396	NH1	ARG A 193	26.082	8.759	69.170	1.00	46.77
	1397	NH2	ARG A 193	27.649	10.048	68.096	1.00	50.46
	1398	C	ARG A 193	19.316	11.877	67.032	1.00	44.00
	1399	O	ARG A 193	18.916	11.683	65.884	1.00	42.42
	1400	N	ASP A 194	18.556	11.648	68.094	1.00	36.34
30	1401	CA	ASP A 194	17.200	11.124	67.945	1.00	33.93
	1402	CB	ASP A 194	16.856	10.204	69.114	1.00	36.54
	1403	CG	ASP A 194	17.866	9.102	69.308	1.00	34.55
	1404	OD1	ASP A 194	18.675	8.865	68.376	1.00	34.00
	1405	OD2	ASP A 194	17.833	8.474	70.398	1.00	33.59
35	1406	C	ASP A 194	16.093	12.181	67.840	1.00	32.88
	1407	O	ASP A 194	15.891	12.988	68.742	1.00	31.68
	1408	N	PRO A 195	15.341	12.163	66.739	1.00	34.77
	1409	CD	PRO A 195	15.303	11.124	65.699	1.00	55.68
	1410	CA	PRO A 195	14.260	13.130	66.563	1.00	34.35
40	1411	CB	PRO A 195	13.481	12.560	65.388	1.00	55.61
	1412	CG	PRO A 195	14.515	11.795	64.628	1.00	56.45
	1413	C	PRO A 195	13.412	13.119	67.813	1.00	34.92
	1414	O	PRO A 195	13.217	12.067	68.404	1.00	35.19

	1415	N	ASP A 196	12.916	14.277	68.226	1.00	38.18
	1416	CA	ASP A 196	12.043	14.355	69.394	1.00	39.88
	1417	CB	ASP A 196	12.166	15.717	70.073	1.00	55.77
	1418	CG	ASP A 196	13.510	15.921	70.733	1.00	59.88
5	1419	OD1	ASP A 196	13.796	17.056	71.157	1.00	61.23
	1420	OD2	ASP A 196	14.282	14.951	70.842	1.00	60.04
	1421	C	ASP A 196	10.642	14.204	68.837	1.00	40.38
	1422	O	ASP A 196	9.694	13.901	69.555	1.00	40.86
	1423	N	LEU A 197	10.529	14.414	67.528	1.00	58.18
10	1424	CA	LEU A 197	9.251	14.329	66.847	1.00	59.97
	1425	CB	LEU A 197	8.507	15.638	67.063	1.00	39.96
	1426	CG	LEU A 197	7.114	15.766	66.476	1.00	38.32
	1427	CD1	LEU A 197	6.247	14.726	67.120	1.00	38.54
	1428	CD2	LEU A 197	6.561	17.156	66.733	1.00	38.84
15	1429	C	LEU A 197	9.378	14.031	65.346	1.00	61.27
	1430	O	LEU A 197	10.228	14.581	64.654	1.00	63.27
	1431	N	ILE A 198	8.513	13.152	64.859	1.00	51.40
	1432	CA	ILE A 198	8.478	12.748	63.456	1.00	51.63
	1433	CB	ILE A 198	8.564	11.212	63.339	1.00	32.05
20	1434	CG2	ILE A 198	8.183	10.775	61.968	1.00	29.63
	1435	CG1	ILE A 198	9.982	10.743	63.666	1.00	31.32
	1436	CD1	ILE A 198	10.132	9.251	63.781	1.00	24.89
	1437	C	ILE A 198	7.150	13.219	62.870	1.00	54.08
	1438	O	ILE A 198	6.130	13.140	63.545	1.00	55.97
25	1439	N	ILE A 199	7.149	13.709	61.629	1.00	55.58
	1440	CA	ILE A 199	5.903	14.182	61.011	1.00	57.03
	1441	CB	ILE A 199	5.928	15.712	60.782	1.00	61.40
	1442	CG2	ILE A 199	4.650	16.145	60.110	1.00	61.59
	1443	CG1	ILE A 199	6.074	16.447	62.115	1.00	60.67
30	1444	CD1	ILE A 199	6.203	17.943	61.985	1.00	57.19
	1445	C	ILE A 199	5.585	13.509	59.674	1.00	58.15
	1446	O	ILE A 199	6.399	13.520	58.748	1.00	59.57
	1447	N	ARG A 200	4.394	12.925	59.586	1.00	40.62
	1448	CA	ARG A 200	3.949	12.251	58.369	1.00	41.42
35	1449	CB	ARG A 200	3.544	10.795	58.658	1.00	57.13
	1450	CG	ARG A 200	3.372	9.936	57.402	1.00	54.89
	1451	CD	ARG A 200	4.638	10.052	56.544	1.00	53.92
	1452	NE	ARG A 200	4.596	9.341	55.268	1.00	52.83
	1453	CZ	ARG A 200	4.486	8.024	55.138	1.00	51.74
40	1454	NH1	ARG A 200	4.398	7.247	56.212	1.00	52.92
	1455	NH2	ARG A 200	4.487	7.485	53.928	1.00	50.95
	1456	C	ARG A 200	2.749	12.986	57.804	1.00	43.70
	1457	O	ARG A 200	1.723	13.129	58.477	1.00	42.74

	1458	N	THR A 201	2.877	13.448	56.565	1.00	71.25
	1459	CA	THR A 201	1.798	14.174	55.908	1.00	74.12
	1460	CB	THR A 201	2.360	15.272	55.001	1.00	73.23
	1461	OG1	THR A 201	2.913	14.673	53.828	1.00	76.28
5	1462	CG2	THR A 201	3.459	16.038	55.711	1.00	74.06
	1463	C	THR A 201	0.958	13.224	55.049	1.00	76.46
	1464	O	THR A 201	1.174	12.011	55.048	1.00	78.25
	1465	N	SER A 202	-0.007	13.784	54.328	1.00	55.00
	1466	CA	SER A 202	-0.872	13.006	53.448	1.00	54.41
10	1467	CB	SER A 202	-0.103	12.603	52.196	1.00	53.35
	1468	OG	SER A 202	-0.890	11.747	51.391	1.00	52.76
	1469	C	SER A 202	-1.486	11.762	54.074	1.00	54.42
	1470	O	SER A 202	-1.379	10.675	53.522	1.00	54.50
	1471	N	GLY A 203	-2.131	11.934	55.224	1.00	69.79
15	1472	CA	GLY A 203	-2.782	10.835	55.918	1.00	70.25
	1473	C	GLY A 203	-2.218	9.446	55.678	1.00	71.00
	1474	O	GLY A 203	-2.812	8.639	54.968	1.00	71.94
	1475	N	GLU A 204	-1.069	9.160	56.275	1.00	65.14
	1476	CA	GLU A 204	-0.430	7.863	56.133	1.00	64.58
20	1477	CB	GLU A 204	0.783	7.975	55.207	1.00	89.40
	1478	CG	GLU A 204	0.451	8.231	53.750	1.00	92.38
	1479	CD	GLU A 204	0.034	6.970	53.018	1.00	94.85
	1480	OE1	GLU A 204	-0.825	6.234	53.549	1.00	94.30
	1481	OE2	GLU A 204	0.561	6.717	51.910	1.00	96.15
25	1482	C	GLU A 204	0.025	7.430	57.516	1.00	63.86
	1483	O	GLU A 204	0.831	8.120	58.146	1.00	64.30
	1484	N	LEU A 205	-0.485	6.300	57.998	1.00	77.27
	1485	CA	LEU A 205	-0.083	5.810	59.312	1.00	75.81
	1486	CB	LEU A 205	-1.307	5.355	60.110	1.00	73.73
30	1487	CG	LEU A 205	-2.419	6.400	60.268	1.00	73.58
	1488	CD1	LEU A 205	-3.189	6.111	61.540	1.00	72.43
	1489	CD2	LEU A 205	-1.840	7.801	60.327	1.00	73.40
	1490	C	LEU A 205	0.961	4.690	59.233	1.00	74.05
	1491	O	LEU A 205	0.782	3.609	59.797	1.00	73.90
35	1492	N	ARG A 206	2.046	4.978	58.516	1.00	44.09
	1493	CA	ARG A 206	3.179	4.081	58.336	1.00	43.58
	1494	CB	ARG A 206	3.292	3.601	56.888	1.00	79.95
	1495	CG	ARG A 206	2.135	2.805	56.349	1.00	82.38
	1496	CD	ARG A 206	2.503	2.233	54.984	1.00	86.62
40	1497	NE	ARG A 206	1.323	2.040	54.148	1.00	90.07
	1498	CZ	ARG A 206	0.615	3.034	53.615	1.00	91.34
	1499	NH1	ARG A 206	0.973	4.292	53.824	1.00	90.96
	1500	NH2	ARG A 206	-0.458	2.772	52.879	1.00	92.02

	1501	C	ARG A 206	4.452	4.871	58.653	1.00	42.29
	1502	O	ARG A 206	4.483	6.100	58.531	1.00	40.58
	1503	N	LEU A 207	5.516	4.176	59.042	1.00	70.66
	1504	CA	LEU A 207	6.755	4.889	59.327	1.00	68.57
5	1505	CB	LEU A 207	7.466	4.298	60.552	1.00	67.93
	1506	CG	LEU A 207	8.184	5.399	61.344	1.00	69.26
	1507	CD1	LEU A 207	7.131	6.282	61.992	1.00	67.83
	1508	CD2	LEU A 207	9.114	4.820	62.390	1.00	69.87
	1509	C	LEU A 207	7.683	4.883	58.100	1.00	66.21
10	1510	O	LEU A 207	8.649	5.645	58.031	1.00	66.27
	1511	N	SER A 208	7.384	4.017	57.138	1.00	48.52
	1512	CA	SER A 208	8.152	3.937	55.895	1.00	44.95
	1513	CB	SER A 208	7.897	5.193	55.061	1.00	49.44
	1514	OG	SER A 208	6.505	5.438	54.934	1.00	53.00
15	1515	C	SER A 208	9.655	3.741	56.049	1.00	42.59
	1516	O	SER A 208	10.449	4.413	55.379	1.00	40.02
	1517	N	ASN A 209	10.039	2.817	56.924	1.00	46.75
	1518	CA	ASN A 209	11.446	2.513	57.161	1.00	45.16
	1519	CB	ASN A 209	11.987	1.709	55.972	1.00	44.54
20	1520	CG	ASN A 209	13.424	1.310	56.151	1.00	44.36
	1521	OD1	ASN A 209	13.830	0.867	57.223	1.00	47.22
	1522	ND2	ASN A 209	14.208	1.459	55.101	1.00	45.74
	1523	C	ASN A 209	12.302	3.767	57.402	1.00	42.89
	1524	O	ASN A 209	13.460	3.825	57.003	1.00	41.55
25	1525	N	PHE A 210	11.725	4.756	58.079	1.00	39.22
	1526	CA	PHE A 210	12.399	6.024	58.365	1.00	37.27
	1527	CB	PHE A 210	11.457	7.183	58.032	1.00	38.93
	1528	CG	PHE A 210	12.001	8.538	58.390	1.00	38.93
	1529	CD1	PHE A 210	13.245	8.957	57.920	1.00	39.50
30	1530	CD2	PHE A 210	11.251	9.419	59.157	1.00	39.49
	1531	CE1	PHE A 210	13.724	10.234	58.211	1.00	36.40
	1532	CE2	PHE A 210	11.723	10.687	59.448	1.00	37.74
	1533	CZ	PHE A 210	12.957	11.092	58.973	1.00	37.09
	1534	C	PHE A 210	12.854	6.153	59.815	1.00	35.77
35	1535	O	PHE A 210	12.034	6.273	60.724	1.00	37.28
	1536	N	LEU A 211	14.165	6.135	60.024	1.00	30.72
	1537	CA	LEU A 211	14.740	6.266	61.356	1.00	29.17
	1538	CB	LEU A 211	14.562	7.710	61.849	1.00	30.75
	1539	CG	LEU A 211	15.282	8.795	61.043	1.00	31.54
40	1540	CD1	LEU A 211	14.887	10.158	61.551	1.00	30.37
	1541	CD2	LEU A 211	16.788	8.607	61.149	1.00	29.89
	1542	C	LEU A 211	14.149	5.282	62.371	1.00	28.83
	1543	O	LEU A 211	13.727	5.666	63.461	1.00	30.11

	1544	N	PRO A 212	14.144	3.989	62.038	1.00	21.34
	1545	CD	PRO A 212	14.827	3.341	60.910	1.00	25.09
	1546	CA	PRO A 212	13.594	2.992	62.950	1.00	20.84
	1547	CB	PRO A 212	13.783	1.686	62.182	1.00	24.56
5	1548	CG	PRO A 212	15.013	1.931	61.407	1.00	25.67
	1549	C	PRO A 212	14.275	2.986	64.311	1.00	19.94
	1550	O	PRO A 212	13.606	2.967	65.341	1.00	17.23
	1551	N	TRP A 213	15.607	3.016	64.308	1.00	28.93
	1552	CA	TRP A 213	16.364	3.005	65.550	1.00	28.92
10	1553	CB	TRP A 213	17.858	2.729	65.280	1.00	27.61
	1554	CG	TRP A 213	18.739	2.778	66.544	1.00	27.10
	1555	CD2	TRP A 213	19.294	1.661	67.264	1.00	27.80
	1556	CE2	TRP A 213	19.977	2.186	68.395	1.00	25.65
	1557	CE3	TRP A 213	19.277	0.271	67.071	1.00	27.47
15	1558	CD1	TRP A 213	19.106	3.896	67.253	1.00	25.51
	1559	NE1	TRP A 213	19.843	3.547	68.362	1.00	25.34
	1560	CZ2	TRP A 213	20.634	1.369	69.325	1.00	26.78
	1561	CZ3	TRP A 213	19.927	-0.537	67.997	1.00	27.71
	1562	CH2	TRP A 213	20.600	0.018	69.114	1.00	26.89
20	1563	C	TRP A 213	16.206	4.322	66.307	1.00	29.52
	1564	O	TRP A 213	15.844	4.325	67.479	1.00	30.08
	1565	N	GLN A 214	16.461	5.436	65.626	1.00	25.53
	1566	CA	GLN A 214	16.397	6.752	66.244	1.00	27.09
	1567	CB	GLN A 214	16.892	7.820	65.265	1.00	32.69
25	1568	CG	GLN A 214	18.366	7.748	64.882	1.00	31.73
	1569	CD	GLN A 214	18.632	6.807	63.743	1.00	33.51
	1570	OE1	GLN A 214	19.768	6.664	63.304	1.00	31.73
	1571	NE2	GLN A 214	17.588	6.148	63.254	1.00	35.57
	1572	C	GLN A 214	15.039	7.176	66.763	1.00	29.77
30	1573	O	GLN A 214	14.952	7.775	67.830	1.00	30.98
	1574	N	GLY A 215	13.979	6.872	66.012	1.00	31.51
	1575	CA	GLY A 215	12.636	7.283	66.414	1.00	29.71
	1576	C	GLY A 215	11.951	6.363	67.397	1.00	30.52
	1577	O	GLY A 215	10.723	6.406	67.593	1.00	30.83
35	1578	N	ALA A 216	12.769	5.536	68.032	1.00	27.55
	1579	CA	ALA A 216	12.288	4.564	68.982	1.00	26.70
	1580	CB	ALA A 216	13.457	3.904	69.675	1.00	23.13
	1581	C	ALA A 216	11.335	5.186	69.980	1.00	27.72
	1582	O	ALA A 216	10.348	4.574	70.351	1.00	28.13
40	1583	N	TYR A 217	11.608	6.407	70.417	1.00	31.29
	1584	CA	TYR A 217	10.696	7.033	71.369	1.00	33.23
	1585	CB	TYR A 217	11.362	7.203	72.725	1.00	36.13
	1586	CG	TYR A 217	11.285	5.961	73.584	1.00	36.90



	1587	CD1	TYR A 217	12.329	5.033	73.619	1.00	35.40
	1588	CE1	TYR A 217	12.241	3.899	74.421	1.00	39.13
	1589	CD2	TYR A 217	10.153	5.717	74.366	1.00	38.96
	1590	CE2	TYR A 217	10.052	4.593	75.165	1.00	38.12
5	1591	CZ	TYR A 217	11.093	3.687	75.197	1.00	40.37
	1592	OH	TYR A 217	10.976	2.595	76.032	1.00	39.19
	1593	C	TYR A 217	10.155	8.356	70.914	1.00	32.99
	1594	O	TYR A 217	9.539	9.073	71.687	1.00	34.63
	1595	N	SER A 218	10.375	8.659	69.643	1.00	29.75
10	1596	CA	SER A 218	9.933	9.904	69.054	1.00	32.78
	1597	CB	SER A 218	10.368	9.977	67.592	1.00	51.24
	1598	OG	SER A 218	11.777	9.986	67.465	1.00	56.29
	1599	C	SER A 218	8.429	10.009	69.123	1.00	34.88
	1600	O	SER A 218	7.734	9.020	68.899	1.00	35.86
15	1601	N	GLU A 219	7.927	11.199	69.453	1.00	50.24
	1602	CA	GLU A 219	6.487	11.431	69.495	1.00	51.43
	1603	CB	GLU A 219	6.170	12.752	70.184	1.00	42.72
	1604	CG	GLU A 219	6.133	12.682	71.698	1.00	42.50
	1605	CD	GLU A 219	4.957	11.880	72.219	1.00	44.60
20	1606	OE1	GLU A 219	3.985	11.711	71.458	1.00	45.34
	1607	OE2	GLU A 219	4.992	11.430	73.386	1.00	45.20
	1608	C	GLU A 219	6.072	11.485	68.031	1.00	52.41
	1609	O	GLU A 219	6.756	12.076	67.206	1.00	52.72
	1610	N	LEU A 220	4.958	10.861	67.705	1.00	39.96
25	1611	CA	LEU A 220	4.515	10.819	66.330	1.00	40.25
	1612	CB	LEU A 220	4.058	9.395	66.014	1.00	26.28
	1613	CG	LEU A 220	5.132	8.374	66.411	1.00	19.24
	1614	CD1	LEU A 220	4.691	7.002	66.044	1.00	19.92
	1615	CD2	LEU A 220	6.427	8.699	65.703	1.00	15.40
30	1616	C	LEU A 220	3.404	11.806	66.040	1.00	44.14
	1617	O	LEU A 220	2.561	12.072	66.891	1.00	45.70
	1618	N	TYR A 221	3.402	12.358	64.835	1.00	53.92
	1619	CA	TYR A 221	2.366	13.304	64.443	1.00	57.45
	1620	CB	TYR A 221	2.864	14.740	64.649	1.00	63.62
35	1621	CG	TYR A 221	1.885	15.812	64.207	1.00	66.26
	1622	CD1	TYR A 221	0.565	15.809	64.647	1.00	66.77
	1623	CE1	TYR A 221	-0.323	16.776	64.233	1.00	66.77
	1624	CD2	TYR A 221	2.282	16.824	63.339	1.00	67.06
	1625	CE2	TYR A 221	1.400	17.788	62.926	1.00	67.52
40	1626	CZ	TYR A 221	0.106	17.758	63.373	1.00	67.28
	1627	OH	TYR A 221	-0.765	18.716	62.938	1.00	69.40
	1628	C	TYR A 221	1.924	13.074	62.990	1.00	58.86
	1629	O	TYR A 221	2.717	13.187	62.048	1.00	59.20

	1630	N	PHE	A	222	0.649	12.741	62.821	1.00	60.95
	1631	CA	PHE	A	222	0.089	12.490	61.503	1.00	62.79
	1632	CB	PHE	A	222	-0.612	11.134	61.521	1.00	58.23
	1633	CG	PHE	A	222	0.307	9.989	61.848	1.00	58.94
5	1634	CD1	PHE	A	222	0.060	9.167	62.945	1.00	58.55
	1635	CD2	PHE	A	222	1.438	9.743	61.071	1.00	58.48
	1636	CE1	PHE	A	222	0.923	8.123	63.265	1.00	58.44
	1637	CE2	PHE	A	222	2.303	8.704	61.384	1.00	56.86
	1638	CZ	PHE	A	222	2.043	7.893	62.486	1.00	58.47
10	1639	C	PHE	A	222	-0.879	13.600	61.066	1.00	64.53
	1640	O	PHE	A	222	-1.436	14.312	61.897	1.00	65.86
	1641	N	THR	A	223	-1.073	13.749	59.761	1.00	53.11
	1642	CA	THR	A	223	-1.965	14.774	59.236	1.00	55.50
	1643	CB	THR	A	223	-1.342	16.165	59.311	1.00	74.89
15	1644	OG1	THR	A	223	-2.132	17.070	58.527	1.00	76.56
	1645	CG2	THR	A	223	0.091	16.146	58.765	1.00	75.02
	1646	C	THR	A	223	-2.299	14.542	57.778	1.00	56.91
	1647	O	THR	A	223	-1.409	14.522	56.926	1.00	57.65
	1648	N	ASP	A	224	-3.588	14.414	57.486	1.00	75.10
20	1649	CA	ASP	A	224	-4.050	14.176	56.124	1.00	75.82
	1650	CB	ASP	A	224	-5.566	14.070	56.114	1.00	72.96
	1651	CG	ASP	A	224	-6.087	13.245	57.269	1.00	74.62
	1652	OD1	ASP	A	224	-6.195	13.791	58.389	1.00	76.73
	1653	OD2	ASP	A	224	-6.374	12.045	57.066	1.00	74.53
25	1654	C	ASP	A	224	-3.599	15.245	55.138	1.00	76.24
	1655	O	ASP	A	224	-3.628	15.034	53.927	1.00	77.12
	1656	N	THR	A	225	-3.168	16.387	55.655	1.00	47.98
	1657	CA	THR	A	225	-2.719	17.478	54.807	1.00	49.10
	1658	CB	THR	A	225	-2.165	18.619	55.655	1.00	84.57
30	1659	OG1	THR	A	225	-1.082	18.129	56.453	1.00	86.07
	1660	CG2	THR	A	225	-3.245	19.162	56.573	1.00	85.13
	1661	C	THR	A	225	-1.636	17.020	53.849	1.00	48.17
	1662	O	THR	A	225	-0.790	16.225	54.216	1.00	49.64
	1663	N	LEU	A	226	-1.674	17.506	52.615	1.00	51.52
35	1664	CA	LEU	A	226	-0.657	17.143	51.636	1.00	52.64
	1665	CB	LEU	A	226	-1.046	17.626	50.237	1.00	72.33
	1666	CG	LEU	A	226	-1.979	16.711	49.441	1.00	72.59
	1667	CD1	LEU	A	226	-1.197	15.499	48.962	1.00	73.13
	1668	CD2	LEU	A	226	-3.171	16.290	50.295	1.00	71.25
40	1669	C	LEU	A	226	0.616	17.825	52.097	1.00	53.19
	1670	O	LEU	A	226	0.578	18.561	53.081	1.00	53.08
	1671	N	TRP	A	227	1.725	17.610	51.388	1.00	66.66
	1672	CA	TRP	A	227	3.005	18.185	51.797	1.00	67.22

	1673	CB	TRP A 227	4.169	17.289	51.358	1.00	60.56
	1674	CG	TRP A 227	5.518	17.915	51.606	1.00	58.17
	1675	CD2	TRP A 227	5.999	18.478	52.837	1.00	57.18
	1676	CE2	TRP A 227	7.291	18.995	52.583	1.00	57.49
5	1677	CE3	TRP A 227	5.466	18.598	54.127	1.00	56.47
	1678	CD1	TRP A 227	6.514	18.105	50.688	1.00	58.25
	1679	NE1	TRP A 227	7.579	18.753	51.266	1.00	58.32
	1680	CZ2	TRP A 227	8.056	19.624	53.573	1.00	56.36
	1681	CZ3	TRP A 227	6.232	19.226	55.113	1.00	55.66
10	1682	CH2	TRP A 227	7.511	19.729	54.826	1.00	55.52
	1683	C	TRP A 227	3.311	19.618	51.392	1.00	68.58
	1684	O	TRP A 227	3.833	20.385	52.195	1.00	68.87
	1685	N	PRO A 228	3.034	19.999	50.142	1.00	87.77
	1686	CD	PRO A 228	2.724	19.233	48.927	1.00	98.49
15	1687	CA	PRO A 228	3.349	21.391	49.810	1.00	88.87
	1688	CB	PRO A 228	3.046	21.462	48.318	1.00	99.05
	1689	CG	PRO A 228	3.378	20.082	47.858	1.00	99.11
	1690	C	PRO A 228	2.468	22.325	50.637	1.00	88.93
	1691	O	PRO A 228	2.716	23.530	50.717	1.00	88.53
20	1692	N	ASP A 229	1.448	21.736	51.260	1.00	95.84
	1693	CA	ASP A 229	0.490	22.450	52.105	1.00	95.31
	1694	CB	ASP A 229	-0.862	21.732	52.076	1.00	72.45
	1695	CG	ASP A 229	-1.597	21.940	50.779	1.00	72.47
	1696	OD1	ASP A 229	-2.571	21.198	50.517	1.00	73.15
25	1697	OD2	ASP A 229	-1.201	22.856	50.030	1.00	72.04
	1698	C	ASP A 229	0.941	22.593	53.563	1.00	95.53
	1699	O	ASP A 229	0.234	23.193	54.384	1.00	95.46
	1700	N	PHE A 230	2.103	22.033	53.889	1.00	72.23
	1701	CA	PHE A 230	2.616	22.122	55.246	1.00	69.91
30	1702	CB	PHE A 230	3.607	20.983	55.533	1.00	60.91
	1703	CG	PHE A 230	3.646	20.566	56.982	1.00	58.00
	1704	CD1	PHE A 230	2.548	19.941	57.566	1.00	55.95
	1705	CD2	PHE A 230	4.756	20.848	57.774	1.00	57.16
	1706	CE1	PHE A 230	2.550	19.611	58.911	1.00	54.54
35	1707	CE2	PHE A 230	4.764	20.523	59.119	1.00	54.72
	1708	CZ	PHE A 230	3.657	19.904	59.687	1.00	54.36
	1709	C	PHE A 230	3.303	23.473	55.349	1.00	69.25
	1710	O	PHE A 230	4.409	23.662	54.837	1.00	67.25
	1711	N	ASP A 231	2.616	24.407	56.008	1.00	105.50
40	1712	CA	ASP A 231	3.085	25.778	56.202	1.00	105.80
	1713	CB	ASP A 231	1.940	26.755	55.898	1.00	68.25
	1714	CG	ASP A 231	0.672	26.438	56.683	1.00	66.13
	1715	OD1	ASP A 231	-0.354	27.100	56.448	1.00	66.14

	1716	OD2	ASP	A	231	0.696	25.531	57.534	1.00	63.85
	1717	C	ASP	A	231	3.592	26.022	57.617	1.00	106.25
	1718	O	ASP	A	231	3.441	25.169	58.493	1.00	105.19
	1719	N	GLU	A	232	4.198	27.185	57.837	1.00	75.85
5	1720	CA	GLU	A	232	4.689	27.513	59.166	1.00	75.73
	1721	CB	GLU	A	232	5.089	28.981	59.261	1.00	74.39
	1722	CG	GLU	A	232	5.796	29.299	60.559	1.00	75.53
	1723	CD	GLU	A	232	6.249	30.743	60.655	1.00	76.43
	1724	OE1	GLU	A	232	6.592	31.336	59.605	1.00	75.83
10	1725	OE2	GLU	A	232	6.284	31.276	61.788	1.00	75.29
	1726	C	GLU	A	232	3.535	27.246	60.118	1.00	75.70
	1727	O	GLU	A	232	3.719	26.713	61.213	1.00	75.51
	1728	N	ALA	A	233	2.338	27.617	59.679	1.00	66.62
	1729	CA	ALA	A	233	1.132	27.406	60.472	1.00	66.81
15	1730	CB	ALA	A	233	-0.110	27.612	59.608	1.00	42.16
	1731	C	ALA	A	233	1.164	25.980	60.987	1.00	67.42
	1732	O	ALA	A	233	1.145	25.733	62.195	1.00	66.72
	1733	N	ALA	A	234	1.223	25.049	60.040	1.00	105.33
	1734	CA	ALA	A	234	1.263	23.627	60.332	1.00	104.96
20	1735	CB	ALA	A	234	1.372	22.840	59.036	1.00	70.15
	1736	C	ALA	A	234	2.447	23.318	61.229	1.00	104.98
	1737	O	ALA	A	234	2.283	22.770	62.317	1.00	105.25
	1738	N	LEU	A	235	3.639	23.676	60.768	1.00	81.94
	1739	CA	LEU	A	235	4.843	23.427	61.536	1.00	81.18
25	1740	CB	LEU	A	235	5.962	24.363	61.087	1.00	60.77
	1741	CG	LEU	A	235	7.367	24.051	61.602	1.00	59.54
	1742	CD1	LEU	A	235	7.388	24.143	63.099	1.00	59.47
	1743	CD2	LEU	A	235	7.784	22.668	61.169	1.00	59.88
	1744	C	LEU	A	235	4.549	23.653	63.005	1.00	82.00
30	1745	O	LEU	A	235	4.577	22.720	63.809	1.00	82.42
	1746	N	GLN	A	236	4.258	24.901	63.351	1.00	79.63
	1747	CA	GLN	A	236	3.968	25.252	64.735	1.00	79.41
	1748	CB	GLN	A	236	3.717	26.758	64.864	1.00	86.03
	1749	CG	GLN	A	236	4.727	27.619	64.115	1.00	87.53
35	1750	CD	GLN	A	236	4.724	29.069	64.564	1.00	88.57
	1751	OE1	GLN	A	236	5.310	29.932	63.913	1.00	88.30
	1752	NE2	GLN	A	236	4.075	29.339	65.688	1.00	90.39
	1753	C	GLN	A	236	2.748	24.480	65.203	1.00	78.24
	1754	O	GLN	A	236	2.694	24.014	66.339	1.00	78.33
40	1755	N	GLU	A	237	1.774	24.342	64.311	1.00	75.22
	1756	CA	GLU	A	237	0.551	23.624	64.625	1.00	74.35
	1757	CB	GLU	A	237	-0.287	23.438	63.362	1.00	83.36
	1758	CG	GLU	A	237	-1.792	23.489	63.582	1.00	85.49

	1759	CD	GLU A 237	-2.290	22.464	64.592	1.00	86.68
	1760	OE1	GLU A 237	-1.986	22.616	65.796	1.00	87.49
	1761	OE2	GLU A 237	-2.989	21.506	64.181	1.00	86.25
	1762	C	GLU A 237	0.945	22.269	65.199	1.00	73.31
5	1763	O	GLU A 237	0.373	21.810	66.189	1.00	72.96
	1764	N	ALA A 238	1.937	21.636	64.580	1.00	68.54
	1765	CA	ALA A 238	2.418	20.337	65.043	1.00	67.12
	1766	CB	ALA A 238	3.490	19.794	64.096	1.00	47.92
	1767	C	ALA A 238	3.001	20.507	66.440	1.00	65.44
10	1768	O	ALA A 238	2.659	19.769	67.368	1.00	64.92
	1769	N	ILE A 239	3.878	21.493	66.590	1.00	55.00
	1770	CA	ILE A 239	4.489	21.727	67.881	1.00	54.40
	1771	CB	ILE A 239	5.429	22.917	67.829	1.00	40.35
	1772	CG2	ILE A 239	6.326	22.929	69.059	1.00	39.90
15	1773	CG1	ILE A 239	6.297	22.805	66.587	1.00	37.77
	1774	CD1	ILE A 239	7.497	23.715	66.621	1.00	39.44
	1775	C	ILE A 239	3.426	21.939	68.955	1.00	56.09
	1776	O	ILE A 239	3.558	21.442	70.072	1.00	55.65
	1777	N	LEU A 240	2.363	22.663	68.624	1.00	65.76
20	1778	CA	LEU A 240	1.312	22.871	69.606	1.00	67.84
	1779	CB	LEU A 240	0.124	23.614	68.990	1.00	93.15
	1780	CG	LEU A 240	-1.019	24.084	69.907	1.00	93.89
	1781	CD1	LEU A 240	-2.066	24.781	69.047	1.00	94.06
	1782	CD2	LEU A 240	-1.659	22.920	70.662	1.00	92.97
25	1783	C	LEU A 240	0.885	21.473	70.035	1.00	68.53
	1784	O	LEU A 240	0.593	21.226	71.205	1.00	68.37
	1785	N	ALA A 241	0.865	20.553	69.080	1.00	78.77
	1786	CA	ALA A 241	0.475	19.185	69.373	1.00	81.17
	1787	CB	ALA A 241	0.189	18.439	68.082	1.00	73.59
30	1788	C	ALA A 241	1.561	18.464	70.171	1.00	82.11
	1789	O	ALA A 241	1.288	17.894	71.228	1.00	81.41
	1790	N	TYR A 242	2.789	18.496	69.665	1.00	68.88
	1791	CA	TYR A 242	3.914	17.838	70.329	1.00	69.93
	1792	CB	TYR A 242	5.236	18.367	69.789	1.00	63.62
35	1793	CG	TYR A 242	6.402	18.047	70.678	1.00	61.34
	1794	CD1	TYR A 242	6.937	16.767	70.719	1.00	61.47
	1795	CE1	TYR A 242	8.002	16.465	71.565	1.00	60.57
	1796	CD2	TYR A 242	6.957	19.023	71.505	1.00	60.00
	1797	CE2	TYR A 242	8.015	18.733	72.350	1.00	59.45
40	1798	CZ	TYR A 242	8.530	17.454	72.375	1.00	59.81
	1799	OH	TYR A 242	9.569	17.158	73.212	1.00	59.44
	1800	C	TYR A 242	3.893	18.043	71.831	1.00	72.10
	1801	O	TYR A 242	4.059	17.097	72.603	1.00	72.12

	1802	N	ASN A 243	3.710	19.295	72.232	1.00	93.74
	1803	CA	ASN A 243	3.652	19.653	73.640	1.00	95.67
	1804	CB	ASN A 243	3.680	21.178	73.798	1.00	70.69
	1805	CG	ASN A 243	4.971	21.804	73.293	1.00	69.64
5	1806	OD1	ASN A 243	6.042	21.594	73.862	1.00	69.41
	1807	ND2	ASN A 243	4.873	22.582	72.221	1.00	69.43
	1808	C	ASN A 243	2.349	19.101	74.214	1.00	97.80
	1809	O	ASN A 243	1.300	19.736	74.103	1.00	98.52
	1810	N	ARG A 244	2.400	17.917	74.816	1.00	104.20
10	1811	CA	ARG A 244	1.185	17.357	75.379	1.00	106.41
	1812	CB	ARG A 244	0.165	17.143	74.260	1.00	103.89
	1813	CG	ARG A 244	-1.281	17.007	74.730	1.00	106.87
	1814	CD	ARG A 244	-1.869	18.333	75.239	1.00	108.89
	1815	NE	ARG A 244	-3.308	18.223	75.496	1.00	110.50
15	1816	CZ	ARG A 244	-4.089	19.222	75.902	1.00	111.26
	1817	NH1	ARG A 244	-3.584	20.432	76.109	1.00	111.93
	1818	NH2	ARG A 244	-5.381	19.009	76.098	1.00	110.31
	1819	C	ARG A 244	1.303	16.075	76.214	1.00	107.62
	1820	O	ARG A 244	0.346	15.727	76.909	1.00	108.53
20	1821	N	ARG A 245	2.434	15.365	76.179	1.00	78.99
	1822	CA	ARG A 245	2.495	14.147	76.988	1.00	79.54
	1823	CB	ARG A 245	1.434	13.158	76.489	1.00	81.06
	1824	CG	ARG A 245	1.700	12.580	75.099	1.00	80.96
	1825	CD	ARG A 245	1.776	13.652	74.001	1.00	79.38
25	1826	NE	ARG A 245	1.818	13.056	72.661	1.00	80.03
	1827	CZ	ARG A 245	1.481	13.697	71.546	1.00	79.70
	1828	NH1	ARG A 245	1.077	14.959	71.615	1.00	80.22
	1829	NH2	ARG A 245	1.531	13.079	70.368	1.00	78.91
	1830	C	ARG A 245	3.817	13.396	77.136	1.00	80.60
30	1831	O	ARG A 245	3.925	12.500	77.981	1.00	80.72
	1832	N	HIS A 246	4.813	13.741	76.328	1.00	120.09
	1833	CA	HIS A 246	6.101	13.053	76.381	1.00	120.59
	1834	CB	HIS A 246	7.234	14.022	76.044	1.00	97.52
	1835	CG	HIS A 246	8.143	13.528	74.961	1.00	96.91
35	1836	CD2	HIS A 246	8.207	12.332	74.331	1.00	96.71
	1837	ND1	HIS A 246	9.139	14.305	74.411	1.00	97.74
	1838	CE1	HIS A 246	9.778	13.608	73.489	1.00	97.35
	1839	NE2	HIS A 246	9.233	12.408	73.420	1.00	96.55
	1840	C	HIS A 246	6.359	12.382	77.727	1.00	121.22
40	1841	O	HIS A 246	6.496	13.042	78.755	1.00	121.75
	1842	N	ARG A 247	6.406	11.057	77.700	1.00	78.16
	1843	CA	ARG A 247	6.626	10.232	78.888	1.00	79.80
	1844	CB	ARG A 247	5.289	9.585	79.285	1.00	91.32

	1845	CG	ARG A 247	5.304	8.487	80.351	1.00	94.26
	1846	CD	ARG A 247	3.868	8.005	80.558	1.00	96.03
	1847	NE	ARG A 247	3.758	6.592	80.920	1.00	96.92
	1848	CZ	ARG A 247	2.638	5.878	80.794	1.00	97.32
5	1849	NH1	ARG A 247	1.540	6.452	80.313	1.00	97.34
	1850	NH2	ARG A 247	2.615	4.592	81.139	1.00	97.79
	1851	C	ARG A 247	7.688	9.168	78.571	1.00	79.63
	1852	O	ARG A 247	7.713	8.084	79.165	1.00	78.61
	1853	N	ARG A 248	8.567	9.512	77.629	1.00	154.67
10	1854	CA	ARG A 248	9.652	8.645	77.165	1.00	153.82
	1855	CB	ARG A 248	10.791	9.474	76.559	1.00	115.47
	1856	CG	ARG A 248	10.540	9.967	75.143	1.00	115.68
	1857	CD	ARG A 248	11.821	10.526	74.520	1.00	116.07
	1858	NE	ARG A 248	11.612	11.027	73.160	1.00	117.85
15	1859	CZ	ARG A 248	12.588	11.430	72.348	1.00	118.27
	1860	NH1	ARG A 248	13.856	11.394	72.748	1.00	118.12
	1861	NH2	ARG A 248	12.294	11.873	71.134	1.00	117.73
	1862	C	ARG A 248	10.256	7.722	78.204	1.00	153.01
	1863	O	ARG A 248	10.017	7.861	79.399	1.00	152.98
20	1864	N	PHE A 249	11.058	6.779	77.720	1.00	104.87
	1865	CA	PHE A 249	11.735	5.811	78.574	1.00	104.55
	1866	CB	PHE A 249	12.807	6.523	79.422	1.00	82.94
	1867	CG	PHE A 249	14.025	5.679	79.716	1.00	82.52
	1868	CD1	PHE A 249	13.993	4.687	80.695	1.00	82.75
25	1869	CD2	PHE A 249	15.206	5.865	78.993	1.00	81.44
	1870	CE1	PHE A 249	15.124	3.891	80.950	1.00	81.36
	1871	CE2	PHE A 249	16.334	5.076	79.241	1.00	80.65
	1872	CZ	PHE A 249	16.290	4.089	80.221	1.00	79.85
	1873	C	PHE A 249	10.708	5.148	79.481	1.00	104.71
30	1874	O	PHE A 249	11.071	4.514	80.473	1.00	105.55
	1875	N	GLY A 250	9.428	5.288	79.133	1.00	72.46
	1876	CA	GLY A 250	8.385	4.714	79.965	1.00	72.36
	1877	C	GLY A 250	8.435	5.429	81.306	1.00	72.32
	1878	O	GLY A 250	8.392	6.669	81.347	1.00	71.99
35	1879	N	GLY A 251	8.537	4.667	82.397	1.00	72.26
	1880	CA	GLY A 251	8.620	5.270	83.720	1.00	71.88
	1881	C	GLY A 251	7.308	5.804	84.253	1.00	71.75
	1882	O	GLY A 251	6.323	5.882	83.523	1.00	71.62
	1883	N	VAL A 252	7.292	6.177	85.529	1.00	71.62
40	1884	CA	VAL A 252	6.072	6.696	86.149	1.00	70.92
	1885	CB	VAL A 252	6.124	6.602	87.709	1.00	70.44
	1886	CG1	VAL A 252	4.700	6.684	88.293	1.00	68.98
	1887	CG2	VAL A 252	6.814	5.309	88.138	1.00	69.75

	1888	C	VAL A	252	5.852	8.154	85.753	1.00	70.83
	1889	O	VAL A	252	5.835	9.023	86.656	1.00	71.48
	1890	OT	VAL A	252	5.701	8.406	84.538	1.00	70.06
	1891	CB	THR B	17	-12.423	-6.704	52.606	1.00	87.12
5	1892	OG1	THR B	17	-12.848	-7.646	51.608	1.00	86.46
	1893	CG2	THR B	17	-12.991	-5.325	52.295	1.00	87.67
	1894	C	THR B	17	-10.335	-7.977	53.162	1.00	100.27
	1895	O	THR B	17	-11.030	-8.998	53.142	1.00	100.77
	1896	N	THR B	17	-10.323	-6.301	51.307	1.00	101.49
10	1897	CA	THR B	17	-10.878	-6.643	52.647	1.00	101.01
	1898	N	GLN B	18	-9.091	-7.959	53.630	1.00	79.67
	1899	CA	GLN B	18	-8.461	-9.166	54.144	1.00	78.05
	1900	CB	GLN B	18	-7.052	-9.321	53.555	1.00	86.36
	1901	CG	GLN B	18	-6.837	-10.616	52.770	1.00	87.41
15	1902	CD	GLN B	18	-7.190	-11.866	53.569	1.00	88.41
	1903	OE1	GLN B	18	-8.343	-12.069	53.953	1.00	89.02
	1904	NE2	GLN B	18	-6.195	-12.709	53.820	1.00	87.06
	1905	C	GLN B	18	-8.372	-9.158	55.664	1.00	76.01
	1906	O	GLN B	18	-9.238	-8.618	56.353	1.00	75.68
20	1907	N	VAL B	19	-7.313	-9.785	56.168	1.00	71.83
	1908	CA	VAL B	19	-7.042	-9.865	57.596	1.00	67.90
	1909	CB	VAL B	19	-7.644	-11.153	58.237	1.00	75.52
	1910	CG1	VAL B	19	-6.887	-12.387	57.771	1.00	74.84
	1911	CG2	VAL B	19	-7.594	-11.055	59.752	1.00	75.66
25	1912	C	VAL B	19	-5.528	-9.868	57.796	1.00	64.95
	1913	O	VAL B	19	-4.806	-10.685	57.216	1.00	63.38
	1914	N	PRO B	20	-5.023	-8.929	58.602	1.00	62.59
	1915	CD	PRO B	20	-5.723	-7.955	59.456	1.00	72.33
	1916	CA	PRO B	20	-3.581	-8.891	58.833	1.00	59.03
30	1917	CB	PRO B	20	-3.429	-7.768	59.860	1.00	69.19
	1918	CG	PRO B	20	-4.748	-7.784	60.588	1.00	71.98
	1919	C	PRO B	20	-3.096	-10.244	59.355	1.00	55.41
	1920	O	PRO B	20	-3.694	-10.822	60.265	1.00	54.15
	1921	N	ALA B	21	-2.019	-10.754	58.770	1.00	41.89
35	1922	CA	ALA B	21	-1.485	-12.036	59.197	1.00	39.88
	1923	CB	ALA B	21	-0.457	-12.520	58.190	1.00	24.71
	1924	C	ALA B	21	-0.862	-11.968	60.591	1.00	39.26
	1925	O	ALA B	21	-1.073	-12.853	61.419	1.00	38.42
	1926	N	HIS B	22	-0.111	-10.899	60.843	1.00	43.99
40	1927	CA	HIS B	22	0.593	-10.688	62.104	1.00	42.13
	1928	CB	HIS B	22	2.108	-10.740	61.807	1.00	40.21
	1929	CG	HIS B	22	3.006	-10.564	62.998	1.00	40.93
	1930	CD2	HIS B	22	2.741	-10.285	64.297	1.00	40.22



	1931	ND1	HIS	B	22	4.377	-10.673	62.904	1.00	38.93
	1932	CE1	HIS	B	22	4.916	-10.472	64.093	1.00	38.31
	1933	NE2	HIS	B	22	3.945	-10.233	64.956	1.00	36.66
	1934	C	HIS	B	22	0.173	-9.327	62.671	1.00	41.73
5	1935	O	HIS	B	22	0.357	-8.286	62.032	1.00	40.36
	1936	N	ILE	B	23	-0.407	-9.335	63.868	1.00	33.95
	1937	CA	ILE	B	23	-0.830	-8.089	64.495	1.00	33.82
	1938	CB	ILE	B	23	-2.318	-8.139	64.915	1.00	38.56
	1939	CG2	ILE	B	23	-2.645	-6.976	65.811	1.00	36.62
10	1940	CG1	ILE	B	23	-3.202	-8.061	63.673	1.00	39.29
	1941	CD1	ILE	B	23	-4.680	-8.107	63.957	1.00	41.41
	1942	C	ILE	B	23	0.027	-7.726	65.702	1.00	34.13
	1943	O	ILE	B	23	0.252	-8.551	66.590	1.00	32.41
	1944	N	GLY	B	24	0.504	-6.477	65.700	1.00	44.73
15	1945	CA	GLY	B	24	1.346	-5.952	66.765	1.00	45.81
	1946	C	GLY	B	24	0.523	-5.247	67.817	1.00	45.73
	1947	O	GLY	B	24	-0.185	-4.283	67.533	1.00	45.53
	1948	N	ILE	B	25	0.647	-5.706	69.052	1.00	42.38
	1949	CA	ILE	B	25	-0.149	-5.142	70.122	1.00	41.58
20	1950	CB	ILE	B	25	-1.129	-6.221	70.650	1.00	52.65
	1951	CG2	ILE	B	25	-1.847	-5.723	71.902	1.00	54.44
	1952	CG1	ILE	B	25	-2.121	-6.597	69.538	1.00	53.88
	1953	CD1	ILE	B	25	-2.758	-7.956	69.705	1.00	49.67
	1954	C	ILE	B	25	0.623	-4.552	71.288	1.00	40.50
25	1955	O	ILE	B	25	1.365	-5.264	71.983	1.00	39.91
	1956	N	ILE	B	26	0.410	-3.245	71.487	1.00	32.40
	1957	CA	ILE	B	26	1.023	-2.466	72.577	1.00	31.55
	1958	CB	ILE	B	26	1.585	-1.093	72.085	1.00	25.90
	1959	CG2	ILE	B	26	2.341	-0.414	73.213	1.00	21.48
30	1960	CG1	ILE	B	26	2.569	-1.302	70.930	1.00	22.02
	1961	CD1	ILE	B	26	2.977	-0.027	70.225	1.00	17.82
	1962	C	ILE	B	26	-0.040	-2.202	73.658	1.00	30.99
	1963	O	ILE	B	26	-0.712	-1.172	73.659	1.00	28.62
	1964	N	MET	B	27	-0.167	-3.160	74.571	1.00	41.44
35	1965	CA	MET	B	27	-1.139	-3.117	75.661	1.00	40.45
	1966	CB	MET	B	27	-1.240	-4.520	76.287	1.00	21.61
	1967	CG	MET	B	27	-1.282	-5.592	75.241	1.00	13.83
	1968	SD	MET	B	27	-1.504	-7.178	75.938	1.00	19.30
	1969	CE	MET	B	27	0.103	-7.602	76.540	1.00	19.71
40	1970	C	MET	B	27	-0.813	-2.061	76.729	1.00	41.87
	1971	O	MET	B	27	-0.378	-2.384	77.847	1.00	43.35
	1972	N	ASP	B	28	-1.045	-0.800	76.382	1.00	29.88
	1973	CA	ASP	B	28	-0.775	0.295	77.294	1.00	34.13

	1974	CB	ASP	B	28	0.153	1.308	76.624	1.00	54.15
	1975	CG	ASP	B	28	0.627	2.363	77.577	1.00	58.01
	1976	OD1	ASP	B	28	0.216	3.528	77.427	1.00	60.01
	1977	OD2	ASP	B	28	1.400	2.014	78.488	1.00	59.19
5	1978	C	ASP	B	28	-2.041	1.000	77.771	1.00	36.52
	1979	O	ASP	B	28	-3.146	0.707	77.310	1.00	35.77
	1980	N	GLY	B	29	-1.866	1.939	78.698	1.00	63.12
	1981	CA	GLY	B	29	-2.992	2.684	79.230	1.00	66.55
	1982	C	GLY	B	29	-3.588	2.063	80.476	1.00	67.60
10	1983	O	GLY	B	29	-4.499	2.631	81.079	1.00	68.24
	1984	N	ASN	B	30	-3.078	0.899	80.861	1.00	66.36
	1985	CA	ASN	B	30	-3.568	0.207	82.039	1.00	68.38
	1986	CB	ASN	B	30	-2.530	-0.791	82.535	1.00	58.69
	1987	CG	ASN	B	30	-2.591	-2.099	81.795	1.00	58.18
15	1988	OD1	ASN	B	30	-1.676	-2.919	81.876	1.00	57.88
	1989	ND2	ASN	B	30	-3.680	-2.310	81.068	1.00	58.20
	1990	C	ASN	B	30	-3.896	1.175	83.155	1.00	70.84
	1991	O	ASN	B	30	-5.065	1.422	83.441	1.00	72.79
	1992	N	GLY	B	31	-2.854	1.719	83.781	1.00	62.10
20	1993	CA	GLY	B	31	-3.032	2.660	84.876	1.00	64.11
	1994	C	GLY	B	31	-4.227	3.584	84.737	1.00	64.87
	1995	O	GLY	B	31	-5.142	3.536	85.552	1.00	64.57
	1996	N	ARG	B	32	-4.215	4.425	83.708	1.00	71.53
	1997	CA	ARG	B	32	-5.302	5.356	83.459	1.00	75.20
25	1998	CB	ARG	B	32	-5.179	5.956	82.051	1.00	77.54
	1999	CG	ARG	B	32	-4.204	7.119	81.952	1.00	77.74
	2000	CD	ARG	B	32	-2.944	6.768	81.154	1.00	79.03
	2001	NE	ARG	B	32	-3.179	6.751	79.711	1.00	78.76
	2002	CZ	ARG	B	32	-2.233	6.568	78.795	1.00	77.81
30	2003	NH1	ARG	B	32	-0.972	6.381	79.162	1.00	78.00
	2004	NH2	ARG	B	32	-2.546	6.579	77.507	1.00	76.36
	2005	C	ARG	B	32	-6.676	4.706	83.634	1.00	76.60
	2006	O	ARG	B	32	-7.658	5.396	83.924	1.00	76.18
	2007	N	TRP	B	33	-6.737	3.384	83.470	1.00	103.51
35	2008	CA	TRP	B	33	-7.987	2.629	83.609	1.00	105.52
	2009	CB	TRP	B	33	-7.861	1.285	82.901	1.00	62.77
	2010	CG	TRP	B	33	-9.127	0.503	82.840	1.00	62.81
	2011	CD2	TRP	B	33	-9.455	-0.669	83.606	1.00	62.73
	2012	CE2	TRP	B	33	-10.702	-1.136	83.142	1.00	62.39
40	2013	CE3	TRP	B	33	-8.812	-1.373	84.635	1.00	62.13
	2014	CD1	TRP	B	33	-10.169	0.701	81.981	1.00	62.96
	2015	NE1	TRP	B	33	-11.117	-0.283	82.153	1.00	61.92
	2016	CZ2	TRP	B	33	-11.317	-2.276	83.669	1.00	60.94

	2017	CZ3	TRP	B	33	-9.434	-2.512	85.157	1.00	60.65
	2018	CH2	TRP	B	33	-10.666	-2.946	84.671	1.00	59.84
	2019	C	TRP	B	33	-8.357	2.384	85.075	1.00	106.64
	2020	O	TRP	B	33	-9.452	2.739	85.524	1.00	107.39
5	2021	N	ALA	B	34	-7.446	1.757	85.812	1.00	88.38
	2022	CA	ALA	B	34	-7.670	1.486	87.221	1.00	88.89
	2023	CB	ALA	B	34	-6.387	0.966	87.853	1.00	72.86
	2024	C	ALA	B	34	-8.121	2.777	87.909	1.00	89.23
	2025	O	ALA	B	34	-8.953	2.757	88.813	1.00	90.02
10	2026	N	LYS	B	35	-7.571	3.903	87.467	1.00	69.65
	2027	CA	LYS	B	35	-7.921	5.192	88.039	1.00	70.39
	2028	CB	LYS	B	35	-7.142	6.319	87.377	1.00	70.75
	2029	CG	LYS	B	35	-7.455	7.668	87.980	1.00	70.72
	2030	CD	LYS	B	35	-6.750	8.792	87.242	1.00	71.05
15	2031	CE	LYS	B	35	-6.735	10.086	88.071	1.00	71.73
	2032	NZ	LYS	B	35	-5.928	9.964	89.330	1.00	72.08
	2033	C	LYS	B	35	-9.396	5.437	87.838	1.00	71.29
	2034	O	LYS	B	35	-10.167	5.322	88.777	1.00	71.56
	2035	N	LYS	B	36	-9.786	5.776	86.612	1.00	79.02
20	2036	CA	LYS	B	36	-11.189	6.034	86.294	1.00	80.84
	2037	CB	LYS	B	36	-11.451	5.817	84.801	1.00	99.56
	2038	CG	LYS	B	36	-10.465	6.499	83.869	1.00	100.17
	2039	CD	LYS	B	36	-10.473	8.005	84.014	1.00	100.22
	2040	CE	LYS	B	36	-9.414	8.627	83.118	1.00	100.12
25	2041	NZ	LYS	B	36	-9.350	10.106	83.267	1.00	98.40
	2042	C	LYS	B	36	-12.103	5.108	87.101	1.00	81.22
	2043	O	LYS	B	36	-13.009	5.559	87.795	1.00	80.91
	2044	N	ARG	B	37	-11.858	3.809	87.010	1.00	94.69
	2045	CA	ARG	B	37	-12.666	2.848	87.741	1.00	95.89
30	2046	CB	ARG	B	37	-12.681	1.518	86.984	1.00	94.83
	2047	CG	ARG	B	37	-13.043	1.673	85.510	1.00	93.94
	2048	CD	ARG	B	37	-13.101	0.340	84.768	1.00	93.08
	2049	NE	ARG	B	37	-14.256	-0.475	85.144	1.00	91.80
	2050	CZ	ARG	B	37	-14.302	-1.294	86.190	1.00	90.45
35	2051	NH1	ARG	B	37	-13.250	-1.434	86.990	1.00	90.29
	2052	NH2	ARG	B	37	-15.415	-1.968	86.445	1.00	89.39
	2053	C	ARG	B	37	-12.085	2.677	89.147	1.00	97.33
	2054	O	ARG	B	37	-12.011	1.569	89.687	1.00	97.61
	2055	N	MET	B	38	-11.684	3.805	89.725	1.00	91.53
40	2056	CA	MET	B	38	-11.085	3.887	91.054	1.00	92.11
	2057	CB	MET	B	38	-12.076	4.556	92.008	1.00	93.22
	2058	CG	MET	B	38	-12.462	5.948	91.530	1.00	94.17
	2059	SD	MET	B	38	-13.037	7.063	92.811	1.00	95.59

	2060	CE	MET	B	38	-14.801	7.030	92.538	1.00	94.62
	2061	C	MET	B	38	-10.529	2.587	91.645	1.00	92.10
	2062	O	MET	B	38	-11.264	1.745	92.155	1.00	92.13
	2063	N	GLN	B	39	-9.207	2.461	91.572	1.00	81.20
5	2064	CA	GLN	B	39	-8.469	1.295	92.053	1.00	81.39
	2065	CB	GLN	B	39	-8.767	0.097	91.157	1.00	92.88
	2066	CG	GLN	B	39	-10.150	-0.474	91.255	1.00	94.20
	2067	CD	GLN	B	39	-10.186	-1.696	92.132	1.00	94.58
	2068	OE1	GLN	B	39	-11.172	-2.435	92.144	1.00	93.61
10	2069	NE2	GLN	B	39	-9.106	-1.923	92.875	1.00	94.98
	2070	C	GLN	B	39	-6.964	1.593	91.947	1.00	81.67
	2071	O	GLN	B	39	-6.565	2.596	91.358	1.00	81.59
	2072	N	PRO	B	40	-6.111	0.722	92.517	1.00	99.47
	2073	CD	PRO	B	40	-6.451	-0.298	93.529	1.00	59.47
15	2074	CA	PRO	B	40	-4.654	0.929	92.444	1.00	100.02
	2075	CB	PRO	B	40	-4.135	0.159	93.661	1.00	59.71
	2076	CG	PRO	B	40	-5.117	-0.981	93.780	1.00	59.56
	2077	C	PRO	B	40	-4.063	0.411	91.107	1.00	101.07
	2078	O	PRO	B	40	-4.734	-0.312	90.361	1.00	100.64
20	2079	N	ARG	B	41	-2.815	0.780	90.807	1.00	141.54
	2080	CA	ARG	B	41	-2.157	0.357	89.561	1.00	141.61
	2081	CB	ARG	B	41	-0.910	1.208	89.281	1.00	87.25
	2082	CG	ARG	B	41	-1.167	2.453	88.434	1.00	86.59
	2083	CD	ARG	B	41	0.144	3.118	88.026	1.00	86.60
25	2084	NE	ARG	B	41	0.921	2.302	87.096	1.00	86.22
	2085	CZ	ARG	B	41	0.717	2.269	85.784	1.00	85.79
	2086	NH1	ARG	B	41	-0.237	3.011	85.242	1.00	84.40
	2087	NH2	ARG	B	41	1.465	1.492	85.014	1.00	84.49
	2088	C	ARG	B	41	-1.762	-1.116	89.507	1.00	141.89
30	2089	O	ARG	B	41	-0.588	-1.453	89.339	1.00	142.57
	2090	N	VAL	B	42	-2.756	-1.985	89.639	1.00	90.29
	2091	CA	VAL	B	42	-2.550	-3.426	89.594	1.00	89.85
	2092	CB	VAL	B	42	-2.078	-3.986	90.952	1.00	84.26
	2093	CG1	VAL	B	42	-0.679	-3.496	91.259	1.00	83.43
35	2094	CG2	VAL	B	42	-3.033	-3.560	92.049	1.00	84.11
	2095	C	VAL	B	42	-3.888	-4.053	89.239	1.00	90.28
	2096	O	VAL	B	42	-3.957	-5.219	88.836	1.00	91.05
	2097	N	PHE	B	43	-4.951	-3.264	89.403	1.00	98.05
	2098	CA	PHE	B	43	-6.306	-3.707	89.088	1.00	97.79
40	2099	CB	PHE	B	43	-7.326	-3.090	90.051	1.00	118.68
	2100	CG	PHE	B	43	-8.656	-3.802	90.067	1.00	119.62
	2101	CD1	PHE	B	43	-8.780	-5.058	90.659	1.00	120.15
	2102	CD2	PHE	B	43	-9.784	-3.220	89.490	1.00	120.97

	2103	CE1	PHE	B	43	-10.008	-5.726	90.679	1.00121.23
	2104	CE2	PHE	B	43	-11.016	-3.877	89.504	1.00122.66
	2105	CZ	PHE	B	43	-11.127	-5.133	90.101	1.00122.54
	2106	C	PHE	B	43	-6.598	-3.250	87.664	1.00 96.64
5	2107	O	PHE	B	43	-7.752	-3.096	87.264	1.00 97.00
	2108	N	GLY	B	44	-5.522	-3.015	86.918	1.00 88.55
	2109	CA	GLY	B	44	-5.617	-2.600	85.530	1.00 85.20
	2110	C	GLY	B	44	-4.860	-3.654	84.751	1.00 82.76
	2111	O	GLY	B	44	-5.278	-4.117	83.691	1.00 82.40
10	2112	N	HIS	B	45	-3.721	-4.038	85.300	1.00 63.82
	2113	CA	HIS	B	45	-2.924	-5.065	84.687	1.00 62.64
	2114	CB	HIS	B	45	-1.584	-5.164	85.410	1.00 65.12
	2115	CG	HIS	B	45	-0.769	-3.911	85.311	1.00 65.52
	2116	CD2	HIS	B	45	-0.695	-2.974	84.335	1.00 64.09
15	2117	ND1	HIS	B	45	0.086	-3.491	86.308	1.00 65.46
	2118	CE1	HIS	B	45	0.646	-2.348	85.951	1.00 64.57
	2119	NE2	HIS	B	45	0.189	-2.014	84.757	1.00 63.16
	2120	C	HIS	B	45	-3.740	-6.341	84.842	1.00 62.02
	2121	O	HIS	B	45	-3.728	-7.211	83.967	1.00 62.48
20	2122	N	LYS	B	46	-4.479	-6.431	85.946	1.00 61.20
	2123	CA	LYS	B	46	-5.303	-7.606	86.215	1.00 59.45
	2124	CB	LYS	B	46	-6.043	-7.450	87.545	1.00 82.81
	2125	CG	LYS	B	46	-6.610	-8.756	88.065	1.00 84.51
	2126	CD	LYS	B	46	-7.524	-8.566	89.262	1.00 85.01
25	2127	CE	LYS	B	46	-7.977	-9.917	89.805	1.00 84.85
	2128	NZ	LYS	B	46	-8.478	-10.821	88.724	1.00 84.70
	2129	C	LYS	B	46	-6.306	-7.800	85.081	1.00 57.37
	2130	O	LYS	B	46	-6.408	-8.878	84.505	1.00 56.25
	2131	N	ALA	B	47	-7.053	-6.755	84.759	1.00 52.63
30	2132	CA	ALA	B	47	-8.011	-6.861	83.675	1.00 52.93
	2133	CB	ALA	B	47	-8.868	-5.611	83.588	1.00 60.24
	2134	C	ALA	B	47	-7.158	-6.985	82.443	1.00 53.48
	2135	O	ALA	B	47	-7.557	-7.588	81.449	1.00 53.23
	2136	N	GLY	B	48	-5.972	-6.396	82.522	1.00 66.56
35	2137	CA	GLY	B	48	-5.056	-6.449	81.406	1.00 67.38
	2138	C	GLY	B	48	-5.073	-7.831	80.796	1.00 67.72
	2139	O	GLY	B	48	-5.451	-7.993	79.635	1.00 68.41
	2140	N	MET	B	49	-4.673	-8.829	81.581	1.00 79.25
	2141	CA	MET	B	49	-4.653	-10.197	81.096	1.00 81.10
40	2142	CB	MET	B	49	-4.373	-11.181	82.228	1.00 79.82
	2143	CG	MET	B	49	-2.946	-11.218	82.715	1.00 81.45
	2144	SD	MET	B	49	-2.730	-12.516	83.968	1.00 85.43
	2145	CE	MET	B	49	-1.616	-13.592	83.168	1.00 83.64

	2146	C	MET	B	49	-5.995	-10.534	80.473	1.00	81.46
	2147	O	MET	B	49	-6.052	-11.142	79.405	1.00	81.66
	2148	N	GLU	B	50	-7.077	-10.138	81.139	1.00	71.82
	2149	CA	GLU	B	50	-8.414	-10.421	80.628	1.00	70.76
5	2150	CB	GLU	B	50	-9.486	-9.793	81.528	1.00	97.62
	2151	CG	GLU	B	50	-10.926	-10.156	81.142	1.00	99.47
	2152	CD	GLU	B	50	-11.259	-11.619	81.390	1.00	100.36
	2153	OE1	GLU	B	50	-12.328	-12.078	80.935	1.00	100.03
	2154	OE2	GLU	B	50	-10.452	-12.309	82.047	1.00	99.68
10	2155	C	GLU	B	50	-8.531	-9.873	79.214	1.00	68.88
	2156	O	GLU	B	50	-8.764	-10.618	78.264	1.00	68.46
	2157	N	ALA	B	51	-8.354	-8.564	79.086	1.00	62.81
	2158	CA	ALA	B	51	-8.432	-7.905	77.789	1.00	61.79
	2159	CB	ALA	B	51	-7.819	-6.517	77.879	1.00	46.87
15	2160	C	ALA	B	51	-7.708	-8.739	76.739	1.00	61.23
	2161	O	ALA	B	51	-8.218	-8.945	75.640	1.00	60.66
	2162	N	LEU	B	52	-6.514	-9.216	77.084	1.00	83.57
	2163	CA	LEU	B	52	-5.728	-10.042	76.172	1.00	82.15
	2164	CB	LEU	B	52	-4.370	-10.407	76.798	1.00	56.18
20	2165	CG	LEU	B	52	-3.353	-11.210	75.965	1.00	54.09
	2166	CD1	LEU	B	52	-2.925	-10.405	74.754	1.00	53.03
	2167	CD2	LEU	B	52	-2.141	-11.552	76.806	1.00	52.15
	2168	C	LEU	B	52	-6.520	-11.312	75.892	1.00	81.48
	2169	O	LEU	B	52	-6.957	-11.538	74.762	1.00	82.41
25	2170	N	GLN	B	53	-6.723	-12.116	76.941	1.00	67.96
	2171	CA	GLN	B	53	-7.445	-13.389	76.849	1.00	64.60
	2172	CB	GLN	B	53	-7.975	-13.824	78.215	1.00	47.34
	2173	CG	GLN	B	53	-8.439	-15.274	78.231	1.00	48.38
	2174	CD	GLN	B	53	-7.327	-16.255	77.871	1.00	48.32
30	2175	OE1	GLN	B	53	-6.665	-16.103	76.844	1.00	50.08
	2176	NE2	GLN	B	53	-7.124	-17.270	78.709	1.00	45.96
	2177	C	GLN	B	53	-8.596	-13.391	75.865	1.00	63.50
	2178	O	GLN	B	53	-8.851	-14.394	75.217	1.00	61.67
	2179	N	THR	B	54	-9.290	-12.270	75.745	1.00	76.29
35	2180	CA	THR	B	54	-10.401	-12.203	74.816	1.00	77.08
	2181	CB	THR	B	54	-11.461	-11.177	75.285	1.00	61.70
	2182	OG1	THR	B	54	-11.135	-9.874	74.790	1.00	63.58
	2183	CG2	THR	B	54	-11.507	-11.129	76.806	1.00	60.45
	2184	C	THR	B	54	-9.926	-11.862	73.396	1.00	77.03
40	2185	O	THR	B	54	-10.481	-12.376	72.421	1.00	78.84
	2186	N	VAL	B	55	-8.903	-11.015	73.265	1.00	59.23
	2187	CA	VAL	B	55	-8.408	-10.660	71.934	1.00	58.00
	2188	CB	VAL	B	55	-7.476	-9.405	71.940	1.00	51.37

	2189	CG1	VAL	B	55	-7.026	-9.102	70.525	1.00	50.53
	2190	CG2	VAL	B	55	-8.188	-8.188	72.504	1.00	50.40
	2191	C	VAL	B	55	-7.610	-11.821	71.361	1.00	57.34
	2192	O	VAL	B	55	-7.819	-12.226	70.223	1.00	57.56
5	2193	N	THR	B	56	-6.699	-12.362	72.160	1.00	37.64
	2194	CA	THR	B	56	-5.866	-13.453	71.707	1.00	37.95
	2195	CB	THR	B	56	-4.785	-13.832	72.769	1.00	44.07
	2196	OG1	THR	B	56	-4.186	-15.085	72.423	1.00	43.93
	2197	CG2	THR	B	56	-5.376	-13.941	74.156	1.00	44.86
10	2198	C	THR	B	56	-6.694	-14.661	71.327	1.00	40.56
	2199	O	THR	B	56	-6.175	-15.628	70.767	1.00	41.59
	2200	N	LYS	B	57	-7.987	-14.611	71.623	1.00	84.82
	2201	CA	LYS	B	57	-8.895	-15.706	71.274	1.00	87.03
	2202	CB	LYS	B	57	-9.887	-15.977	72.418	1.00	87.57
15	2203	CG	LYS	B	57	-9.386	-16.968	73.480	1.00	89.45
	2204	CD	LYS	B	57	-10.319	-17.045	74.700	1.00	90.23
	2205	CE	LYS	B	57	-11.744	-17.458	74.339	1.00	91.29
	2206	NZ	LYS	B	57	-12.654	-17.472	75.526	1.00	91.63
	2207	C	LYS	B	57	-9.646	-15.288	70.011	1.00	86.89
20	2208	O	LYS	B	57	-9.739	-16.037	69.031	1.00	86.65
	2209	N	ALA	B	58	-10.180	-14.076	70.055	1.00	67.53
	2210	CA	ALA	B	58	-10.897	-13.527	68.929	1.00	68.45
	2211	CB	ALA	B	58	-11.269	-12.066	69.200	1.00	41.64
	2212	C	ALA	B	58	-9.974	-13.624	67.729	1.00	70.12
25	2213	O	ALA	B	58	-10.342	-14.180	66.701	1.00	70.67
	2214	N	ALA	B	59	-8.760	-13.105	67.878	1.00	66.34
	2215	CA	ALA	B	59	-7.795	-13.121	66.792	1.00	66.05
	2216	CB	ALA	B	59	-6.532	-12.410	67.207	1.00	50.09
	2217	C	ALA	B	59	-7.474	-14.530	66.304	1.00	66.88
30	2218	O	ALA	B	59	-7.297	-14.731	65.099	1.00	66.90
	2219	N	ASN	B	60	-7.390	-15.507	67.213	1.00	51.60
	2220	CA	ASN	B	60	-7.104	-16.875	66.780	1.00	52.22
	2221	CB	ASN	B	60	-6.854	-17.810	67.960	1.00	61.88
	2222	CG	ASN	B	60	-6.720	-19.280	67.527	1.00	61.60
35	2223	OD1	ASN	B	60	-5.985	-19.612	66.584	1.00	58.76
	2224	ND2	ASN	B	60	-7.430	-20.165	68.227	1.00	60.65
	2225	C	ASN	B	60	-8.297	-17.372	65.995	1.00	53.73
	2226	O	ASN	B	60	-8.222	-18.391	65.311	1.00	53.33
	2227	N	LYS	B	61	-9.400	-16.634	66.101	1.00	95.49
40	2228	CA	LYS	B	61	-10.635	-16.955	65.394	1.00	96.30
	2229	CB	LYS	B	61	-11.848	-16.527	66.223	1.00	88.98
	2230	CG	LYS	B	61	-13.132	-16.374	65.404	1.00	90.20
	2231	CD	LYS	B	61	-14.339	-16.018	66.276	1.00	90.77

	2232	CE	LYS B	61	-14.195	-14.644	66.925	1.00	89.85
	2233	NZ	LYS B	61	-15.255	-14.374	67.945	1.00	88.15
	2234	C	LYS B	61	-10.691	-16.264	64.036	1.00	95.56
	2235	O	LYS B	61	-10.621	-16.918	63.001	1.00	96.30
5	2236	N	LEU B	62	-10.815	-14.939	64.055	1.00	66.60
	2237	CA	LEU B	62	-10.897	-14.136	62.838	1.00	64.51
	2238	CB	LEU B	62	-10.819	-12.643	63.174	1.00	69.48
	2239	CG	LEU B	62	-11.977	-12.000	63.941	1.00	69.62
	2240	CD1	LEU B	62	-11.949	-12.413	65.407	1.00	68.87
10	2241	CD2	LEU B	62	-11.867	-10.489	63.815	1.00	69.12
	2242	C	LEU B	62	-9.875	-14.442	61.736	1.00	62.85
	2243	O	LEU B	62	-9.966	-13.876	60.645	1.00	63.30
	2244	N	GLY B	63	-8.901	-15.309	62.006	1.00	53.05
	2245	CA	GLY B	63	-7.928	-15.646	60.974	1.00	50.87
15	2246	C	GLY B	63	-6.470	-15.252	61.152	1.00	48.86
	2247	O	GLY B	63	-5.592	-15.877	60.548	1.00	49.29
	2248	N	VAL B	64	-6.220	-14.227	61.973	1.00	42.54
	2249	CA	VAL B	64	-4.877	-13.703	62.251	1.00	39.17
	2250	CB	VAL B	64	-4.914	-12.615	63.335	1.00	46.78
20	2251	CG1	VAL B	64	-3.506	-12.190	63.699	1.00	45.63
	2252	CG2	VAL B	64	-5.699	-11.422	62.836	1.00	45.54
	2253	C	VAL B	64	-3.916	-14.775	62.703	1.00	37.14
	2254	O	VAL B	64	-4.107	-15.374	63.755	1.00	34.75
	2255	N	LYS B	65	-2.874	-14.972	61.895	1.00	60.65
25	2256	CA	LYS B	65	-1.828	-15.970	62.113	1.00	58.92
	2257	CB	LYS B	65	-0.966	-16.074	60.851	1.00	54.39
	2258	CG	LYS B	65	-1.609	-16.794	59.672	1.00	57.12
	2259	CD	LYS B	65	-1.613	-18.310	59.885	1.00	59.89
	2260	CE	LYS B	65	-1.931	-19.090	58.611	1.00	59.99
30	2261	NZ	LYS B	65	-1.870	-20.564	58.836	1.00	56.81
	2262	C	LYS B	65	-0.911	-15.750	63.322	1.00	57.23
	2263	O	LYS B	65	-0.540	-16.709	64.011	1.00	58.47
	2264	N	VAL B	66	-0.529	-14.497	63.567	1.00	48.68
	2265	CA	VAL B	66	0.365	-14.168	64.682	1.00	47.17
35	2266	CB	VAL B	66	1.866	-14.139	64.243	1.00	38.98
	2267	CG1	VAL B	66	2.737	-13.732	65.405	1.00	38.59
	2268	CG2	VAL B	66	2.305	-15.490	63.732	1.00	38.64
	2269	C	VAL B	66	0.083	-12.808	65.306	1.00	45.92
	2270	O	VAL B	66	-0.203	-11.838	64.602	1.00	47.39
40	2271	N	ILE B	67	0.148	-12.746	66.632	1.00	29.82
	2272	CA	ILE B	67	-0.018	-11.481	67.321	1.00	29.07
	2273	CB	ILE B	67	-1.405	-11.346	67.992	1.00	43.61
	2274	CG2	ILE B	67	-2.490	-11.664	66.978	1.00	44.35



	2275	CG1	ILE	B	67	-1.505	-12.231	69.235	1.00	45.50
	2276	CD1	ILE	B	67	-1.183	-11.497	70.534	1.00	45.09
	2277	C	ILE	B	67	1.117	-11.388	68.358	1.00	29.05
	2278	O	ILE	B	67	1.382	-12.344	69.110	1.00	25.41
5	2279	N	THR	B	68	1.822	-10.253	68.344	1.00	36.80
	2280	CA	THR	B	68	2.931	-10.006	69.256	1.00	33.90
	2281	CB	THR	B	68	4.226	-9.635	68.485	1.00	29.12
	2282	OG1	THR	B	68	4.684	-10.781	67.751	1.00	30.17
	2283	CG2	THR	B	68	5.319	-9.192	69.441	1.00	27.04
10	2284	C	THR	B	68	2.505	-8.875	70.164	1.00	33.51
	2285	O	THR	B	68	2.225	-7.758	69.710	1.00	30.56
	2286	N	VAL	B	69	2.436	-9.184	71.455	1.00	26.40
	2287	CA	VAL	B	69	2.008	-8.204	72.454	1.00	28.99
	2288	CB	VAL	B	69	1.015	-8.807	73.453	1.00	37.15
15	2289	CG1	VAL	B	69	-0.389	-8.722	72.899	1.00	36.17
	2290	CG2	VAL	B	69	1.418	-10.247	73.761	1.00	37.07
	2291	C	VAL	B	69	3.125	-7.607	73.277	1.00	28.98
	2292	O	VAL	B	69	4.024	-8.314	73.762	1.00	26.82
	2293	N	TYR	B	70	3.025	-6.300	73.463	1.00	27.67
20	2294	CA	TYR	B	70	4.006	-5.577	74.229	1.00	30.51
	2295	CB	TYR	B	70	4.026	-4.135	73.750	1.00	33.17
	2296	CG	TYR	B	70	5.353	-3.462	73.934	1.00	32.94
	2297	CD1	TYR	B	70	6.439	-4.147	74.473	1.00	31.43
	2298	CE1	TYR	B	70	7.639	-3.517	74.670	1.00	29.58
25	2299	CD2	TYR	B	70	5.517	-2.133	73.596	1.00	28.94
	2300	CE2	TYR	B	70	6.710	-1.505	73.790	1.00	30.65
	2301	CZ	TYR	B	70	7.758	-2.196	74.326	1.00	30.60
	2302	OH	TYR	B	70	8.930	-1.537	74.521	1.00	30.30
	2303	C	TYR	B	70	3.654	-5.673	75.723	1.00	34.02
30	2304	O	TYR	B	70	2.864	-4.891	76.259	1.00	33.42
	2305	N	ALA	B	71	4.261	-6.645	76.387	1.00	45.31
	2306	CA	ALA	B	71	4.010	-6.898	77.794	1.00	48.29
	2307	CB	ALA	B	71	4.290	-8.363	78.088	1.00	41.40
	2308	C	ALA	B	71	4.786	-6.020	78.772	1.00	50.20
35	2309	O	ALA	B	71	4.192	-5.331	79.601	1.00	50.83
	2310	N	PHE	B	72	6.117	-6.073	78.688	1.00	55.08
	2311	CA	PHE	B	72	7.011	-5.305	79.567	1.00	55.92
	2312	CB	PHE	B	72	7.424	-6.167	80.763	1.00	50.50
	2313	CG	PHE	B	72	7.970	-5.385	81.935	1.00	49.88
40	2314	CD1	PHE	B	72	7.130	-4.597	82.716	1.00	50.76
	2315	CD2	PHE	B	72	9.322	-5.467	82.274	1.00	49.65
	2316	CE1	PHE	B	72	7.625	-3.912	83.811	1.00	50.29
	2317	CE2	PHE	B	72	9.820	-4.786	83.362	1.00	49.87

	2318	CZ	PHE B	72	8.971	-4.008	84.134	1.00	49.55
	2319	C	PHE B	72	8.263	-4.888	78.797	1.00	56.53
	2320	O	PHE B	72	9.014	-5.747	78.324	1.00	54.61
	2321	N	SER B	73	8.481	-3.576	78.684	1.00	60.57
5	2322	CA	SER B	73	9.636	-3.036	77.965	1.00	62.60
	2323	CB	SER B	73	9.285	-1.705	77.295	1.00	75.13
	2324	OG	SER B	73	9.047	-0.678	78.242	1.00	76.91
	2325	C	SER B	73	10.841	-2.826	78.872	1.00	63.53
	2326	O	SER B	73	10.711	-2.363	80.001	1.00	64.98
10	2327	N	THR B	74	12.012	-3.178	78.357	1.00	52.25
	2328	CA	THR B	74	13.263	-3.036	79.082	1.00	52.50
	2329	CB	THR B	74	14.486	-3.228	78.118	1.00	45.83
	2330	OG1	THR B	74	14.254	-2.553	76.867	1.00	43.16
	2331	CG2	THR B	74	14.716	-4.708	77.842	1.00	46.92
15	2332	C	THR B	74	13.371	-1.685	79.793	1.00	54.40
	2333	O	THR B	74	14.142	-1.538	80.737	1.00	54.29
	2334	N	GLU B	75	12.592	-0.708	79.339	1.00	49.84
	2335	CA	GLU B	75	12.608	0.625	79.932	1.00	52.76
	2336	CB	GLU B	75	12.311	1.704	78.881	1.00	52.24
20	2337	CG	GLU B	75	13.315	1.833	77.744	1.00	49.68
	2338	CD	GLU B	75	13.231	0.694	76.747	1.00	49.37
	2339	OE1	GLU B	75	13.822	-0.366	77.008	1.00	49.15
	2340	OE2	GLU B	75	12.566	0.851	75.702	1.00	48.77
	2341	C	GLU B	75	11.576	0.751	81.046	1.00	56.12
25	2342	O	GLU B	75	11.457	1.805	81.670	1.00	56.93
	2343	N	ASN B	76	10.819	-0.310	81.299	1.00	77.79
	2344	CA	ASN B	76	9.809	-0.239	82.344	1.00	81.56
	2345	CB	ASN B	76	8.525	-0.951	81.903	1.00	85.37
	2346	CG	ASN B	76	7.638	-0.056	81.055	1.00	85.73
30	2347	OD1	ASN B	76	7.471	1.132	81.358	1.00	86.16
	2348	ND2	ASN B	76	7.060	-0.617	79.995	1.00	85.50
	2349	C	ASN B	76	10.262	-0.740	83.710	1.00	84.02
	2350	O	ASN B	76	9.475	-1.272	84.485	1.00	84.31
	2351	N	TRP B	77	11.539	-0.552	84.008	1.00	100.98
35	2352	CA	TRP B	77	12.066	-0.950	85.298	1.00	103.06
	2353	CB	TRP B	77	13.422	-1.639	85.120	1.00	100.08
	2354	CG	TRP B	77	13.328	-3.151	85.188	1.00	102.77
	2355	CD2	TRP B	77	13.394	-4.072	84.092	1.00	103.22
	2356	CE2	TRP B	77	13.235	-5.372	84.627	1.00	103.87
40	2357	CE3	TRP B	77	13.570	-3.926	82.711	1.00	103.80
	2358	CD1	TRP B	77	13.136	-3.912	86.310	1.00	103.91
	2359	NE1	TRP B	77	13.080	-5.246	85.980	1.00	104.55
	2360	CZ2	TRP B	77	13.249	-6.514	83.832	1.00	104.90

	2361	CZ3	TRP	B	77	13.581	-5.065	81.918	1.00104.96
	2362	CH2	TRP	B	77	13.421	-6.342	82.483	1.00106.06
	2363	C	TRP	B	77	12.174	0.315	86.148	1.00103.61
	2364	O	TRP	B	77	12.478	0.264	87.338	1.00104.36
5	2365	N	THR	B	78	11.897	1.452	85.517	1.00 67.76
	2366	CA	THR	B	78	11.929	2.755	86.178	1.00 68.98
	2367	CB	THR	B	78	12.236	3.891	85.156	1.00 61.27
	2368	OG1	THR	B	78	11.110	4.082	84.290	1.00 60.24
	2369	CG2	THR	B	78	13.449	3.530	84.303	1.00 59.39
10	2370	C	THR	B	78	10.537	2.964	86.778	1.00 69.99
	2371	O	THR	B	78	10.022	4.084	86.869	1.00 69.56
	2372	N	ARG	B	79	9.941	1.850	87.180	1.00 73.72
	2373	CA	ARG	B	79	8.603	1.832	87.751	1.00 76.03
	2374	CB	ARG	B	79	7.771	0.756	87.034	1.00 80.00
15	2375	CG	ARG	B	79	6.391	1.197	86.550	1.00 82.26
	2376	CD	ARG	B	79	6.478	2.146	85.368	1.00 84.20
	2377	NE	ARG	B	79	6.113	1.520	84.097	1.00 86.95
	2378	CZ	ARG	B	79	4.927	0.976	83.837	1.00 89.12
	2379	NH1	ARG	B	79	3.976	0.969	84.761	1.00 89.94
20	2380	NH2	ARG	B	79	4.685	0.452	82.643	1.00 90.19
	2381	C	ARG	B	79	8.703	1.517	89.249	1.00 76.04
	2382	O	ARG	B	79	9.733	1.026	89.709	1.00 75.74
	2383	N	PRO	B	80	7.636	1.800	90.024	1.00 79.82
	2384	CD	PRO	B	80	6.375	2.454	89.636	1.00 73.77
25	2385	CA	PRO	B	80	7.634	1.535	91.459	1.00 80.67
	2386	CB	PRO	B	80	6.179	1.769	91.845	1.00 73.72
	2387	CG	PRO	B	80	5.810	2.890	90.980	1.00 73.71
	2388	C	PRO	B	80	8.115	0.130	91.802	1.00 82.00
	2389	O	PRO	B	80	7.709	-0.859	91.187	1.00 81.64
30	2390	N	ASP	B	81	8.986	0.080	92.804	1.00121.28
	2391	CA	ASP	B	81	9.597	-1.141	93.301	1.00122.10
	2392	CB	ASP	B	81	10.239	-0.855	94.657	1.00120.79
	2393	CG	ASP	B	81	11.310	-1.850	95.011	1.00122.23
	2394	OD1	ASP	B	81	11.021	-3.061	94.987	1.00122.99
35	2395	OD2	ASP	B	81	12.442	-1.420	95.317	1.00123.05
	2396	C	ASP	B	81	8.631	-2.313	93.424	1.00121.97
	2397	O	ASP	B	81	8.986	-3.446	93.105	1.00121.97
	2398	N	GLN	B	82	7.414	-2.049	93.888	1.00 95.10
	2399	CA	GLN	B	82	6.435	-3.120	94.044	1.00 95.24
40	2400	CB	GLN	B	82	5.402	-2.756	95.109	1.00 96.25
	2401	CG	GLN	B	82	5.943	-2.900	96.534	1.00 97.17
	2402	CD	GLN	B	82	6.653	-4.241	96.776	1.00 97.46
	2403	OE1	GLN	B	82	7.740	-4.490	96.246	1.00 97.11

	2404	NE2	GLN	B	82	6.033	-5.106	97.575	1.00	97.19
	2405	C	GLN	B	82	5.756	-3.522	92.747	1.00	94.98
	2406	O	GLN	B	82	5.577	-4.711	92.487	1.00	94.54
	2407	N	GLU	B	83	5.359	-2.551	91.932	1.00	120.68
5	2408	CA	GLU	B	83	4.778	-2.909	90.648	1.00	120.50
	2409	CB	GLU	B	83	4.324	-1.667	89.877	1.00	93.98
	2410	CG	GLU	B	83	3.731	-1.984	88.508	1.00	93.63
	2411	CD	GLU	B	83	3.334	-0.741	87.736	1.00	93.74
	2412	OE1	GLU	B	83	3.083	-0.849	86.521	1.00	93.84
10	2413	OE2	GLU	B	83	3.267	0.346	88.340	1.00	94.14
	2414	C	GLU	B	83	5.996	-3.545	89.978	1.00	120.39
	2415	O	GLU	B	83	7.087	-3.506	90.546	1.00	121.16
	2416	N	VAL	B	84	5.839	-4.110	88.785	1.00	101.60
	2417	CA	VAL	B	84	6.951	-4.774	88.089	1.00	100.63
15	2418	CB	VAL	B	84	8.197	-3.844	87.882	1.00	66.48
	2419	CG1	VAL	B	84	7.812	-2.385	88.071	1.00	65.73
	2420	CG2	VAL	B	84	9.342	-4.253	88.806	1.00	65.12
	2421	C	VAL	B	84	7.366	-6.000	88.902	1.00	100.20
	2422	O	VAL	B	84	7.736	-7.033	88.348	1.00	100.66
20	2423	N	LYS	B	85	7.323	-5.866	90.223	1.00	100.82
	2424	CA	LYS	B	85	7.634	-6.969	91.113	1.00	100.07
	2425	CB	LYS	B	85	7.884	-6.461	92.529	1.00	90.57
	2426	CG	LYS	B	85	7.988	-7.552	93.577	1.00	90.50
	2427	CD	LYS	B	85	8.244	-6.935	94.942	1.00	92.14
25	2428	CE	LYS	B	85	8.266	-7.970	96.056	1.00	92.89
	2429	NZ	LYS	B	85	8.412	-7.328	97.397	1.00	92.61
	2430	C	LYS	B	85	6.335	-7.742	91.065	1.00	99.73
	2431	O	LYS	B	85	6.316	-8.970	91.066	1.00	99.77
	2432	N	PHE	B	86	5.248	-6.979	91.003	1.00	102.16
30	2433	CA	PHE	B	86	3.894	-7.509	90.924	1.00	101.13
	2434	CB	PHE	B	86	2.893	-6.409	91.278	1.00	113.66
	2435	CG	PHE	B	86	1.509	-6.649	90.743	1.00	114.40
	2436	CD1	PHE	B	86	0.714	-7.668	91.255	1.00	114.81
	2437	CD2	PHE	B	86	1.001	-5.851	89.724	1.00	114.98
35	2438	CE1	PHE	B	86	-0.571	-7.888	90.759	1.00	114.89
	2439	CE2	PHE	B	86	-0.282	-6.061	89.220	1.00	115.52
	2440	CZ	PHE	B	86	-1.070	-7.082	89.740	1.00	115.63
	2441	C	PHE	B	86	3.630	-7.989	89.502	1.00	100.03
	2442	O	PHE	B	86	2.933	-8.981	89.278	1.00	99.84
40	2443	N	ILE	B	87	4.197	-7.262	88.547	1.00	97.93
	2444	CA	ILE	B	87	4.039	-7.570	87.136	1.00	95.43
	2445	CB	ILE	B	87	4.503	-6.380	86.285	1.00	81.14
	2446	CG2	ILE	B	87	4.756	-6.811	84.847	1.00	80.92

	2447	CG1	ILE	B	87	3.457	-5.267	86.400	1.00	80.86
	2448	CD1	ILE	B	87	3.761	-4.026	85.599	1.00	80.16
	2449	C	ILE	B	87	4.747	-8.848	86.706	1.00	94.34
	2450	O	ILE	B	87	4.154	-9.659	86.006	1.00	94.45
5	2451	N	MET	B	88	5.999	-9.038	87.115	1.00	74.37
	2452	CA	MET	B	88	6.720	-10.258	86.752	1.00	73.04
	2453	CB	MET	B	88	8.167	-10.206	87.249	1.00	61.11
	2454	CG	MET	B	88	8.995	-9.098	86.641	1.00	55.57
	2455	SD	MET	B	88	8.876	-9.101	84.868	1.00	49.46
10	2456	CE	MET	B	88	9.988	-10.409	84.463	1.00	46.35
	2457	C	MET	B	88	6.013	-11.456	87.382	1.00	74.98
	2458	O	MET	B	88	6.336	-12.612	87.104	1.00	75.44
	2459	N	ASN	B	89	5.032	-11.156	88.226	1.00	104.83
	2460	CA	ASN	B	89	4.255	-12.168	88.923	1.00	106.29
15	2461	CB	ASN	B	89	3.975	-11.685	90.348	1.00	120.06
	2462	CG	ASN	B	89	3.468	-12.787	91.264	1.00	121.27
	2463	OD1	ASN	B	89	3.206	-12.548	92.445	1.00	122.22
	2464	ND2	ASN	B	89	3.332	-13.998	90.729	1.00	120.54
	2465	C	ASN	B	89	2.939	-12.460	88.197	1.00	106.39
20	2466	O	ASN	B	89	2.072	-13.142	88.733	1.00	106.68
	2467	N	LEU	B	90	2.791	-11.942	86.981	1.00	90.06
	2468	CA	LEU	B	90	1.573	-12.163	86.199	1.00	90.00
	2469	CB	LEU	B	90	1.215	-10.919	85.378	1.00	79.88
	2470	CG	LEU	B	90	1.285	-9.555	86.066	1.00	79.44
25	2471	CD1	LEU	B	90	0.605	-8.508	85.190	1.00	79.03
	2472	CD2	LEU	B	90	0.618	-9.629	87.420	1.00	80.11
	2473	C	LEU	B	90	1.720	-13.360	85.259	1.00	90.05
	2474	O	LEU	B	90	0.837	-14.216	85.189	1.00	90.12
	2475	N	PRO	B	91	2.834	-13.434	84.511	1.00	79.89
30	2476	CD	PRO	B	91	3.962	-12.502	84.355	1.00	71.65
	2477	CA	PRO	B	91	2.985	-14.577	83.612	1.00	79.87
	2478	CB	PRO	B	91	4.366	-14.352	83.003	1.00	72.08
	2479	CG	PRO	B	91	4.484	-12.869	82.990	1.00	72.08
	2480	C	PRO	B	91	2.915	-15.850	84.438	1.00	80.26
35	2481	O	PRO	B	91	2.921	-16.960	83.909	1.00	80.69
	2482	N	VAL	B	92	2.853	-15.668	85.750	1.00	103.06
	2483	CA	VAL	B	92	2.779	-16.785	86.666	1.00	103.66
	2484	CB	VAL	B	92	3.088	-16.338	88.097	1.00	99.37
	2485	CG1	VAL	B	92	3.325	-17.556	88.984	1.00	99.98
40	2486	CG2	VAL	B	92	4.299	-15.416	88.094	1.00	99.29
	2487	C	VAL	B	92	1.383	-17.375	86.620	1.00	103.81
	2488	O	VAL	B	92	1.208	-18.528	86.237	1.00	103.87
	2489	N	GLU	B	93	0.390	-16.578	86.999	1.00	97.39

	2490	CA	GLU	B	93	-0.994	-17.039	86.998	1.00	97.95
	2491	CB	GLU	B	93	-1.898	-16.008	87.659	1.00	104.76
	2492	CG	GLU	B	93	-1.562	-15.767	89.105	1.00	105.93
	2493	CD	GLU	B	93	-2.590	-14.905	89.784	1.00	106.78
5	2494	OE1	GLU	B	93	-2.849	-13.789	89.284	1.00	106.92
	2495	OE2	GLU	B	93	-3.138	-15.347	90.817	1.00	107.30
	2496	C	GLU	B	93	-1.489	-17.324	85.589	1.00	98.10
	2497	O	GLU	B	93	-2.440	-18.090	85.393	1.00	98.29
	2498	N	PHE	B	94	-0.850	-16.694	84.608	1.00	83.01
10	2499	CA	PHE	B	94	-1.209	-16.909	83.214	1.00	81.14
	2500	CB	PHE	B	94	-0.125	-16.301	82.301	1.00	66.71
	2501	CG	PHE	B	94	-0.572	-16.058	80.876	1.00	64.83
	2502	CD1	PHE	B	94	-1.745	-15.349	80.603	1.00	65.30
	2503	CD2	PHE	B	94	0.192	-16.520	79.809	1.00	62.64
15	2504	CE1	PHE	B	94	-2.145	-15.109	79.298	1.00	63.65
	2505	CE2	PHE	B	94	-0.199	-16.285	78.501	1.00	62.92
	2506	CZ	PHE	B	94	-1.368	-15.580	78.244	1.00	63.25
	2507	C	PHE	B	94	-1.267	-18.432	83.050	1.00	81.18
	2508	O	PHE	B	94	-2.339	-19.006	82.825	1.00	81.17
20	2509	N	TYR	B	95	-0.106	-19.069	83.220	1.00	80.38
	2510	CA	TYR	B	95	0.053	-20.518	83.097	1.00	80.54
	2511	CB	TYR	B	95	1.527	-20.896	83.270	1.00	78.06
	2512	CG	TYR	B	95	1.789	-22.383	83.409	1.00	76.98
	2513	CD1	TYR	B	95	1.588	-23.255	82.342	1.00	76.74
25	2514	CE1	TYR	B	95	1.802	-24.624	82.484	1.00	76.63
	2515	CD2	TYR	B	95	2.214	-22.917	84.622	1.00	76.15
	2516	CE2	TYR	B	95	2.428	-24.275	84.775	1.00	75.60
	2517	CZ	TYR	B	95	2.221	-25.124	83.708	1.00	76.18
	2518	OH	TYR	B	95	2.423	-26.473	83.878	1.00	75.63
30	2519	C	TYR	B	95	-0.783	-21.324	84.076	1.00	81.67
	2520	O	TYR	B	95	-0.694	-22.550	84.107	1.00	81.45
	2521	N	ASP	B	96	-1.599	-20.651	84.876	1.00	108.10
	2522	CA	ASP	B	96	-2.426	-21.370	85.829	1.00	107.20
	2523	CB	ASP	B	96	-2.168	-20.860	87.247	1.00	120.67
35	2524	CG	ASP	B	96	-0.785	-21.246	87.758	1.00	123.02
	2525	OD1	ASP	B	96	-0.415	-22.436	87.651	1.00	122.56
	2526	OD2	ASP	B	96	-0.067	-20.363	88.271	1.00	125.22
	2527	C	ASP	B	96	-3.908	-21.326	85.497	1.00	105.88
	2528	O	ASP	B	96	-4.584	-22.347	85.587	1.00	106.66
40	2529	N	ASN	B	97	-4.424	-20.165	85.109	1.00	68.95
	2530	CA	ASN	B	97	-5.840	-20.099	84.760	1.00	66.85
	2531	CB	ASN	B	97	-6.703	-19.729	85.983	1.00	101.14
	2532	CG	ASN	B	97	-6.162	-18.551	86.761	1.00	102.03

	2533	OD1 ASN B	97	-5.106	-18.641	87.382	1.00102.34
	2534	ND2 ASN B	97	-6.892	-17.441	86.742	1.00101.15
	2535	C ASN B	97	-6.190	-19.208	83.573	1.00 64.22
	2536	O ASN B	97	-7.180	-18.469	83.583	1.00 63.87
5	2537	N TYR B	98	-5.376	-19.301	82.534	1.00 75.26
	2538	CA TYR B	98	-5.615	-18.539	81.321	1.00 71.28
	2539	CB TYR B	98	-5.102	-17.108	81.464	1.00 77.09
	2540	CG TYR B	98	-6.096	-16.119	82.040	1.00 76.65
	2541	CD1 TYR B	98	-5.965	-15.647	83.346	1.00 77.07
10	2542	CE1 TYR B	98	-6.830	-14.672	83.854	1.00 77.23
	2543	CD2 TYR B	98	-7.123	-15.601	81.254	1.00 76.44
	2544	CE2 TYR B	98	-7.995	-14.627	81.748	1.00 77.96
	2545	CZ TYR B	98	-7.841	-14.164	83.047	1.00 78.71
	2546	OH TYR B	98	-8.683	-13.184	83.529	1.00 78.63
15	2547	C TYR B	98	-4.910	-19.228	80.166	1.00 68.10
	2548	O TYR B	98	-5.395	-19.222	79.031	1.00 67.14
	2549	N VAL B	99	-3.771	-19.839	80.469	1.00 52.36
	2550	CA VAL B	99	-3.000	-20.528	79.455	1.00 50.02
	2551	CB VAL B	99	-1.556	-20.836	79.962	1.00 72.59
20	2552	CG1 VAL B	99	-1.365	-22.318	80.221	1.00 73.06
	2553	CG2 VAL B	99	-0.543	-20.349	78.949	1.00 72.98
	2554	C VAL B	99	-3.684	-21.809	78.974	1.00 48.99
	2555	O VAL B	99	-3.793	-22.024	77.770	1.00 47.94
	2556	N PRO B	100	-4.176	-22.662	79.900	1.00 63.99
25	2557	CD PRO B	100	-4.250	-22.451	81.354	1.00 75.93
	2558	CA PRO B	100	-4.847	-23.919	79.546	1.00 62.58
	2559	CB PRO B	100	-5.438	-24.371	80.870	1.00 74.62
	2560	CG PRO B	100	-4.478	-23.847	81.850	1.00 76.59
	2561	C PRO B	100	-5.924	-23.723	78.492	1.00 60.55
30	2562	O PRO B	100	-5.922	-24.370	77.449	1.00 59.34
	2563	N GLU B	101	-6.854	-22.830	78.785	1.00 44.90
	2564	CA GLU B	101	-7.932	-22.530	77.857	1.00 45.84
	2565	CB GLU B	101	-8.804	-21.398	78.396	1.00 49.35
	2566	CG GLU B	101	-10.195	-21.358	77.791	1.00 47.33
35	2567	CD GLU B	101	-10.590	-19.978	77.330	1.00 47.28
	2568	OE1 GLU B	101	-10.287	-19.005	78.061	1.00 47.78
	2569	OE2 GLU B	101	-11.209	-19.872	76.242	1.00 47.31
	2570	C GLU B	101	-7.311	-22.085	76.545	1.00 46.84
	2571	O GLU B	101	-7.765	-22.468	75.464	1.00 46.83
40	2572	N LEU B	102	-6.275	-21.255	76.654	1.00 74.24
	2573	CA LEU B	102	-5.568	-20.748	75.486	1.00 73.45
	2574	CB LEU B	102	-4.427	-19.820	75.915	1.00 48.87
	2575	CG LEU B	102	-4.195	-18.645	74.966	1.00 48.82

	2576	CD1	LEU	B	102	-5.437	-17.773	74.932	1.00	48.94
	2577	CD2	LEU	B	102	-3.010	-17.829	75.414	1.00	48.43
	2578	C	LEU	B	102	-5.013	-21.956	74.740	1.00	73.31
	2579	O	LEU	B	102	-5.144	-22.070	73.521	1.00	74.19
5	2580	N	HIS	B	103	-4.408	-22.866	75.493	1.00	53.31
	2581	CA	HIS	B	103	-3.846	-24.080	74.921	1.00	52.67
	2582	CB	HIS	B	103	-3.189	-24.930	76.007	1.00	49.27
	2583	CG	HIS	B	103	-2.755	-26.277	75.528	1.00	47.83
	2584	CD2	HIS	B	103	-2.969	-27.514	76.031	1.00	47.86
10	2585	ND1	HIS	B	103	-1.959	-26.449	74.417	1.00	47.89
	2586	CE1	HIS	B	103	-1.695	-27.733	74.260	1.00	47.87
	2587	NE2	HIS	B	103	-2.296	-28.402	75.227	1.00	46.77
	2588	C	HIS	B	103	-4.961	-24.877	74.277	1.00	52.89
	2589	O	HIS	B	103	-4.774	-25.529	73.251	1.00	52.96
15	2590	N	ALA	B	104	-6.128	-24.819	74.904	1.00	65.91
	2591	CA	ALA	B	104	-7.293	-25.536	74.418	1.00	64.27
	2592	CB	ALA	B	104	-8.442	-25.377	75.402	1.00	71.86
	2593	C	ALA	B	104	-7.707	-25.041	73.039	1.00	62.67
	2594	O	ALA	B	104	-8.449	-25.719	72.332	1.00	62.50
20	2595	N	ASN	B	105	-7.226	-23.861	72.656	1.00	47.98
	2596	CA	ASN	B	105	-7.576	-23.313	71.357	1.00	45.58
	2597	CB	ASN	B	105	-7.847	-21.811	71.446	1.00	54.12
	2598	CG	ASN	B	105	-9.263	-21.501	71.886	1.00	56.71
	2599	OD1	ASN	B	105	-9.745	-20.387	71.704	1.00	59.11
25	2600	ND2	ASN	B	105	-9.935	-22.483	72.472	1.00	55.23
	2601	C	ASN	B	105	-6.522	-23.573	70.305	1.00	43.04
	2602	O	ASN	B	105	-6.677	-23.164	69.158	1.00	41.89
	2603	N	ASN	B	106	-5.453	-24.256	70.689	1.00	42.40
	2604	CA	ASN	B	106	-4.408	-24.560	69.734	1.00	41.78
30	2605	CB	ASN	B	106	-5.065	-25.049	68.431	1.00	35.23
	2606	CG	ASN	B	106	-4.067	-25.596	67.419	1.00	35.10
	2607	OD1	ASN	B	106	-3.123	-26.293	67.772	1.00	31.82
	2608	ND2	ASN	B	106	-4.296	-25.299	66.144	1.00	34.37
	2609	C	ASN	B	106	-3.551	-23.304	69.505	1.00	41.86
35	2610	O	ASN	B	106	-3.160	-22.996	68.383	1.00	41.51
	2611	N	VAL	B	107	-3.262	-22.570	70.574	1.00	36.53
	2612	CA	VAL	B	107	-2.439	-21.374	70.449	1.00	36.77
	2613	CB	VAL	B	107	-2.909	-20.252	71.365	1.00	41.29
	2614	CG1	VAL	B	107	-1.866	-19.142	71.395	1.00	40.11
40	2615	CG2	VAL	B	107	-4.224	-19.699	70.861	1.00	39.98
	2616	C	VAL	B	107	-1.016	-21.705	70.834	1.00	36.27
	2617	O	VAL	B	107	-0.786	-22.407	71.824	1.00	36.31
	2618	N	LYS	B	108	-0.064	-21.206	70.045	1.00	37.74



	2619	CA	LYS B 108	1.347	-21.446	70.320	1.00	38.20
	2620	CB	LYS B 108	2.132	-21.626	69.023	1.00	35.34
	2621	CG	LYS B 108	3.556	-22.154	69.195	1.00	31.10
	2622	CD	LYS B 108	4.229	-22.225	67.841	1.00	29.42
5	2623	CE	LYS B 108	4.827	-23.580	67.563	1.00	35.50
	2624	NZ	LYS B 108	6.010	-23.855	68.417	1.00	35.85
	2625	C	LYS B 108	1.813	-20.199	71.026	1.00	40.31
	2626	O	LYS B 108	1.692	-19.095	70.492	1.00	40.92
	2627	N	ILE B 109	2.327	-20.366	72.235	1.00	41.22
10	2628	CA	ILE B 109	2.781	-19.225	72.993	1.00	41.51
	2629	CB	ILE B 109	2.355	-19.322	74.439	1.00	56.24
	2630	CG2	ILE B 109	2.539	-17.969	75.109	1.00	58.01
	2631	CG1	ILE B 109	0.898	-19.773	74.519	1.00	55.38
	2632	CD1	ILE B 109	0.382	-19.886	75.929	1.00	56.07
15	2633	C	ILE B 109	4.272	-19.204	72.963	1.00	41.98
	2634	O	ILE B 109	4.907	-20.253	73.030	1.00	43.40
	2635	N	GLN B 110	4.826	-18.006	72.858	1.00	36.15
	2636	CA	GLN B 110	6.271	-17.819	72.826	1.00	37.97
	2637	CB	GLN B 110	6.811	-17.960	71.408	1.00	53.31
20	2638	CG	GLN B 110	6.930	-19.375	70.914	1.00	55.45
	2639	CD	GLN B 110	7.289	-19.416	69.458	1.00	57.54
	2640	OE1	GLN B 110	7.436	-20.488	68.877	1.00	60.83
	2641	NE2	GLN B 110	7.435	-18.235	68.848	1.00	58.77
	2642	C	GLN B 110	6.588	-16.434	73.325	1.00	37.62
25	2643	O	GLN B 110	5.815	-15.502	73.104	1.00	36.55
	2644	N	MET B 111	7.733	-16.296	73.978	1.00	53.13
	2645	CA	MET B 111	8.135	-15.008	74.505	1.00	54.09
	2646	CB	MET B 111	8.562	-15.154	75.958	1.00	56.34
	2647	CG	MET B 111	9.991	-15.644	76.105	1.00	59.89
30	2648	SD	MET B 111	10.417	-16.019	77.807	1.00	68.27
	2649	CE	MET B 111	11.002	-17.781	77.663	1.00	60.47
	2650	C	MET B 111	9.298	-14.418	73.731	1.00	53.12
	2651	O	MET B 111	10.188	-15.136	73.283	1.00	52.47
	2652	N	ILE B 112	9.274	-13.105	73.556	1.00	46.96
35	2653	CA	ILE B 112	10.385	-12.421	72.907	1.00	47.13
	2654	CB	ILE B 112	9.986	-11.711	71.571	1.00	39.77
	2655	CG2	ILE B 112	9.273	-12.684	70.663	1.00	39.16
	2656	CG1	ILE B 112	9.085	-10.514	71.833	1.00	38.91
	2657	CD1	ILE B 112	8.806	-9.718	70.598	1.00	39.08
40	2658	C	ILE B 112	10.874	-11.403	73.947	1.00	47.40
	2659	O	ILE B 112	10.085	-10.646	74.523	1.00	47.07
	2660	N	GLY B 113	12.172	-11.429	74.222	1.00	35.58
	2661	CA	GLY B 113	12.728	-10.521	75.198	1.00	38.29

	2662	C	GLY B 113	14.091	-11.023	75.587	1.00	41.35
	2663	O	GLY B 113	14.670	-11.817	74.849	1.00	42.26
	2664	N	GLU B 114	14.611	-10.539	76.714	1.00	70.53
	2665	CA	GLU B 114	15.908	-10.973	77.221	1.00	73.56
5	2666	CB	GLU B 114	16.800	-9.767	77.604	1.00	59.45
	2667	CG	GLU B 114	17.509	-9.108	76.389	1.00	58.05
	2668	CD	GLU B 114	18.417	-7.912	76.727	1.00	57.77
	2669	OE1	GLU B 114	17.925	-6.842	77.153	1.00	53.67
	2670	OE2	GLU B 114	19.642	-8.042	76.546	1.00	58.81
10	2671	C	GLU B 114	15.618	-11.862	78.424	1.00	76.37
	2672	O	GLU B 114	15.347	-11.382	79.519	1.00	76.96
	2673	N	THR B 115	15.659	-13.169	78.176	1.00	55.29
	2674	CA	THR B 115	15.390	-14.215	79.166	1.00	57.55
	2675	CB	THR B 115	15.788	-15.591	78.619	1.00	78.62
15	2676	OG1	THR B 115	17.216	-15.645	78.466	1.00	79.08
	2677	CG2	THR B 115	15.111	-15.844	77.274	1.00	76.28
	2678	C	THR B 115	16.079	-14.062	80.516	1.00	58.59
	2679	O	THR B 115	15.432	-14.138	81.561	1.00	56.92
	2680	N	ASP B 116	17.396	-13.878	80.486	1.00	74.93
20	2681	CA	ASP B 116	18.179	-13.721	81.712	1.00	76.99
	2682	CB	ASP B 116	19.616	-13.265	81.384	1.00	75.42
	2683	CG	ASP B 116	19.667	-12.063	80.448	1.00	78.98
	2684	OD1	ASP B 116	19.396	-12.231	79.236	1.00	81.29
	2685	OD2	ASP B 116	19.981	-10.953	80.930	1.00	78.72
25	2686	C	ASP B 116	17.539	-12.757	82.711	1.00	76.51
	2687	O	ASP B 116	16.916	-13.179	83.674	1.00	77.02
	2688	N	ARG B 117	17.699	-11.466	82.470	1.00	70.65
	2689	CA	ARG B 117	17.146	-10.434	83.329	1.00	71.11
	2690	CB	ARG B 117	16.833	-9.199	82.487	1.00	116.12
30	2691	CG	ARG B 117	17.914	-8.830	81.485	1.00	120.52
	2692	CD	ARG B 117	17.423	-7.782	80.493	1.00	124.25
	2693	NE	ARG B 117	17.610	-6.408	80.955	1.00	127.70
	2694	CZ	ARG B 117	17.063	-5.886	82.050	1.00	129.66
	2695	NH1	ARG B 117	16.278	-6.615	82.830	1.00	130.44
35	2696	NH2	ARG B 117	17.301	-4.622	82.368	1.00	129.30
	2697	C	ARG B 117	15.882	-10.847	84.092	1.00	69.75
	2698	O	ARG B 117	15.673	-10.414	85.216	1.00	71.37
	2699	N	LEU B 118	15.040	-11.670	83.475	1.00	64.17
	2700	CA	LEU B 118	13.773	-12.131	84.068	1.00	61.87
40	2701	CB	LEU B 118	13.018	-13.008	83.063	1.00	72.78
	2702	CG	LEU B 118	12.401	-12.488	81.766	1.00	71.93
	2703	CD1	LEU B 118	12.465	-13.576	80.692	1.00	70.47
	2704	CD2	LEU B 118	10.973	-12.060	82.039	1.00	68.98

	2705	C	LEU B 118	13.934	-12.957	85.337	1.00	60.71
	2706	O	LEU B 118	14.890	-13.711	85.457	1.00	62.34
	2707	N	PRO B 119	12.985	-12.848	86.289	1.00	45.07
	2708	CD	PRO B 119	11.879	-11.879	86.339	1.00	56.09
5	2709	CA	PRO B 119	13.042	-13.612	87.541	1.00	44.37
	2710	CB	PRO B 119	11.681	-13.344	88.162	1.00	55.31
	2711	CG	PRO B 119	11.453	-11.939	87.804	1.00	55.13
	2712	C	PRO B 119	13.278	-15.112	87.330	1.00	44.61
	2713	O	PRO B 119	13.812	-15.552	86.303	1.00	42.91
10	2714	N	LYS B 120	12.884	-15.897	88.323	1.00	70.02
	2715	CA	LYS B 120	13.030	-17.344	88.249	1.00	70.37
	2716	CB	LYS B 120	13.904	-17.865	89.397	1.00	70.42
	2717	CG	LYS B 120	14.040	-19.387	89.433	1.00	71.73
	2718	CD	LYS B 120	13.490	-19.997	90.722	1.00	71.51
15	2719	CE	LYS B 120	13.312	-21.503	90.582	1.00	71.92
	2720	NZ	LYS B 120	14.506	-22.170	89.963	1.00	70.24
	2721	C	LYS B 120	11.632	-17.906	88.371	1.00	70.03
	2722	O	LYS B 120	11.300	-18.934	87.792	1.00	69.09
	2723	N	GLN B 121	10.805	-17.201	89.123	1.00	60.63
20	2724	CA	GLN B 121	9.446	-17.635	89.323	1.00	60.71
	2725	CB	GLN B 121	8.835	-16.899	90.510	1.00	98.66
	2726	CG	GLN B 121	7.611	-17.571	91.087	1.00	102.22
	2727	CD	GLN B 121	7.531	-17.401	92.587	1.00	104.86
	2728	OE1	GLN B 121	7.506	-16.281	93.094	1.00	105.24
25	2729	NE2	GLN B 121	7.499	-18.516	93.309	1.00	104.95
	2730	C	GLN B 121	8.677	-17.340	88.055	1.00	60.00
	2731	O	GLN B 121	7.541	-17.782	87.895	1.00	60.82
	2732	N	THR B 122	9.300	-16.599	87.144	1.00	69.70
	2733	CA	THR B 122	8.632	-16.262	85.897	1.00	67.18
30	2734	CB	THR B 122	8.682	-14.770	85.622	1.00	55.92
	2735	OG1	THR B 122	8.099	-14.064	86.719	1.00	53.62
	2736	CG2	THR B 122	7.888	-14.454	84.382	1.00	55.74
	2737	C	THR B 122	9.207	-16.991	84.702	1.00	64.99
	2738	O	THR B 122	8.494	-17.699	84.007	1.00	66.19
35	2739	N	PHE B 123	10.495	-16.814	84.453	1.00	36.51
	2740	CA	PHE B 123	11.140	-17.494	83.335	1.00	34.52
	2741	CB	PHE B 123	12.655	-17.340	83.393	1.00	42.68
	2742	CG	PHE B 123	13.382	-18.176	82.384	1.00	40.47
	2743	CD1	PHE B 123	13.620	-17.697	81.110	1.00	39.38
40	2744	CD2	PHE B 123	13.812	-19.454	82.708	1.00	40.82
	2745	CE1	PHE B 123	14.279	-18.473	80.167	1.00	40.63
	2746	CE2	PHE B 123	14.470	-20.243	81.774	1.00	40.39
	2747	CZ	PHE B 123	14.705	-19.747	80.497	1.00	41.21

	2748	C	PHE B 123	10.828	-18.981	83.341	1.00	35.82
	2749	O	PHE B 123	11.105	-19.671	82.370	1.00	36.42
	2750	N	GLU B 124	10.289	-19.489	84.445	1.00	66.96
	2751	CA	GLU B 124	9.940	-20.903	84.520	1.00	66.62
5	2752	CB	GLU B 124	10.226	-21.453	85.914	1.00	65.43
	2753	CG	GLU B 124	11.688	-21.818	86.134	1.00	66.19
	2754	CD	GLU B 124	11.911	-22.603	87.429	1.00	67.66
	2755	OE1	GLU B 124	13.024	-23.177	87.602	1.00	66.06
	2756	OE2	GLU B 124	10.970	-22.635	88.265	1.00	66.27
10	2757	C	GLU B 124	8.473	-21.106	84.153	1.00	66.16
	2758	O	GLU B 124	8.124	-22.094	83.518	1.00	64.89
	2759	N	ALA B 125	7.621	-20.164	84.549	1.00	58.96
	2760	CA	ALA B 125	6.203	-20.241	84.227	1.00	58.99
	2761	CB	ALA B 125	5.448	-19.112	84.877	1.00	38.66
15	2762	C	ALA B 125	6.058	-20.144	82.722	1.00	60.08
	2763	O	ALA B 125	5.526	-21.045	82.079	1.00	59.86
	2764	N	LEU B 126	6.530	-19.041	82.160	1.00	48.31
	2765	CA	LEU B 126	6.457	-18.854	80.724	1.00	46.89
	2766	CB	LEU B 126	7.208	-17.586	80.299	1.00	42.59
20	2767	CG	LEU B 126	6.743	-16.228	80.849	1.00	42.89
	2768	CD1	LEU B 126	7.765	-15.144	80.475	1.00	41.81
	2769	CD2	LEU B 126	5.360	-15.894	80.311	1.00	41.27
	2770	C	LEU B 126	7.053	-20.065	80.015	1.00	46.18
	2771	O	LEU B 126	6.478	-20.556	79.062	1.00	44.20
25	2772	N	THR B 127	8.192	-20.562	80.477	1.00	48.66
	2773	CA	THR B 127	8.792	-21.716	79.814	1.00	50.75
	2774	CB	THR B 127	10.086	-22.191	80.518	1.00	47.16
	2775	OG1	THR B 127	11.104	-21.205	80.372	1.00	49.12
	2776	CG2	THR B 127	10.593	-23.466	79.898	1.00	45.81
30	2777	C	THR B 127	7.802	-22.876	79.781	1.00	52.28
	2778	O	THR B 127	7.664	-23.569	78.768	1.00	52.35
	2779	N	LYS B 128	7.119	-23.101	80.894	1.00	74.85
	2780	CA	LYS B 128	6.154	-24.180	80.934	1.00	75.58
	2781	CB	LYS B 128	5.455	-24.217	82.302	1.00	61.03
35	2782	CG	LYS B 128	6.371	-24.725	83.447	1.00	61.84
	2783	CD	LYS B 128	5.730	-24.603	84.846	1.00	61.50
	2784	CE	LYS B 128	5.503	-23.136	85.243	1.00	62.42
	2785	NZ	LYS B 128	4.871	-22.919	86.577	1.00	60.58
	2786	C	LYS B 128	5.174	-23.907	79.803	1.00	75.32
40	2787	O	LYS B 128	4.990	-24.741	78.917	1.00	76.48
	2788	N	ALA B 129	4.587	-22.715	79.815	1.00	50.74
	2789	CA	ALA B 129	3.634	-22.306	78.786	1.00	48.88
	2790	CB	ALA B 129	3.346	-20.815	78.896	1.00	31.58

	2791	C	ALA B 129	4.113	-22.617	77.379	1.00	48.48
	2792	O	ALA B 129	3.307	-22.708	76.465	1.00	48.10
	2793	N	GLU B 130	5.420	-22.752	77.194	1.00	50.31
	2794	CA	GLU B 130	5.965	-23.052	75.876	1.00	49.93
5	2795	CB	GLU B 130	7.434	-22.653	75.786	1.00	54.74
	2796	CG	GLU B 130	7.689	-21.182	75.568	1.00	55.29
	2797	CD	GLU B 130	9.162	-20.890	75.379	1.00	56.14
	2798	OE1	GLU B 130	9.835	-21.690	74.704	1.00	55.87
	2799	OE2	GLU B 130	9.651	-19.862	75.890	1.00	59.52
10	2800	C	GLU B 130	5.861	-24.533	75.614	1.00	50.88
	2801	O	GLU B 130	5.186	-24.975	74.689	1.00	53.45
	2802	N	GLU B 131	6.540	-25.302	76.449	1.00	50.32
	2803	CA	GLU B 131	6.551	-26.744	76.315	1.00	49.92
	2804	CB	GLU B 131	7.272	-27.346	77.511	1.00	63.87
15	2805	CG	GLU B 131	8.586	-26.657	77.807	1.00	66.98
	2806	CD	GLU B 131	9.078	-26.934	79.209	1.00	69.64
	2807	OE1	GLU B 131	8.313	-26.676	80.173	1.00	71.86
	2808	OE2	GLU B 131	10.233	-27.401	79.342	1.00	71.71
	2809	C	GLU B 131	5.136	-27.289	76.215	1.00	48.18
20	2810	O	GLU B 131	4.908	-28.304	75.577	1.00	47.85
	2811	N	LEU B 132	4.186	-26.609	76.840	1.00	51.42
	2812	CA	LEU B 132	2.801	-27.056	76.804	1.00	51.74
	2813	CB	LEU B 132	1.928	-26.213	77.743	1.00	54.74
	2814	CG	LEU B 132	0.417	-26.490	77.681	1.00	55.90
25	2815	CD1	LEU B 132	0.053	-27.593	78.633	1.00	54.96
	2816	CD2	LEU B 132	-0.359	-25.246	78.041	1.00	54.85
	2817	C	LEU B 132	2.233	-26.958	75.399	1.00	51.53
	2818	O	LEU B 132	1.652	-27.919	74.883	1.00	53.35
	2819	N	THR B 133	2.408	-25.790	74.785	1.00	42.27
30	2820	CA	THR B 133	1.880	-25.522	73.452	1.00	38.90
	2821	CB	THR B 133	1.236	-24.126	73.396	1.00	38.41
	2822	OG1	THR B 133	2.258	-23.120	73.332	1.00	39.51
	2823	CG2	THR B 133	0.385	-23.901	74.625	1.00	37.08
	2824	C	THR B 133	2.900	-25.603	72.325	1.00	38.27
35	2825	O	THR B 133	2.620	-25.200	71.193	1.00	38.93
	2826	N	LYS B 134	4.075	-26.139	72.605	1.00	47.91
	2827	CA	LYS B 134	5.073	-26.199	71.564	1.00	46.51
	2828	CB	LYS B 134	6.342	-26.851	72.084	1.00	36.10
	2829	CG	LYS B 134	6.329	-28.335	72.151	1.00	35.70
40	2830	CD	LYS B 134	7.736	-28.840	71.908	1.00	39.26
	2831	CE	LYS B 134	7.834	-30.357	71.972	1.00	40.32
	2832	NZ	LYS B 134	7.828	-30.849	73.385	1.00	42.00
	2833	C	LYS B 134	4.609	-26.920	70.312	1.00	46.96

	2834	O	LYS B 134	5.324	-26.957	69.331	1.00	46.52
	2835	N	ASN B 135	3.410	-27.482	70.318	1.00	42.04
	2836	CA	ASN B 135	2.968	-28.206	69.139	1.00	39.89
	2837	CB	ASN B 135	2.786	-29.682	69.478	1.00	46.16
5	2838	CG	ASN B 135	4.075	-30.338	69.937	1.00	49.11
	2839	OD1	ASN B 135	5.120	-30.189	69.309	1.00	51.05
	2840	ND2	ASN B 135	4.005	-31.077	71.030	1.00	48.36
	2841	C	ASN B 135	1.708	-27.660	68.497	1.00	39.99
	2842	O	ASN B 135	1.342	-28.080	67.407	1.00	39.33
10	2843	N	ASN B 136	1.041	-26.730	69.166	1.00	40.14
	2844	CA	ASN B 136	-0.168	-26.132	68.619	1.00	40.76
	2845	CB	ASN B 136	-0.676	-25.043	69.549	1.00	46.89
	2846	CG	ASN B 136	-1.121	-25.587	70.878	1.00	48.32
	2847	OD1	ASN B 136	-0.728	-26.689	71.281	1.00	47.19
15	2848	ND2	ASN B 136	-1.936	-24.814	71.583	1.00	45.41
	2849	C	ASN B 136	0.111	-25.527	67.253	1.00	40.88
	2850	O	ASN B 136	1.131	-24.868	67.048	1.00	43.10
	2851	N	THR B 137	-0.814	-25.730	66.327	1.00	32.40
	2852	CA	THR B 137	-0.668	-25.228	64.970	1.00	27.29
20	2853	CB	THR B 137	-0.973	-26.349	63.996	1.00	25.13
	2854	OG1	THR B 137	-2.336	-26.749	64.158	1.00	28.80
	2855	CG2	THR B 137	-0.089	-27.531	64.272	1.00	20.78
	2856	C	THR B 137	-1.562	-24.021	64.641	1.00	27.10
	2857	O	THR B 137	-1.773	-23.689	63.478	1.00	25.52
25	2858	N	GLY B 138	-2.071	-23.350	65.670	1.00	29.04
	2859	CA	GLY B 138	-2.951	-22.210	65.450	1.00	27.90
	2860	C	GLY B 138	-2.261	-20.872	65.548	1.00	28.97
	2861	O	GLY B 138	-1.085	-20.760	65.239	1.00	30.50
	2862	N	LEU B 139	-2.978	-19.844	65.965	1.00	30.10
30	2863	CA	LEU B 139	-2.354	-18.547	66.082	1.00	32.70
	2864	CB	LEU B 139	-3.391	-17.500	66.420	1.00	24.09
	2865	CG	LEU B 139	-2.868	-16.272	67.135	1.00	21.46
	2866	CD1	LEU B 139	-3.595	-15.021	66.673	1.00	23.42
	2867	CD2	LEU B 139	-3.054	-16.497	68.607	1.00	23.71
35	2868	C	LEU B 139	-1.268	-18.569	67.143	1.00	36.48
	2869	O	LEU B 139	-1.408	-19.227	68.186	1.00	37.87
	2870	N	ILE B 140	-0.175	-17.857	66.866	1.00	39.83
	2871	CA	ILE B 140	0.943	-17.784	67.797	1.00	40.00
	2872	CB	ILE B 140	2.279	-17.600	67.082	1.00	33.99
40	2873	CG2	ILE B 140	3.408	-17.695	68.083	1.00	32.14
	2874	CG1	ILE B 140	2.473	-18.661	66.008	1.00	32.36
	2875	CD1	ILE B 140	3.919	-18.717	65.474	1.00	30.06
	2876	C	ILE B 140	0.787	-16.590	68.719	1.00	39.79

	2877	O	ILE B 140	0.551	-15.474	68.260	1.00	40.70
	2878	N	LEU B 141	0.902	-16.823	70.020	1.00	31.20
	2879	CA	LEU B 141	0.817	-15.731	70.969	1.00	33.93
	2880	CB	LEU B 141	0.155	-16.160	72.260	1.00	44.06
5	2881	CG	LEU B 141	0.265	-14.993	73.236	1.00	45.51
	2882	CD1	LEU B 141	-0.330	-13.731	72.620	1.00	43.84
	2883	CD2	LEU B 141	-0.428	-15.379	74.527	1.00	47.62
	2884	C	LEU B 141	2.244	-15.334	71.256	1.00	36.13
	2885	O	LEU B 141	3.006	-16.098	71.857	1.00	36.58
10	2886	N	ASN B 142	2.598	-14.132	70.827	1.00	42.08
	2887	CA	ASN B 142	3.948	-13.614	70.980	1.00	43.17
	2888	CB	ASN B 142	4.360	-12.997	69.644	1.00	56.80
	2889	CG	ASN B 142	5.821	-13.164	69.352	1.00	59.07
	2890	OD1	ASN B 142	6.336	-14.280	69.267	1.00	61.13
15	2891	ND2	ASN B 142	6.505	-12.048	69.193	1.00	58.39
	2892	C	ASN B 142	4.040	-12.582	72.115	1.00	43.12
	2893	O	ASN B 142	3.704	-11.400	71.942	1.00	44.00
	2894	N	PHE B 143	4.491	-13.044	73.279	1.00	50.33
	2895	CA	PHE B 143	4.632	-12.193	74.464	1.00	50.62
20	2896	CB	PHE B 143	4.475	-13.017	75.744	1.00	65.61
	2897	CG	PHE B 143	3.168	-12.811	76.442	1.00	69.53
	2898	CD1	PHE B 143	2.231	-13.828	76.501	1.00	70.32
	2899	CD2	PHE B 143	2.874	-11.591	77.044	1.00	71.07
	2900	CE1	PHE B 143	1.021	-13.635	77.148	1.00	71.14
25	2901	CE2	PHE B 143	1.667	-11.387	77.694	1.00	70.89
	2902	CZ	PHE B 143	0.739	-12.413	77.746	1.00	70.99
	2903	C	PHE B 143	5.988	-11.525	74.503	1.00	49.15
	2904	O	PHE B 143	7.014	-12.204	74.547	1.00	49.20
	2905	N	ALA B 144	6.003	-10.198	74.483	1.00	39.26
30	2906	CA	ALA B 144	7.273	-9.478	74.537	1.00	36.58
	2907	CB	ALA B 144	7.248	-8.258	73.615	1.00	37.37
	2908	C	ALA B 144	7.460	-9.050	75.977	1.00	35.58
	2909	O	ALA B 144	6.923	-8.034	76.402	1.00	36.04
	2910	N	LEU B 145	8.216	-9.840	76.727	1.00	35.08
35	2911	CA	LEU B 145	8.442	-9.549	78.125	1.00	35.23
	2912	CB	LEU B 145	8.215	-10.804	78.969	1.00	55.88
	2913	CG	LEU B 145	7.290	-10.717	80.189	1.00	58.67
	2914	CD1	LEU B 145	8.019	-11.242	81.415	1.00	59.98
	2915	CD2	LEU B 145	6.822	-9.289	80.415	1.00	58.81
40	2916	C	LEU B 145	9.865	-9.070	78.314	1.00	34.06
	2917	O	LEU B 145	10.805	-9.742	77.873	1.00	29.79
	2918	N	ASN B 146	10.026	-7.911	78.960	1.00	34.72
	2919	CA	ASN B 146	11.354	-7.394	79.200	1.00	32.11

	2920	CB	ASN B 146	12.028	-8.326	80.201	1.00	40.89
	2921	CG	ASN B 146	13.512	-8.320	80.102	1.00	43.20
	2922	OD1	ASN B 146	14.131	-7.271	79.942	1.00	43.84
	2923	ND2	ASN B 146	14.111	-9.501	80.214	1.00	44.60
5	2924	C	ASN B 146	12.011	-7.393	77.825	1.00	30.73
	2925	O	ASN B 146	13.079	-7.974	77.597	1.00	30.58
	2926	N	TYR B 147	11.310	-6.741	76.898	1.00	30.68
	2927	CA	TYR B 147	11.736	-6.615	75.507	1.00	30.27
	2928	CB	TYR B 147	10.681	-7.200	74.549	1.00	31.47
10	2929	CG	TYR B 147	10.869	-6.780	73.104	1.00	31.31
	2930	CD1	TYR B 147	11.642	-7.526	72.237	1.00	31.34
	2931	CE1	TYR B 147	11.899	-7.085	70.954	1.00	31.50
	2932	CD2	TYR B 147	10.351	-5.579	72.644	1.00	29.89
	2933	CE2	TYR B 147	10.606	-5.129	71.377	1.00	29.93
15	2934	CZ	TYR B 147	11.381	-5.880	70.530	1.00	32.26
	2935	OH	TYR B 147	11.650	-5.406	69.260	1.00	33.08
	2936	C	TYR B 147	11.961	-5.163	75.136	1.00	30.06
	2937	O	TYR B 147	11.210	-4.279	75.554	1.00	26.56
	2938	N	GLY B 148	12.983	-4.944	74.315	1.00	32.92
20	2939	CA	GLY B 148	13.315	-3.609	73.862	1.00	32.00
	2940	C	GLY B 148	13.881	-3.680	72.461	1.00	31.94
	2941	O	GLY B 148	14.705	-4.535	72.160	1.00	31.87
	2942	N	GLY B 149	13.427	-2.777	71.602	1.00	31.24
	2943	CA	GLY B 149	13.897	-2.750	70.233	1.00	29.45
25	2944	C	GLY B 149	15.399	-2.690	70.162	1.00	27.44
	2945	O	GLY B 149	16.051	-3.652	69.749	1.00	26.39
	2946	N	ARG B 150	15.942	-1.550	70.574	1.00	30.93
	2947	CA	ARG B 150	17.382	-1.334	70.575	1.00	31.02
	2948	CB	ARG B 150	17.697	-0.038	71.288	1.00	20.21
30	2949	CG	ARG B 150	16.928	1.107	70.715	1.00	18.79
	2950	CD	ARG B 150	17.302	2.445	71.302	1.00	17.44
	2951	NE	ARG B 150	16.939	3.522	70.395	1.00	20.30
	2952	CZ	ARG B 150	17.275	4.788	70.579	1.00	22.73
	2953	NH1	ARG B 150	17.979	5.125	71.643	1.00	23.04
35	2954	NH2	ARG B 150	16.928	5.710	69.695	1.00	23.32
	2955	C	ARG B 150	18.068	-2.499	71.265	1.00	30.95
	2956	O	ARG B 150	19.091	-2.996	70.804	1.00	31.34
	2957	N	ALA B 151	17.503	-2.945	72.373	1.00	22.01
	2958	CA	ALA B 151	18.082	-4.076	73.048	1.00	22.37
40	2959	CB	ALA B 151	17.266	-4.445	74.232	1.00	17.65
	2960	C	ALA B 151	18.113	-5.241	72.075	1.00	24.04
	2961	O	ALA B 151	19.139	-5.891	71.919	1.00	25.91
	2962	N	GLU B 152	16.994	-5.506	71.410	1.00	26.34



	2963	CA	GLU B 152	16.947	-6.624	70.484	1.00	26.11
	2964	CB	GLU B 152	15.541	-6.815	69.924	1.00	23.93
	2965	CG	GLU B 152	15.466	-7.801	68.769	1.00	24.82
	2966	CD	GLU B 152	14.049	-8.044	68.279	1.00	26.88
5	2967	OE1	GLU B 152	13.238	-7.099	68.238	1.00	24.60
	2968	OE2	GLU B 152	13.743	-9.184	67.903	1.00	28.89
	2969	C	GLU B 152	17.922	-6.475	69.338	1.00	26.60
	2970	O	GLU B 152	18.587	-7.436	68.945	1.00	23.14
	2971	N	ILE B 153	18.037	-5.283	68.783	1.00	22.34
10	2972	CA	ILE B 153	18.954	-5.191	67.677	1.00	24.01
	2973	CB	ILE B 153	18.881	-3.840	66.963	1.00	23.73
	2974	CG2	ILE B 153	19.736	-3.887	65.711	1.00	20.22
	2975	CG1	ILE B 153	17.435	-3.535	66.579	1.00	23.89
	2976	CD1	ILE B 153	17.275	-2.385	65.614	1.00	20.64
15	2977	C	ILE B 153	20.366	-5.433	68.160	1.00	26.64
	2978	O	ILE B 153	21.191	-5.989	67.429	1.00	25.13
	2979	N	THR B 154	20.643	-5.046	69.402	1.00	30.24
	2980	CA	THR B 154	21.993	-5.196	69.935	1.00	30.03
	2981	CB	THR B 154	22.153	-4.515	71.296	1.00	26.73
20	2982	OG1	THR B 154	21.750	-3.148	71.207	1.00	25.40
	2983	CG2	THR B 154	23.589	-4.528	71.701	1.00	26.39
	2984	C	THR B 154	22.382	-6.642	70.078	1.00	30.94
	2985	O	THR B 154	23.282	-7.113	69.399	1.00	31.05
	2986	N	GLN B 155	21.688	-7.330	70.972	1.00	32.53
25	2987	CA	GLN B 155	21.911	-8.738	71.241	1.00	36.01
	2988	CB	GLN B 155	20.715	-9.329	71.995	1.00	51.24
	2989	CG	GLN B 155	20.345	-10.766	71.600	1.00	57.08
	2990	CD	GLN B 155	19.233	-10.840	70.549	1.00	59.24
	2991	OE1	GLN B 155	18.982	-11.896	69.960	1.00	59.64
30	2992	NE2	GLN B 155	18.552	-9.722	70.325	1.00	62.49
	2993	C	GLN B 155	22.110	-9.488	69.959	1.00	37.78
	2994	O	GLN B 155	22.701	-10.552	69.952	1.00	39.40
	2995	N	ALA B 156	21.606	-8.940	68.865	1.00	41.71
	2996	CA	ALA B 156	21.752	-9.598	67.580	1.00	43.30
35	2997	CB	ALA B 156	20.494	-9.414	66.739	1.00	25.30
	2998	C	ALA B 156	22.968	-9.082	66.834	1.00	45.02
	2999	O	ALA B 156	23.790	-9.886	66.399	1.00	46.11
	3000	N	LEU B 157	23.101	-7.757	66.691	1.00	53.83
	3001	CA	LEU B 157	24.259	-7.212	65.977	1.00	55.27
40	3002	CB	LEU B 157	24.248	-5.679	65.899	1.00	48.18
	3003	CG	LEU B 157	23.280	-4.992	64.911	1.00	50.98
	3004	CD1	LEU B 157	23.915	-3.704	64.404	1.00	49.50
	3005	CD2	LEU B 157	22.970	-5.888	63.735	1.00	50.05

	3006	C	LEU B 157	25.502	-7.689	66.676	1.00	54.30
	3007	O	LEU B 157	26.601	-7.520	66.184	1.00	53.42
	3008	N	LYS B 158	25.300	-8.284	67.842	1.00	40.58
	3009	CA	LYS B 158	26.378	-8.867	68.602	1.00	42.24
5	3010	CB	LYS B 158	25.984	-9.020	70.062	1.00	54.94
	3011	CG	LYS B 158	26.881	-9.954	70.828	1.00	56.65
	3012	CD	LYS B 158	27.413	-9.295	72.074	1.00	60.75
	3013	CE	LYS B 158	26.296	-8.885	73.014	1.00	62.28
	3014	NZ	LYS B 158	26.847	-8.245	74.244	1.00	65.28
10	3015	C	LYS B 158	26.568	-10.240	67.975	1.00	43.87
	3016	O	LYS B 158	27.272	-10.373	66.974	1.00	43.58
	3017	N	LEU B 159	25.916	-11.248	68.552	1.00	53.59
	3018	CA	LEU B 159	25.998	-12.620	68.058	1.00	53.87
	3019	CB	LEU B 159	24.619	-13.263	68.079	1.00	38.71
15	3020	CG	LEU B 159	24.051	-13.478	69.476	1.00	38.21
	3021	CD1	LEU B 159	22.584	-13.874	69.409	1.00	38.39
	3022	CD2	LEU B 159	24.852	-14.540	70.160	1.00	36.39
	3023	C	LEU B 159	26.569	-12.682	66.651	1.00	55.69
	3024	O	LEU B 159	27.526	-13.408	66.408	1.00	54.95
20	3025	N	ILE B 160	25.980	-11.928	65.723	1.00	47.80
	3026	CA	ILE B 160	26.484	-11.895	64.356	1.00	50.45
	3027	CB	ILE B 160	25.859	-10.715	63.523	1.00	52.45
	3028	CG2	ILE B 160	26.733	-10.390	62.289	1.00	49.79
	3029	CG1	ILE B 160	24.442	-11.074	63.070	1.00	52.17
25	3030	CD1	ILE B 160	23.799	-10.012	62.178	1.00	50.29
	3031	C	ILE B 160	28.002	-11.709	64.426	1.00	52.81
	3032	O	ILE B 160	28.758	-12.637	64.144	1.00	53.75
	3033	N	SER B 161	28.434	-10.512	64.816	1.00	68.73
	3034	CA	SER B 161	29.856	-10.180	64.923	1.00	70.90
30	3035	CB	SER B 161	30.044	-8.927	65.773	1.00	54.73
	3036	OG	SER B 161	29.664	-9.186	67.115	1.00	55.27
	3037	C	SER B 161	30.657	-11.325	65.535	1.00	72.09
	3038	O	SER B 161	31.708	-11.702	65.017	1.00	72.60
	3039	N	GLN B 162	30.178	-11.862	66.652	1.00	65.45
35	3040	CA	GLN B 162	30.866	-12.987	67.270	1.00	67.74
	3041	CB	GLN B 162	29.983	-13.639	68.343	1.00	74.56
	3042	CG	GLN B 162	30.507	-14.968	68.915	1.00	75.31
	3043	CD	GLN B 162	31.504	-14.788	70.050	1.00	76.13
	3044	OE1	GLN B 162	31.219	-14.120	71.042	1.00	76.95
40	3045	NE2	GLN B 162	32.672	-15.394	69.911	1.00	75.35
	3046	C	GLN B 162	31.086	-13.964	66.120	1.00	69.54
	3047	O	GLN B 162	32.216	-14.218	65.703	1.00	70.50
	3048	N	ASP B 163	29.984	-14.483	65.589	1.00	78.04

	3049	CA	ASP B 163	30.041	-15.425	64.485	1.00	79.04
	3050	CB	ASP B 163	28.632	-15.686	63.947	1.00	82.10
	3051	CG	ASP B 163	27.787	-16.498	64.915	1.00	84.42
	3052	OD1	ASP B 163	26.603	-16.761	64.611	1.00	85.70
5	3053	OD2	ASP B 163	28.313	-16.879	65.985	1.00	84.15
	3054	C	ASP B 163	30.974	-14.950	63.376	1.00	79.30
	3055	O	ASP B 163	31.689	-15.757	62.791	1.00	80.39
	3056	N	VAL B 164	30.986	-13.653	63.086	1.00	67.38
	3057	CA	VAL B 164	31.882	-13.150	62.046	1.00	68.00
10	3058	CB	VAL B 164	31.707	-11.641	61.800	1.00	68.44
	3059	CG1	VAL B 164	32.401	-11.250	60.509	1.00	68.71
	3060	CG2	VAL B 164	30.240	-11.282	61.757	1.00	68.53
	3061	C	VAL B 164	33.289	-13.374	62.581	1.00	68.33
	3062	O	VAL B 164	34.187	-13.823	61.866	1.00	66.84
15	3063	N	LEU B 165	33.449	-13.070	63.863	1.00	80.97
	3064	CA	LEU B 165	34.718	-13.216	64.553	1.00	82.49
	3065	CB	LEU B 165	34.545	-12.846	66.035	1.00	79.80
	3066	CG	LEU B 165	35.745	-12.475	66.916	1.00	80.26
	3067	CD1	LEU B 165	36.689	-13.655	67.072	1.00	80.94
20	3068	CD2	LEU B 165	36.460	-11.288	66.302	1.00	80.62
	3069	C	LEU B 165	35.213	-14.650	64.419	1.00	82.96
	3070	O	LEU B 165	36.358	-14.880	64.056	1.00	83.85
	3071	N	ASP B 166	34.349	-15.617	64.697	1.00	68.73
	3072	CA	ASP B 166	34.746	-17.014	64.610	1.00	69.37
25	3073	CB	ASP B 166	33.911	-17.838	65.577	1.00	107.54
	3074	CG	ASP B 166	34.086	-17.388	67.000	1.00	109.41
	3075	OD1	ASP B 166	33.425	-17.953	67.898	1.00	110.51
	3076	OD2	ASP B 166	34.894	-16.460	67.215	1.00	109.83
	3077	C	ASP B 166	34.649	-17.606	63.212	1.00	68.95
30	3078	O	ASP B 166	34.388	-18.798	63.055	1.00	68.96
	3079	N	ALA B 167	34.861	-16.770	62.200	1.00	74.82
	3080	CA	ALA B 167	34.808	-17.202	60.806	1.00	73.74
	3081	CB	ALA B 167	36.122	-17.850	60.416	1.00	71.38
	3082	C	ALA B 167	33.662	-18.160	60.512	1.00	73.42
35	3083	O	ALA B 167	33.684	-18.861	59.503	1.00	73.13
	3084	N	LYS B 168	32.668	-18.193	61.395	1.00	76.94
	3085	CA	LYS B 168	31.518	-19.059	61.209	1.00	76.07
	3086	CB	LYS B 168	30.717	-19.182	62.504	1.00	83.53
	3087	CG	LYS B 168	31.536	-19.542	63.741	1.00	84.67
40	3088	CD	LYS B 168	30.636	-20.145	64.821	1.00	86.13
	3089	CE	LYS B 168	31.271	-20.088	66.201	1.00	85.76
	3090	NZ	LYS B 168	31.243	-18.706	66.753	1.00	86.00
	3091	C	LYS B 168	30.638	-18.476	60.109	1.00	75.99

	3092	O	LYS B 168	29.787	-19.168	59.556	1.00	76.10
	3093	N	ILE B 169	30.831	-17.195	59.809	1.00	56.33
	3094	CA	ILE B 169	30.091	-16.516	58.743	1.00	56.70
	3095	CB	ILE B 169	28.740	-15.943	59.224	1.00	88.89
5	3096	CG2	ILE B 169	27.906	-17.042	59.851	1.00	89.46
	3097	CG1	ILE B 169	28.969	-14.811	60.224	1.00	88.80
	3098	CD1	ILE B 169	27.695	-14.129	60.677	1.00	89.12
	3099	C	ILE B 169	30.969	-15.375	58.243	1.00	56.55
	3100	O	ILE B 169	32.035	-15.131	58.799	1.00	56.78
10	3101	N	ASN B 170	30.527	-14.663	57.213	1.00	71.19
	3102	CA	ASN B 170	31.347	-13.584	56.672	1.00	71.78
	3103	CB	ASN B 170	31.795	-13.965	55.259	1.00	79.14
	3104	CG	ASN B 170	33.252	-13.655	55.001	1.00	78.99
	3105	OD1	ASN B 170	34.140	-14.169	55.688	1.00	79.74
15	3106	ND2	ASN B 170	33.509	-12.818	54.000	1.00	78.04
	3107	C	ASN B 170	30.690	-12.200	56.646	1.00	71.52
	3108	O	ASN B 170	29.479	-12.072	56.457	1.00	70.38
	3109	N	PRO B 171	31.496	-11.140	56.820	1.00	79.18
	3110	CD	PRO B 171	32.952	-11.187	57.033	1.00	96.01
20	3111	CA	PRO B 171	31.020	-9.753	56.819	1.00	78.61
	3112	CB	PRO B 171	32.280	-8.956	57.147	1.00	96.07
	3113	CG	PRO B 171	33.373	-9.814	56.592	1.00	97.33
	3114	C	PRO B 171	30.374	-9.330	55.500	1.00	77.50
	3115	O	PRO B 171	29.636	-8.348	55.447	1.00	78.36
25	3116	N	GLY B 172	30.660	-10.064	54.434	1.00	73.27
	3117	CA	GLY B 172	30.049	-9.747	53.158	1.00	70.47
	3118	C	GLY B 172	28.684	-10.418	53.117	1.00	68.95
	3119	O	GLY B 172	27.865	-10.169	52.229	1.00	68.33
	3120	N	ASP B 173	28.448	-11.282	54.100	1.00	61.89
30	3121	CA	ASP B 173	27.192	-12.009	54.218	1.00	58.97
	3122	CB	ASP B 173	27.444	-13.419	54.740	1.00	67.48
	3123	CG	ASP B 173	28.349	-14.219	53.836	1.00	68.30
	3124	OD1	ASP B 173	27.992	-14.413	52.658	1.00	68.23
	3125	OD2	ASP B 173	29.415	-14.658	54.309	1.00	67.70
35	3126	C	ASP B 173	26.261	-11.289	55.176	1.00	56.51
	3127	O	ASP B 173	25.234	-11.822	55.575	1.00	56.63
	3128	N	ILE B 174	26.636	-10.078	55.556	1.00	58.22
	3129	CA	ILE B 174	25.822	-9.293	56.463	1.00	55.66
	3130	CB	ILE B 174	26.659	-8.252	57.203	1.00	48.35
40	3131	CG2	ILE B 174	25.753	-7.341	57.991	1.00	47.15
	3132	CG1	ILE B 174	27.658	-8.941	58.127	1.00	45.67
	3133	CD1	ILE B 174	28.680	-7.991	58.672	1.00	45.81
	3134	C	ILE B 174	24.758	-8.571	55.665	1.00	53.97

	3135	O	ILE B 174	25.039	-7.617	54.942	1.00	53.77
	3136	N	THR B 175	23.524	-9.023	55.804	1.00	50.65
	3137	CA	THR B 175	22.438	-8.404	55.078	1.00	48.25
	3138	CB	THR B 175	22.167	-9.189	53.814	1.00	47.89
5	3139	OG1	THR B 175	22.080	-10.579	54.141	1.00	47.65
	3140	CG2	THR B 175	23.292	-8.990	52.830	1.00	47.35
	3141	C	THR B 175	21.157	-8.277	55.894	1.00	47.27
	3142	O	THR B 175	20.968	-8.952	56.907	1.00	48.30
	3143	N	GLU B 176	20.283	-7.387	55.449	1.00	40.67
10	3144	CA	GLU B 176	19.031	-7.171	56.133	1.00	38.01
	3145	CB	GLU B 176	18.082	-6.378	55.237	1.00	38.17
	3146	CG	GLU B 176	18.450	-4.914	55.152	1.00	39.37
	3147	CD	GLU B 176	17.625	-4.123	54.157	1.00	41.38
	3148	OE1	GLU B 176	16.373	-4.180	54.216	1.00	42.98
15	3149	OE2	GLU B 176	18.247	-3.431	53.319	1.00	42.31
	3150	C	GLU B 176	18.425	-8.505	56.514	1.00	38.12
	3151	O	GLU B 176	18.053	-8.724	57.663	1.00	37.44
	3152	N	GLU B 177	18.345	-9.409	55.548	1.00	43.72
	3153	CA	GLU B 177	17.775	-10.713	55.812	1.00	46.24
20	3154	CB	GLU B 177	17.830	-11.595	54.564	1.00	86.81
	3155	CG	GLU B 177	17.360	-13.019	54.832	1.00	95.81
	3156	CD	GLU B 177	17.441	-13.921	53.616	1.00	100.82
	3157	OE1	GLU B 177	18.529	-14.011	53.003	1.00	103.81
	3158	OE2	GLU B 177	16.412	-14.548	53.284	1.00	101.00
25	3159	C	GLU B 177	18.532	-11.380	56.951	1.00	44.23
	3160	O	GLU B 177	17.930	-11.859	57.915	1.00	44.32
	3161	N	LEU B 178	19.857	-11.410	56.848	1.00	41.63
	3162	CA	LEU B 178	20.655	-12.029	57.896	1.00	38.74
	3163	CB	LEU B 178	22.134	-11.738	57.676	1.00	44.89
30	3164	CG	LEU B 178	23.040	-12.230	58.803	1.00	44.18
	3165	CD1	LEU B 178	22.852	-13.711	59.013	1.00	41.50
	3166	CD2	LEU B 178	24.471	-11.925	58.462	1.00	43.37
	3167	C	LEU B 178	20.224	-11.493	59.257	1.00	36.74
	3168	O	LEU B 178	19.782	-12.244	60.137	1.00	35.45
35	3169	N	ILE B 179	20.354	-10.182	59.418	1.00	30.73
	3170	CA	ILE B 179	19.985	-9.529	60.663	1.00	28.99
	3171	CB	ILE B 179	19.963	-8.004	60.457	1.00	34.51
	3172	CG2	ILE B 179	19.054	-7.361	61.486	1.00	32.26
	3173	CG1	ILE B 179	21.398	-7.455	60.512	1.00	30.94
40	3174	CD1	ILE B 179	21.549	-6.037	59.974	1.00	28.71
	3175	C	ILE B 179	18.629	-10.021	61.202	1.00	30.52
	3176	O	ILE B 179	18.445	-10.195	62.415	1.00	29.07
	3177	N	GLY B 180	17.694	-10.250	60.283	1.00	35.31

	3178	CA	GLY B 180	16.371	-10.723	60.647	1.00	34.95
	3179	C	GLY B 180	16.430	-12.119	61.220	1.00	35.48
	3180	O	GLY B 180	15.549	-12.540	61.957	1.00	34.62
	3181	N	ASN B 181	17.482	-12.849	60.889	1.00	37.92
5	3182	CA	ASN B 181	17.615	-14.199	61.413	1.00	40.59
	3183	CB	ASN B 181	18.412	-15.067	60.424	1.00	36.21
	3184	CG	ASN B 181	17.604	-15.405	59.165	1.00	36.35
	3185	OD1	ASN B 181	16.837	-14.574	58.668	1.00	36.37
	3186	ND2	ASN B 181	17.779	-16.619	58.647	1.00	36.61
10	3187	C	ASN B 181	18.228	-14.227	62.817	1.00	41.36
	3188	O	ASN B 181	18.143	-15.227	63.512	1.00	39.95
	3189	N	TYR B 182	18.831	-13.125	63.245	1.00	47.60
	3190	CA	TYR B 182	19.420	-13.089	64.575	1.00	47.20
	3191	CB	TYR B 182	20.802	-12.455	64.535	1.00	51.38
15	3192	CG	TYR B 182	21.878	-13.365	63.990	1.00	55.42
	3193	CD1	TYR B 182	21.845	-13.815	62.671	1.00	54.58
	3194	CE1	TYR B 182	22.837	-14.660	62.173	1.00	54.20
	3195	CD2	TYR B 182	22.932	-13.781	64.794	1.00	56.79
	3196	CE2	TYR B 182	23.922	-14.624	64.303	1.00	56.49
20	3197	CZ	TYR B 182	23.867	-15.062	62.997	1.00	55.81
	3198	OH	TYR B 182	24.826	-15.929	62.537	1.00	53.14
	3199	C	TYR B 182	18.540	-12.335	65.556	1.00	47.45
	3200	O	TYR B 182	18.817	-12.329	66.760	1.00	47.85
	3201	N	LEU B 183	17.481	-11.705	65.041	1.00	38.04
25	3202	CA	LEU B 183	16.537	-10.959	65.880	1.00	35.84
	3203	CB	LEU B 183	15.627	-10.122	65.002	1.00	37.83
	3204	CG	LEU B 183	16.337	-8.992	64.272	1.00	37.45
	3205	CD1	LEU B 183	15.406	-8.356	63.274	1.00	36.12
	3206	CD2	LEU B 183	16.777	-7.954	65.273	1.00	37.86
30	3207	C	LEU B 183	15.686	-11.862	66.797	1.00	36.04
	3208	O	LEU B 183	15.612	-13.079	66.623	1.00	34.20
	3209	N	PHE B 184	15.045	-11.266	67.785	1.00	48.34
	3210	CA	PHE B 184	14.237	-12.045	68.700	1.00	48.02
	3211	CB	PHE B 184	13.717	-11.154	69.819	1.00	33.47
35	3212	CG	PHE B 184	14.742	-10.829	70.860	1.00	32.80
	3213	CD1	PHE B 184	14.584	-9.726	71.680	1.00	29.31
	3214	CD2	PHE B 184	15.833	-11.669	71.070	1.00	31.94
	3215	CE1	PHE B 184	15.484	-9.472	72.688	1.00	26.20
	3216	CE2	PHE B 184	16.732	-11.416	72.082	1.00	30.20
40	3217	CZ	PHE B 184	16.555	-10.317	72.891	1.00	27.54
	3218	C	PHE B 184	13.068	-12.738	68.032	1.00	48.12
	3219	O	PHE B 184	12.483	-13.648	68.612	1.00	46.91
	3220	N	THR B 185	12.731	-12.322	66.816	1.00	39.62

	3221	CA	THR	B	185	11.599	-12.913	66.101	1.00	39.60
	3222	CB	THR	B	185	10.800	-11.825	65.398	1.00	33.52
	3223	OG1	THR	B	185	11.706	-10.915	64.772	1.00	36.38
	3224	CG2	THR	B	185	9.959	-11.076	66.371	1.00	31.31
5	3225	C	THR	B	185	11.952	-13.976	65.056	1.00	39.83
	3226	O	THR	B	185	11.160	-14.235	64.148	1.00	40.45
	3227	N	GLN	B	186	13.120	-14.599	65.182	1.00	33.11
	3228	CA	GLN	B	186	13.544	-15.601	64.212	1.00	36.30
	3229	CB	GLN	B	186	14.980	-16.019	64.475	1.00	49.10
10	3230	CG	GLN	B	186	15.221	-16.690	65.814	1.00	51.91
	3231	CD	GLN	B	186	16.706	-16.826	66.113	1.00	53.47
	3232	OE1	GLN	B	186	17.437	-15.836	66.126	1.00	54.44
	3233	NE2	GLN	B	186	17.159	-18.047	66.346	1.00	53.85
	3234	C	GLN	B	186	12.662	-16.820	64.227	1.00	38.04
15	3235	O	GLN	B	186	12.339	-17.364	63.182	1.00	35.86
	3236	N	HIS	B	187	12.278	-17.247	65.423	1.00	52.33
	3237	CA	HIS	B	187	11.429	-18.414	65.599	1.00	55.53
	3238	CB	HIS	B	187	10.948	-18.480	67.042	1.00	82.61
	3239	CG	HIS	B	187	12.034	-18.222	68.036	1.00	89.37
20	3240	CD2	HIS	B	187	12.029	-17.550	69.212	1.00	91.93
	3241	ND1	HIS	B	187	13.325	-18.672	67.855	1.00	91.93
	3242	CE1	HIS	B	187	14.070	-18.286	68.876	1.00	93.79
	3243	NE2	HIS	B	187	13.308	-17.603	69.713	1.00	94.84
	3244	C	HIS	B	187	10.251	-18.368	64.654	1.00	54.83
25	3245	O	HIS	B	187	9.909	-19.371	64.036	1.00	57.33
	3246	N	LEU	B	188	9.632	-17.200	64.539	1.00	44.86
	3247	CA	LEU	B	188	8.497	-17.027	63.647	1.00	44.07
	3248	CB	LEU	B	188	8.013	-15.576	63.680	1.00	44.44
	3249	CG	LEU	B	188	6.694	-15.198	64.372	1.00	45.88
30	3250	CD1	LEU	B	188	6.716	-15.580	65.844	1.00	47.14
	3251	CD2	LEU	B	188	6.468	-13.698	64.223	1.00	43.76
	3252	C	LEU	B	188	8.863	-17.405	62.212	1.00	44.68
	3253	O	LEU	B	188	9.963	-17.149	61.734	1.00	45.59
	3254	N	PRO	B	189	7.942	-18.041	61.508	1.00	44.28
35	3255	CD	PRO	B	189	6.603	-18.477	61.919	1.00	46.24
	3256	CA	PRO	B	189	8.222	-18.429	60.129	1.00	43.98
	3257	CB	PRO	B	189	6.973	-19.197	59.733	1.00	47.15
	3258	CG	PRO	B	189	5.901	-18.545	60.591	1.00	47.38
	3259	C	PRO	B	189	8.455	-17.226	59.232	1.00	44.37
40	3260	O	PRO	B	189	7.685	-16.268	59.260	1.00	44.39
	3261	N	LYS	B	190	9.512	-17.315	58.426	1.00	45.86
	3262	CA	LYS	B	190	9.937	-16.271	57.488	1.00	45.86
	3263	CB	LYS	B	190	10.537	-16.905	56.225	1.00	60.84

	3264	CG	LYS B 190	11.941	-17.470	56.407	1.00	63.63
	3265	CD	LYS B 190	13.019	-16.389	56.223	1.00	66.12
	3266	CE	LYS B 190	14.436	-16.857	56.654	1.00	67.52
	3267	NZ	LYS B 190	15.093	-17.892	55.793	1.00	67.17
5	3268	C	LYS B 190	8.902	-15.242	57.073	1.00	45.92
	3269	O	LYS B 190	9.076	-14.053	57.308	1.00	45.33
	3270	N	ASP B 191	7.821	-15.682	56.453	1.00	41.73
	3271	CA	ASP B 191	6.824	-14.733	55.996	1.00	41.48
	3272	CB	ASP B 191	5.856	-15.402	55.030	1.00	63.45
10	3273	CG	ASP B 191	6.313	-15.294	53.592	1.00	67.43
	3274	OD1	ASP B 191	5.676	-15.921	52.717	1.00	70.88
	3275	OD2	ASP B 191	7.306	-14.577	53.329	1.00	69.09
	3276	C	ASP B 191	6.042	-14.028	57.070	1.00	40.03
	3277	O	ASP B 191	5.336	-13.078	56.775	1.00	39.83
15	3278	N	LEU B 192	6.168	-14.449	58.321	1.00	47.34
	3279	CA	LEU B 192	5.387	-13.798	59.350	1.00	45.66
	3280	CB	LEU B 192	4.504	-14.831	60.040	1.00	38.64
	3281	CG	LEU B 192	3.454	-15.563	59.196	1.00	36.65
	3282	CD1	LEU B 192	2.572	-16.388	60.112	1.00	38.15
20	3283	CD2	LEU B 192	2.590	-14.576	58.447	1.00	34.11
	3284	C	LEU B 192	6.144	-13.000	60.395	1.00	45.53
	3285	O	LEU B 192	5.544	-12.530	61.356	1.00	48.01
	3286	N	ARG B 193	7.445	-12.816	60.216	1.00	37.70
	3287	CA	ARG B 193	8.244	-12.070	61.185	1.00	36.20
25	3288	CB	ARG B 193	9.701	-12.193	60.805	1.00	39.60
	3289	CG	ARG B 193	10.216	-13.599	60.941	1.00	42.31
	3290	CD	ARG B 193	11.435	-13.806	60.087	1.00	43.05
	3291	NE	ARG B 193	12.214	-14.948	60.547	1.00	44.54
	3292	CZ	ARG B 193	13.422	-15.261	60.085	1.00	46.24
30	3293	NH1	ARG B 193	13.997	-14.519	59.135	1.00	44.13
	3294	NH2	ARG B 193	14.072	-16.297	60.598	1.00	46.66
	3295	C	ARG B 193	7.871	-10.590	61.374	1.00	36.40
	3296	O	ARG B 193	7.876	-10.083	62.494	1.00	35.46
	3297	N	ASP B 194	7.543	-9.897	60.289	1.00	43.01
35	3298	CA	ASP B 194	7.169	-8.487	60.382	1.00	43.32
	3299	CB	ASP B 194	7.602	-7.725	59.136	1.00	38.38
	3300	CG	ASP B 194	9.076	-7.825	58.881	1.00	40.95
	3301	OD1	ASP B 194	9.820	-8.219	59.810	1.00	40.39
	3302	OD2	ASP B 194	9.492	-7.500	57.751	1.00	42.29
40	3303	C	ASP B 194	5.678	-8.308	60.532	1.00	42.96
	3304	O	ASP B 194	4.907	-8.962	59.852	1.00	45.54
	3305	N	PRO B 195	5.248	-7.415	61.429	1.00	34.18
	3306	CD	PRO B 195	5.994	-6.877	62.572	1.00	31.05



	3307	CA	PRO B 195	3.824	-7.177	61.626	1.00	33.33
	3308	CB	PRO B 195	3.795	-6.376	62.923	1.00	28.62
	3309	CG	PRO B 195	4.930	-6.870	63.642	1.00	30.37
	3310	C	PRO B 195	3.271	-6.362	60.469	1.00	32.39
5	3311	O	PRO B 195	3.950	-5.469	59.973	1.00	33.28
	3312	N	ASP B 196	2.040	-6.658	60.049	1.00	33.82
	3313	CA	ASP B 196	1.407	-5.894	58.967	1.00	33.08
	3314	CB	ASP B 196	0.356	-6.723	58.213	1.00	40.99
	3315	CG	ASP B 196	0.898	-8.031	57.676	1.00	41.96
10	3316	OD1	ASP B 196	1.002	-9.013	58.450	1.00	42.06
	3317	OD2	ASP B 196	1.215	-8.063	56.467	1.00	43.06
	3318	C	ASP B 196	0.685	-4.704	59.599	1.00	31.99
	3319	O	ASP B 196	0.508	-3.652	58.973	1.00	31.68
	3320	N	LEU B 197	0.281	-4.888	60.851	1.00	40.44
15	3321	CA	LEU B 197	-0.448	-3.867	61.578	1.00	41.69
	3322	CB	LEU B 197	-1.941	-4.217	61.522	1.00	39.81
	3323	CG	LEU B 197	-2.962	-3.590	62.471	1.00	38.39
	3324	CD1	LEU B 197	-3.375	-2.208	61.983	1.00	34.37
	3325	CD2	LEU B 197	-4.163	-4.514	62.546	1.00	40.85
20	3326	C	LEU B 197	0.019	-3.762	63.031	1.00	42.42
	3327	O	LEU B 197	-0.003	-4.757	63.764	1.00	42.95
	3328	N	ILE B 198	0.445	-2.564	63.438	1.00	34.38
	3329	CA	ILE B 198	0.887	-2.335	64.807	1.00	35.37
	3330	CB	ILE B 198	2.266	-1.644	64.850	1.00	26.32
25	3331	CG2	ILE B 198	2.471	-0.929	66.202	1.00	23.20
	3332	CG1	ILE B 198	3.359	-2.690	64.602	1.00	23.88
	3333	CD1	ILE B 198	4.757	-2.179	64.832	1.00	18.24
	3334	C	ILE B 198	-0.141	-1.456	65.484	1.00	36.77
	3335	O	ILE B 198	-0.430	-0.369	64.981	1.00	37.04
30	3336	N	ILE B 199	-0.668	-1.926	66.621	1.00	41.16
	3337	CA	ILE B 199	-1.721	-1.240	67.400	1.00	43.74
	3338	CB	ILE B 199	-2.941	-2.196	67.652	1.00	49.23
	3339	CG2	ILE B 199	-3.835	-1.671	68.767	1.00	45.95
	3340	CG1	ILE B 199	-3.760	-2.355	66.383	1.00	47.61
35	3341	CD1	ILE B 199	-4.875	-3.363	66.540	1.00	49.10
	3342	C	ILE B 199	-1.315	-0.703	68.771	1.00	44.54
	3343	O	ILE B 199	-0.899	-1.468	69.652	1.00	45.29
	3344	N	ARG B 200	-1.479	0.608	68.953	1.00	36.74
	3345	CA	ARG B 200	-1.182	1.270	70.230	1.00	37.18
40	3346	CB	ARG B 200	-0.257	2.482	70.041	1.00	44.70
	3347	CG	ARG B 200	0.216	3.120	71.367	1.00	45.83
	3348	CD	ARG B 200	0.776	2.048	72.313	1.00	46.69
	3349	NE	ARG B 200	1.375	2.561	73.549	1.00	50.52

	3350	CZ	ARG B 200	2.447	3.348	73.608	1.00	49.70
	3351	NH1	ARG B 200	3.055	3.734	72.496	1.00	50.01
	3352	NH2	ARG B 200	2.923	3.730	74.787	1.00	49.31
	3353	C	ARG B 200	-2.499	1.771	70.782	1.00	36.96
5	3354	O	ARG B 200	-3.154	2.597	70.142	1.00	34.80
	3355	N	THR B 201	-2.876	1.293	71.963	1.00	42.28
	3356	CA	THR B 201	-4.134	1.694	72.584	1.00	43.27
	3357	CB	THR B 201	-4.562	0.676	73.635	1.00	26.81
	3358	OG1	THR B 201	-3.507	0.517	74.583	1.00	26.30
10	3359	CG2	THR B 201	-4.892	-0.660	72.999	1.00	24.68
	3360	C	THR B 201	-4.047	3.062	73.268	1.00	46.06
	3361	O	THR B 201	-3.351	3.961	72.795	1.00	47.90
	3362	N	SER B 202	-4.782	3.204	74.373	1.00	44.92
	3363	CA	SER B 202	-4.824	4.414	75.199	1.00	45.07
15	3364	CB	SER B 202	-4.196	4.109	76.561	1.00	68.92
	3365	OG	SER B 202	-2.942	3.461	76.416	1.00	68.80
	3366	C	SER B 202	-4.167	5.653	74.614	1.00	44.69
	3367	O	SER B 202	-3.028	5.967	74.947	1.00	44.52
	3368	N	GLY B 203	-4.908	6.349	73.753	1.00	56.74
20	3369	CA	GLY B 203	-4.432	7.557	73.095	1.00	56.52
	3370	C	GLY B 203	-2.981	7.888	73.357	1.00	57.20
	3371	O	GLY B 203	-2.661	8.422	74.413	1.00	60.64
	3372	N	GLU B 204	-2.112	7.568	72.402	1.00	44.00
	3373	CA	GLU B 204	-0.674	7.815	72.510	1.00	41.03
25	3374	CB	GLU B 204	-0.020	6.803	73.446	1.00	42.47
	3375	CG	GLU B 204	-0.151	7.098	74.908	1.00	44.49
	3376	CD	GLU B 204	0.202	8.529	75.230	1.00	47.65
	3377	OE1	GLU B 204	1.002	9.134	74.484	1.00	47.65
	3378	OE2	GLU B 204	-0.319	9.052	76.238	1.00	50.02
30	3379	C	GLU B 204	-0.036	7.673	71.137	1.00	40.26
	3380	O	GLU B 204	-0.246	6.685	70.444	1.00	39.65
	3381	N	LEU B 205	0.755	8.648	70.732	1.00	40.79
	3382	CA	LEU B 205	1.368	8.543	69.424	1.00	39.70
	3383	CB	LEU B 205	1.054	9.789	68.586	1.00	35.62
35	3384	CG	LEU B 205	-0.410	10.024	68.185	1.00	35.68
	3385	CD1	LEU B 205	-0.414	10.904	66.944	1.00	34.09
	3386	CD2	LEU B 205	-1.150	8.712	67.896	1.00	33.17
	3387	C	LEU B 205	2.868	8.299	69.485	1.00	40.49
	3388	O	LEU B 205	3.674	9.127	69.068	1.00	39.65
40	3389	N	ARG B 206	3.233	7.138	70.005	1.00	38.80
	3390	CA	ARG B 206	4.626	6.759	70.115	1.00	40.82
	3391	CB	ARG B 206	5.175	7.242	71.464	1.00	46.44
	3392	CG	ARG B 206	4.403	6.733	72.680	1.00	49.25

	3393	CD	ARG B 206	5.077	7.119	73.986	1.00	50.40
	3394	NE	ARG B 206	4.926	8.535	74.288	1.00	51.98
	3395	CZ	ARG B 206	4.201	9.012	75.297	1.00	53.40
	3396	NH1	ARG B 206	3.557	8.189	76.111	1.00	51.40
5	3397	NH2	ARG B 206	4.113	10.322	75.491	1.00	54.54
	3398	C	ARG B 206	4.709	5.233	69.988	1.00	40.18
	3399	O	ARG B 206	3.697	4.535	70.141	1.00	40.42
	3400	N	LEU B 207	5.901	4.714	69.694	1.00	40.36
	3401	CA	LEU B 207	6.082	3.267	69.542	1.00	38.78
10	3402	CB	LEU B 207	6.827	2.943	68.248	1.00	34.97
	3403	CG	LEU B 207	5.915	2.949	67.024	1.00	37.95
	3404	CD1	LEU B 207	6.712	3.206	65.771	1.00	37.88
	3405	CD2	LEU B 207	5.166	1.634	66.949	1.00	37.85
	3406	C	LEU B 207	6.835	2.684	70.700	1.00	37.93
15	3407	O	LEU B 207	7.096	1.492	70.737	1.00	39.09
	3408	N	SER B 208	7.194	3.545	71.638	1.00	40.79
	3409	CA	SER B 208	7.930	3.140	72.821	1.00	40.20
	3410	CB	SER B 208	6.946	2.888	73.963	1.00	42.07
	3411	OG	SER B 208	6.207	4.066	74.244	1.00	43.06
20	3412	C	SER B 208	8.858	1.933	72.634	1.00	39.55
	3413	O	SER B 208	8.811	0.973	73.396	1.00	37.18
	3414	N	ASN B 209	9.693	2.001	71.605	1.00	34.58
	3415	CA	ASN B 209	10.670	0.968	71.306	1.00	30.52
	3416	CB	ASN B 209	11.650	0.854	72.473	1.00	26.40
25	3417	CG	ASN B 209	13.036	0.448	72.034	1.00	25.66
	3418	OD1	ASN B 209	13.800	-0.097	72.808	1.00	27.06
	3419	ND2	ASN B 209	13.372	0.730	70.790	1.00	26.24
	3420	C	ASN B 209	10.088	-0.410	71.006	1.00	29.69
	3421	O	ASN B 209	10.634	-1.424	71.434	1.00	30.39
30	3422	N	PHE B 210	8.997	-0.463	70.258	1.00	31.34
	3423	CA	PHE B 210	8.373	-1.751	69.935	1.00	31.64
	3424	CB	PHE B 210	6.864	-1.663	70.147	1.00	33.86
	3425	CG	PHE B 210	6.155	-2.984	70.058	1.00	35.91
	3426	CD1	PHE B 210	6.340	-3.956	71.032	1.00	33.45
35	3427	CD2	PHE B 210	5.266	-3.242	69.020	1.00	36.79
	3428	CE1	PHE B 210	5.649	-5.161	70.984	1.00	33.50
	3429	CE2	PHE B 210	4.575	-4.444	68.964	1.00	33.34
	3430	CZ	PHE B 210	4.770	-5.403	69.953	1.00	35.11
	3431	C	PHE B 210	8.655	-2.205	68.500	1.00	30.79
40	3432	O	PHE B 210	8.164	-1.624	67.545	1.00	31.80
	3433	N	LEU B 211	9.454	-3.243	68.350	1.00	25.80
	3434	CA	LEU B 211	9.761	-3.752	67.032	1.00	24.56
	3435	CB	LEU B 211	8.552	-4.486	66.462	1.00	22.76

	3436	CG	LEU B 211	7.958	-5.587	67.334	1.00	21.58
	3437	CD1	LEU B 211	6.632	-6.017	66.719	1.00	21.38
	3438	CD2	LEU B 211	8.930	-6.746	67.479	1.00	16.04
	3439	C	LEU B 211	10.195	-2.677	66.055	1.00	25.45
5	3440	O	LEU B 211	9.636	-2.542	64.977	1.00	27.46
	3441	N	PRO B 212	11.216	-1.907	66.413	1.00	28.22
	3442	CD	PRO B 212	12.169	-2.103	67.508	1.00	29.78
	3443	CA	PRO B 212	11.695	-0.862	65.524	1.00	28.18
	3444	CB	PRO B 212	12.855	-0.280	66.297	1.00	29.38
10	3445	CG	PRO B 212	13.413	-1.475	66.933	1.00	27.86
	3446	C	PRO B 212	12.141	-1.428	64.179	1.00	30.14
	3447	O	PRO B 212	12.040	-0.748	63.174	1.00	31.16
	3448	N	TRP B 213	12.638	-2.663	64.152	1.00	25.64
	3449	CA	TRP B 213	13.081	-3.241	62.887	1.00	25.84
15	3450	CB	TRP B 213	14.240	-4.216	63.129	1.00	38.97
	3451	CG	TRP B 213	14.743	-4.926	61.887	1.00	40.05
	3452	CD2	TRP B 213	15.990	-4.724	61.220	1.00	39.67
	3453	CE2	TRP B 213	16.012	-5.584	60.106	1.00	39.16
	3454	CE3	TRP B 213	17.093	-3.895	61.453	1.00	40.30
20	3455	CD1	TRP B 213	14.088	-5.870	61.173	1.00	38.83
	3456	NE1	TRP B 213	14.836	-6.273	60.103	1.00	37.40
	3457	CZ2	TRP B 213	17.082	-5.643	59.226	1.00	40.19
	3458	CZ3	TRP B 213	18.160	-3.951	60.573	1.00	43.18
	3459	CH2	TRP B 213	18.144	-4.821	59.471	1.00	41.81
25	3460	C	TRP B 213	11.984	-3.936	62.077	1.00	27.33
	3461	O	TRP B 213	11.794	-3.639	60.891	1.00	25.38
	3462	N	GLN B 214	11.263	-4.856	62.708	1.00	31.07
	3463	CA	GLN B 214	10.218	-5.599	62.016	1.00	32.88
	3464	CB	GLN B 214	9.759	-6.779	62.874	1.00	35.62
30	3465	CG	GLN B 214	10.879	-7.619	63.431	1.00	37.92
	3466	CD	GLN B 214	11.432	-7.075	64.727	1.00	37.06
	3467	OE1	GLN B 214	11.505	-5.867	64.922	1.00	40.55
	3468	NE2	GLN B 214	11.841	-7.965	65.615	1.00	33.87
	3469	C	GLN B 214	8.991	-4.766	61.614	1.00	32.91
35	3470	O	GLN B 214	8.306	-5.093	60.642	1.00	32.25
	3471	N	GLY B 215	8.704	-3.704	62.365	1.00	26.95
	3472	CA	GLY B 215	7.553	-2.882	62.053	1.00	25.25
	3473	C	GLY B 215	7.949	-1.749	61.143	1.00	25.33
	3474	O	GLY B 215	7.160	-0.864	60.841	1.00	26.74
40	3475	N	ALA B 216	9.191	-1.788	60.696	1.00	29.18
	3476	CA	ALA B 216	9.722	-0.751	59.829	1.00	29.54
	3477	CB	ALA B 216	11.004	-1.238	59.167	1.00	56.27
	3478	C	ALA B 216	8.752	-0.268	58.776	1.00	28.81

	3479	O	ALA B 216	8.853	0.871	58.332	1.00	29.21
	3480	N	TYR B 217	7.827	-1.135	58.362	1.00	33.05
	3481	CA	TYR B 217	6.859	-0.762	57.337	1.00	33.52
	3482	CB	TYR B 217	7.129	-1.456	56.006	1.00	26.97
5	3483	CG	TYR B 217	8.494	-1.239	55.375	1.00	27.03
	3484	CD1	TYR B 217	9.606	-2.025	55.751	1.00	28.49
	3485	CE1	TYR B 217	10.823	-1.913	55.083	1.00	26.38
	3486	CD2	TYR B 217	8.657	-0.332	54.325	1.00	27.94
	3487	CE2	TYR B 217	9.867	-0.217	53.658	1.00	29.81
10	3488	CZ	TYR B 217	10.936	-1.012	54.036	1.00	30.32
	3489	OH	TYR B 217	12.096	-0.935	53.320	1.00	35.46
	3490	C	TYR B 217	5.435	-1.091	57.710	1.00	35.00
	3491	O	TYR B 217	4.535	-0.940	56.881	1.00	37.26
	3492	N	SER B 218	5.202	-1.544	58.935	1.00	31.38
15	3493	CA	SER B 218	3.835	-1.880	59.312	1.00	34.90
	3494	CB	SER B 218	3.823	-2.590	60.667	1.00	44.37
	3495	OG	SER B 218	4.843	-2.094	61.506	1.00	49.79
	3496	C	SER B 218	2.885	-0.686	59.316	1.00	34.66
	3497	O	SER B 218	3.316	0.460	59.255	1.00	35.96
20	3498	N	GLU B 219	1.586	-0.980	59.345	1.00	46.39
	3499	CA	GLU B 219	0.540	0.042	59.376	1.00	48.11
	3500	CB	GLU B 219	-0.780	-0.477	58.787	1.00	42.82
	3501	CG	GLU B 219	-0.765	-0.799	57.295	1.00	40.25
	3502	CD	GLU B 219	-0.760	0.443	56.421	1.00	41.75
25	3503	OE1	GLU B 219	-0.641	1.561	56.965	1.00	41.05
	3504	OE2	GLU B 219	-0.869	0.295	55.185	1.00	43.48
	3505	C	GLU B 219	0.305	0.347	60.832	1.00	48.55
	3506	O	GLU B 219	0.145	-0.566	61.651	1.00	49.82
	3507	N	LEU B 220	0.279	1.623	61.168	1.00	42.65
30	3508	CA	LEU B 220	0.062	1.981	62.551	1.00	44.53
	3509	CB	LEU B 220	0.892	3.210	62.912	1.00	34.86
	3510	CG	LEU B 220	2.283	2.957	63.502	1.00	31.02
	3511	CD1	LEU B 220	2.922	1.740	62.852	1.00	29.61
	3512	CD2	LEU B 220	3.133	4.208	63.320	1.00	32.36
35	3513	C	LEU B 220	-1.403	2.250	62.769	1.00	46.39
	3514	O	LEU B 220	-2.089	2.722	61.867	1.00	47.21
	3515	N	TYR B 221	-1.882	1.929	63.964	1.00	53.95
	3516	CA	TYR B 221	-3.278	2.147	64.310	1.00	55.64
	3517	CB	TYR B 221	-4.115	0.923	63.976	1.00	58.57
40	3518	CG	TYR B 221	-5.529	1.036	64.477	1.00	60.14
	3519	CD1	TYR B 221	-6.372	2.048	64.026	1.00	59.26
	3520	CE1	TYR B 221	-7.661	2.176	64.518	1.00	61.05
	3521	CD2	TYR B 221	-6.012	0.155	65.430	1.00	61.11

	3522	CE2	TYR	B	221	-7.294	0.274	65.930	1.00	62.90
	3523	CZ	TYR	B	221	-8.116	1.283	65.476	1.00	62.23
	3524	OH	TYR	B	221	-9.384	1.397	66.009	1.00	60.46
	3525	C	TYR	B	221	-3.451	2.471	65.781	1.00	57.07
5	3526	O	TYR	B	221	-3.361	1.586	66.639	1.00	58.08
	3527	N	PHE	B	222	-3.710	3.749	66.050	1.00	56.47
	3528	CA	PHE	B	222	-3.912	4.262	67.402	1.00	57.27
	3529	CB	PHE	B	222	-3.249	5.630	67.548	1.00	49.96
	3530	CG	PHE	B	222	-1.891	5.695	66.946	1.00	48.78
10	3531	CD1	PHE	B	222	-1.735	5.891	65.589	1.00	47.54
	3532	CD2	PHE	B	222	-0.760	5.524	67.731	1.00	49.19
	3533	CE1	PHE	B	222	-0.476	5.916	65.019	1.00	48.43
	3534	CE2	PHE	B	222	0.504	5.547	67.167	1.00	46.75
	3535	CZ	PHE	B	222	0.643	5.744	65.810	1.00	47.56
15	3536	C	PHE	B	222	-5.393	4.387	67.762	1.00	58.98
	3537	O	PHE	B	222	-6.233	4.773	66.937	1.00	59.22
	3538	N	THR	B	223	-5.700	4.074	69.013	1.00	65.91
	3539	CA	THR	B	223	-7.064	4.137	69.491	1.00	66.56
	3540	CB	THR	B	223	-7.710	2.747	69.429	1.00	68.79
20	3541	OG1	THR	B	223	-9.101	2.874	69.729	1.00	73.73
	3542	CG2	THR	B	223	-7.054	1.784	70.423	1.00	66.05
	3543	C	THR	B	223	-7.092	4.667	70.921	1.00	67.20
	3544	O	THR	B	223	-6.491	4.077	71.823	1.00	68.64
	3545	N	ASP	B	224	-7.793	5.780	71.126	1.00	59.07
25	3546	CA	ASP	B	224	-7.875	6.392	72.450	1.00	57.77
	3547	CB	ASP	B	224	-8.771	7.641	72.413	1.00	59.96
	3548	CG	ASP	B	224	-8.166	8.766	71.589	1.00	62.19
	3549	OD1	ASP	B	224	-7.818	8.503	70.421	1.00	64.70
	3550	OD2	ASP	B	224	-8.031	9.903	72.095	1.00	61.88
30	3551	C	ASP	B	224	-8.340	5.461	73.569	1.00	56.76
	3552	O	ASP	B	224	-8.283	5.837	74.737	1.00	56.94
	3553	N	THR	B	225	-8.781	4.249	73.235	1.00	40.23
	3554	CA	THR	B	225	-9.243	3.326	74.275	1.00	41.21
	3555	CB	THR	B	225	-10.184	2.228	73.710	1.00	69.35
35	3556	OG1	THR	B	225	-9.579	0.943	73.891	1.00	71.55
	3557	CG2	THR	B	225	-10.481	2.466	72.240	1.00	70.88
	3558	C	THR	B	225	-8.111	2.642	75.033	1.00	39.57
	3559	O	THR	B	225	-7.111	2.280	74.443	1.00	38.26
	3560	N	LEU	B	226	-8.288	2.478	76.343	1.00	49.79
40	3561	CA	LEU	B	226	-7.297	1.834	77.202	1.00	50.45
	3562	CB	LEU	B	226	-7.552	2.146	78.679	1.00	73.50
	3563	CG	LEU	B	226	-7.670	3.606	79.135	1.00	75.22
	3564	CD1	LEU	B	226	-6.975	3.744	80.476	1.00	73.87

	3565	CD2	LEU B 226	-7.065	4.561	78.114	1.00	73.91
	3566	C	LEU B 226	-7.346	0.338	77.003	1.00	50.06
	3567	O	LEU B 226	-8.382	-0.213	76.671	1.00	50.52
	3568	N	TRP B 227	-6.220	-0.317	77.238	1.00	56.52
5	3569	CA	TRP B 227	-6.109	-1.749	77.031	1.00	55.63
	3570	CB	TRP B 227	-4.836	-2.282	77.672	1.00	40.08
	3571	CG	TRP B 227	-4.591	-3.710	77.343	1.00	32.65
	3572	CD2	TRP B 227	-4.712	-4.336	76.056	1.00	29.73
	3573	CE2	TRP B 227	-4.357	-5.698	76.220	1.00	29.35
10	3574	CE3	TRP B 227	-5.086	-3.882	74.778	1.00	30.04
	3575	CD1	TRP B 227	-4.183	-4.682	78.202	1.00	32.68
	3576	NE1	TRP B 227	-4.039	-5.877	77.541	1.00	31.63
	3577	CZ2	TRP B 227	-4.362	-6.616	75.158	1.00	27.35
	3578	CZ3	TRP B 227	-5.092	-4.802	73.714	1.00	27.85
15	3579	CH2	TRP B 227	-4.729	-6.154	73.923	1.00	28.92
	3580	C	TRP B 227	-7.272	-2.637	77.446	1.00	57.42
	3581	O	TRP B 227	-7.930	-3.220	76.593	1.00	57.78
	3582	N	PRO B 228	-7.550	-2.758	78.751	1.00	59.57
	3583	CD	PRO B 228	-6.949	-2.138	79.942	1.00	82.42
20	3584	CA	PRO B 228	-8.669	-3.634	79.131	1.00	61.06
	3585	CB	PRO B 228	-8.747	-3.451	80.649	1.00	84.47
	3586	CG	PRO B 228	-7.327	-3.129	81.022	1.00	83.95
	3587	C	PRO B 228	-9.997	-3.339	78.417	1.00	60.86
	3588	O	PRO B 228	-10.852	-4.210	78.278	1.00	59.30
25	3589	N	ASP B 229	-10.157	-2.106	77.960	1.00	63.90
	3590	CA	ASP B 229	-11.363	-1.717	77.257	1.00	65.67
	3591	CB	ASP B 229	-11.548	-0.203	77.324	1.00	66.08
	3592	CG	ASP B 229	-11.601	0.310	78.741	1.00	67.12
	3593	OD1	ASP B 229	-11.670	1.545	78.925	1.00	66.03
30	3594	OD2	ASP B 229	-11.574	-0.527	79.669	1.00	66.23
	3595	C	ASP B 229	-11.248	-2.147	75.805	1.00	66.75
	3596	O	ASP B 229	-12.000	-1.681	74.950	1.00	67.93
	3597	N	PHE B 230	-10.289	-3.021	75.523	1.00	69.70
	3598	CA	PHE B 230	-10.096	-3.506	74.164	1.00	67.90
35	3599	CB	PHE B 230	-8.606	-3.656	73.841	1.00	35.34
	3600	CG	PHE B 230	-8.283	-3.509	72.382	1.00	26.39
	3601	CD1	PHE B 230	-8.216	-2.262	71.801	1.00	21.82
	3602	CD2	PHE B 230	-8.033	-4.622	71.589	1.00	22.39
	3603	CE1	PHE B 230	-7.901	-2.112	70.446	1.00	18.61
40	3604	CE2	PHE B 230	-7.720	-4.476	70.236	1.00	17.21
	3605	CZ	PHE B 230	-7.654	-3.215	69.669	1.00	16.11
	3606	C	PHE B 230	-10.788	-4.859	74.130	1.00	70.82
	3607	O	PHE B 230	-10.607	-5.682	75.032	1.00	70.34

	3608	N	ASP B 231	-11.588	-5.065	73.085	1.00105.90
	3609	CA	ASP B 231	-12.365	-6.285	72.900	1.00107.50
	3610	CB	ASP B 231	-13.781	-6.063	73.415	1.00 85.49
	3611	CG	ASP B 231	-14.412	-4.824	72.820	1.00 87.23
5	3612	OD1	ASP B 231	-14.335	-4.670	71.582	1.00 86.76
	3613	OD2	ASP B 231	-14.973	-4.006	73.580	1.00 88.98
	3614	C	ASP B 231	-12.439	-6.660	71.426	1.00108.26
	3615	O	ASP B 231	-11.697	-6.135	70.601	1.00108.49
	3616	N	GLU B 232	-13.372	-7.547	71.104	1.00 62.60
10	3617	CA	GLU B 232	-13.553	-8.016	69.740	1.00 61.27
	3618	CB	GLU B 232	-14.574	-9.143	69.723	1.00 64.23
	3619	CG	GLU B 232	-14.395	-10.072	68.551	1.00 64.71
	3620	CD	GLU B 232	-15.119	-11.386	68.743	1.00 64.28
	3621	OE1	GLU B 232	-14.865	-12.066	69.766	1.00 62.46
15	3622	OE2	GLU B 232	-15.940	-11.737	67.868	1.00 64.88
	3623	C	GLU B 232	-13.972	-6.925	68.761	1.00 61.20
	3624	O	GLU B 232	-13.516	-6.894	67.620	1.00 61.27
	3625	N	ALA B 233	-14.844	-6.027	69.197	1.00 70.90
	3626	CA	ALA B 233	-15.288	-4.949	68.318	1.00 73.06
20	3627	CB	ALA B 233	-16.464	-4.209	68.938	1.00 93.53
	3628	C	ALA B 233	-14.142	-3.979	68.065	1.00 73.31
	3629	O	ALA B 233	-14.200	-3.153	67.151	1.00 73.80
	3630	N	ALA B 234	-13.102	-4.086	68.888	1.00 71.16
	3631	CA	ALA B 234	-11.932	-3.217	68.777	1.00 70.00
25	3632	CB	ALA B 234	-11.236	-3.120	70.132	1.00 96.43
	3633	C	ALA B 234	-10.957	-3.741	67.725	1.00 67.92
	3634	O	ALA B 234	-10.543	-3.005	66.816	1.00 65.56
	3635	N	LEU B 235	-10.594	-5.015	67.871	1.00 55.18
	3636	CA	LEU B 235	-9.678	-5.668	66.954	1.00 54.73
30	3637	CB	LEU B 235	-9.623	-7.170	67.238	1.00 48.95
	3638	CG	LEU B 235	-8.233	-7.803	67.303	1.00 48.32
	3639	CD1	LEU B 235	-8.335	-9.313	67.500	1.00 46.48
	3640	CD2	LEU B 235	-7.496	-7.479	66.035	1.00 47.32
	3641	C	LEU B 235	-10.235	-5.431	65.567	1.00 56.02
35	3642	O	LEU B 235	-9.517	-5.035	64.643	1.00 54.95
	3643	N	GLN B 236	-11.543	-5.645	65.447	1.00 70.62
	3644	CA	GLN B 236	-12.244	-5.487	64.185	1.00 70.74
	3645	CB	GLN B 236	-13.666	-6.046	64.321	1.00 88.42
	3646	CG	GLN B 236	-13.679	-7.553	64.590	1.00 92.34
40	3647	CD	GLN B 236	-15.072	-8.173	64.557	1.00 94.69
	3648	OE1	GLN B 236	-15.818	-8.002	63.591	1.00 95.25
	3649	NE2	GLN B 236	-15.419	-8.912	65.611	1.00 94.26
	3650	C	GLN B 236	-12.259	-4.058	63.640	1.00 69.80



	3651	O	GLN B 236	-11.933	-3.842	62.477	1.00	70.18
	3652	N	GLU B 237	-12.616	-3.075	64.460	1.00	52.79
	3653	CA	GLU B 237	-12.645	-1.703	63.957	1.00	52.29
	3654	CB	GLU B 237	-13.006	-0.707	65.068	1.00	76.60
5	3655	CG	GLU B 237	-13.056	0.756	64.605	1.00	78.85
	3656	CD	GLU B 237	-14.097	1.005	63.514	1.00	81.46
	3657	OE1	GLU B 237	-15.314	1.018	63.822	1.00	81.02
	3658	OE2	GLU B 237	-13.690	1.184	62.342	1.00	81.65
	3659	C	GLU B 237	-11.266	-1.397	63.413	1.00	51.87
10	3660	O	GLU B 237	-11.099	-0.530	62.552	1.00	51.44
	3661	N	ALA B 238	-10.287	-2.137	63.929	1.00	63.75
	3662	CA	ALA B 238	-8.892	-1.999	63.532	1.00	62.12
	3663	CB	ALA B 238	-7.991	-2.450	64.657	1.00	66.94
	3664	C	ALA B 238	-8.636	-2.842	62.297	1.00	60.80
15	3665	O	ALA B 238	-8.329	-2.299	61.230	1.00	60.24
	3666	N	ILE B 239	-8.758	-4.166	62.453	1.00	40.23
	3667	CA	ILE B 239	-8.555	-5.104	61.348	1.00	39.87
	3668	CB	ILE B 239	-9.165	-6.492	61.642	1.00	35.32
	3669	CG2	ILE B 239	-8.936	-7.420	60.475	1.00	34.94
20	3670	CG1	ILE B 239	-8.528	-7.092	62.886	1.00	32.97
	3671	CD1	ILE B 239	-9.005	-8.480	63.222	1.00	31.96
	3672	C	ILE B 239	-9.272	-4.511	60.148	1.00	42.94
	3673	O	ILE B 239	-8.857	-4.682	59.004	1.00	43.05
	3674	N	LEU B 240	-10.358	-3.802	60.437	1.00	80.50
25	3675	CA	LEU B 240	-11.155	-3.148	59.417	1.00	83.41
	3676	CB	LEU B 240	-12.435	-2.583	60.025	1.00	108.88
	3677	CG	LEU B 240	-13.154	-1.558	59.145	1.00	110.23
	3678	CD1	LEU B 240	-13.680	-2.234	57.881	1.00	109.99
	3679	CD2	LEU B 240	-14.283	-0.912	59.936	1.00	110.96
30	3680	C	LEU B 240	-10.350	-2.011	58.816	1.00	85.14
	3681	O	LEU B 240	-9.800	-2.134	57.719	1.00	86.33
	3682	N	ALA B 241	-10.285	-0.901	59.544	1.00	88.35
	3683	CA	ALA B 241	-9.556	0.265	59.075	1.00	88.88
	3684	CB	ALA B 241	-9.279	1.206	60.227	1.00	57.91
35	3685	C	ALA B 241	-8.258	-0.186	58.429	1.00	89.35
	3686	O	ALA B 241	-7.809	0.404	57.450	1.00	89.34
	3687	N	TYR B 242	-7.663	-1.242	58.973	1.00	68.33
	3688	CA	TYR B 242	-6.430	-1.760	58.410	1.00	69.38
	3689	CB	TYR B 242	-6.063	-3.101	59.040	1.00	61.75
40	3690	CG	TYR B 242	-5.017	-3.847	58.243	1.00	59.73
	3691	CD1	TYR B 242	-3.834	-3.219	57.858	1.00	58.22
	3692	CE1	TYR B 242	-2.886	-3.878	57.083	1.00	57.00
	3693	CD2	TYR B 242	-5.224	-5.164	57.838	1.00	58.12

	3694	CE2	TYR	B	242	-4.275	-5.832	57.062	1.00	57.61
	3695	CZ	TYR	B	242	-3.112	-5.177	56.685	1.00	56.34
	3696	OH	TYR	B	242	-2.198	-5.794	55.871	1.00	56.15
	3697	C	TYR	B	242	-6.621	-1.944	56.913	1.00	70.66
5	3698	O	TYR	B	242	-5.810	-1.486	56.104	1.00	70.96
	3699	N	ASN	B	243	-7.703	-2.621	56.553	1.00	63.54
	3700	CA	ASN	B	243	-8.010	-2.862	55.157	1.00	65.12
	3701	CB	ASN	B	243	-9.069	-3.946	55.033	1.00	62.53
	3702	CG	ASN	B	243	-8.552	-5.293	55.444	1.00	61.37
10	3703	OD1	ASN	B	243	-8.995	-5.852	56.441	1.00	61.93
	3704	ND2	ASN	B	243	-7.600	-5.826	54.680	1.00	61.00
	3705	C	ASN	B	243	-8.482	-1.602	54.451	1.00	66.20
	3706	O	ASN	B	243	-8.280	-1.445	53.245	1.00	65.95
	3707	N	ARG	B	244	-9.109	-0.701	55.199	1.00	64.72
15	3708	CA	ARG	B	244	-9.594	0.540	54.611	1.00	67.47
	3709	CB	ARG	B	244	-10.226	1.424	55.681	1.00	94.83
	3710	CG	ARG	B	244	-11.040	2.574	55.119	1.00	96.30
	3711	CD	ARG	B	244	-12.422	2.113	54.689	1.00	98.16
	3712	NE	ARG	B	244	-13.377	2.045	55.803	1.00	99.54
20	3713	CZ	ARG	B	244	-13.363	1.139	56.781	1.00	99.23
	3714	NH1	ARG	B	244	-12.436	0.191	56.810	1.00	99.50
	3715	NH2	ARG	B	244	-14.286	1.181	57.734	1.00	98.66
	3716	C	ARG	B	244	-8.435	1.290	53.961	1.00	69.17
	3717	O	ARG	B	244	-8.625	2.043	53.006	1.00	69.16
25	3718	N	ARG	B	245	-7.231	1.078	54.483	1.00	90.19
	3719	CA	ARG	B	245	-6.046	1.746	53.960	1.00	92.43
	3720	CB	ARG	B	245	-4.814	1.401	54.805	1.00	79.40
	3721	CG	ARG	B	245	-5.013	1.508	56.315	1.00	78.40
	3722	CD	ARG	B	245	-5.394	2.918	56.755	1.00	78.14
30	3723	NE	ARG	B	245	-5.540	3.030	58.208	1.00	77.20
	3724	CZ	ARG	B	245	-4.539	2.903	59.078	1.00	76.66
	3725	NH1	ARG	B	245	-3.306	2.658	58.650	1.00	76.13
	3726	NH2	ARG	B	245	-4.771	3.019	60.379	1.00	75.87
	3727	C	ARG	B	245	-5.791	1.326	52.522	1.00	94.57
35	3728	O	ARG	B	245	-5.595	0.147	52.235	1.00	94.29
	3729	N	HIS	B	246	-5.813	2.293	51.617	1.00	142.27
	3730	CA	HIS	B	246	-5.547	2.018	50.213	1.00	144.64
	3731	CB	HIS	B	246	-6.640	2.603	49.304	1.00	124.13
	3732	CG	HIS	B	246	-8.010	2.052	49.544	1.00	125.01
40	3733	CD2	HIS	B	246	-9.171	2.669	49.869	1.00	125.08
	3734	ND1	HIS	B	246	-8.313	0.715	49.402	1.00	125.24
	3735	CE1	HIS	B	246	-9.602	0.532	49.627	1.00	125.20
	3736	NE2	HIS	B	246	-10.145	1.702	49.912	1.00	125.75

	3737	C	HIS B 246	-4.250	2.744	49.899	1.00145.61
	3738	O	HIS B 246	-3.154	2.346	50.307	1.00146.34
	3739	N	ARG B 247	-4.434	3.837	49.171	1.00 74.46
	3740	CA	ARG B 247	-3.401	4.755	48.712	1.00 74.85
5	3741	CB	ARG B 247	-2.260	4.001	48.003	1.00 74.20
	3742	CG	ARG B 247	-2.692	2.816	47.140	1.00 72.35
	3743	CD	ARG B 247	-1.503	1.878	46.868	1.00 71.58
	3744	NE	ARG B 247	-1.904	0.644	46.187	1.00 70.02
	3745	CZ	ARG B 247	-2.762	-0.249	46.681	1.00 69.37
10	3746	NH1	ARG B 247	-3.322	-0.059	47.871	1.00 69.43
	3747	NH2	ARG B 247	-3.075	-1.331	45.976	1.00 67.98
	3748	C	ARG B 247	-4.187	5.644	47.750	1.00 75.12
	3749	O	ARG B 247	-3.634	6.502	47.058	1.00 74.84
	3750	N	ARG B 248	-5.505	5.424	47.755	1.00 75.10
15	3751	CA	ARG B 248	-6.450	6.146	46.914	1.00 74.94
	3752	CB	ARG B 248	-6.517	7.627	47.328	1.00 73.91
	3753	CG	ARG B 248	-7.534	8.433	46.515	1.00 72.01
	3754	CD	ARG B 248	-7.514	9.937	46.808	1.00 69.76
	3755	NE	ARG B 248	-8.134	10.702	45.719	1.00 67.75
20	3756	CZ	ARG B 248	-9.384	10.538	45.279	1.00 67.22
	3757	NH1	ARG B 248	-10.189	9.633	45.832	1.00 66.89
	3758	NH2	ARG B 248	-9.827	11.265	44.260	1.00 65.91
	3759	C	ARG B 248	-6.053	6.005	45.437	1.00 75.28
	3760	O	ARG B 248	-5.857	6.997	44.719	1.00 75.09
25	3761	N	PHE B 249	-5.931	4.758	44.990	1.00 75.96
	3762	CA	PHE B 249	-5.554	4.469	43.603	1.00 76.80
	3763	CB	PHE B 249	-4.998	3.035	43.499	1.00 76.98
	3764	CG	PHE B 249	-5.731	2.031	44.357	1.00 77.74
	3765	CD1	PHE B 249	-7.127	1.945	44.323	1.00 77.77
30	3766	CD2	PHE B 249	-5.027	1.177	45.203	1.00 77.66
	3767	CE1	PHE B 249	-7.810	1.024	45.121	1.00 77.84
	3768	CE2	PHE B 249	-5.698	0.250	46.008	1.00 77.54
	3769	CZ	PHE B 249	-7.093	0.173	45.968	1.00 77.55
	3770	C	PHE B 249	-6.722	4.658	42.614	1.00 77.29
35	3771	O	PHE B 249	-7.013	3.708	41.838	1.00 77.59
	3772	OT	PHE B 249	-7.325	5.763	42.625	1.00 77.59
	3773	C01	IPP C 1	3.752	-1.490	77.726	1.00 33.83
	3774	C02	IPP C 1	2.891	-0.835	78.560	1.00 33.83
	3775	C05	IPP C 1	4.416	-2.798	78.081	1.00 33.83
40	3776	C09	IPP C 1	4.097	-0.941	76.373	1.00 33.83
	3777	C12	IPP C 1	5.075	0.215	76.421	1.00 33.83
	3778	O14	IPP C 1	4.843	3.852	77.104	1.00 33.83
	3779	P15	IPP C 1	4.821	2.417	77.787	1.00 33.83

	3780	O16	IPP	C	1	6.225	2.006	78.323	1.00	33.83
	3781	O17	IPP	C	1	4.317	1.406	76.629	1.00	33.83
	3782	O18	IPP	C	1	3.695	2.471	78.827	1.00	33.83
	3783	P19	IPP	C	1	5.684	5.144	77.406	1.00	33.83
5	3784	O20	IPP	C	1	7.110	4.945	76.880	1.00	33.83
	3785	O21	IPP	C	1	4.994	6.358	76.768	1.00	33.83
	3786	O22	IPP	C	1	5.646	5.185	78.935	1.00	33.83
	3787	C01	IPP	C	2	2.307	-3.138	81.526	1.00	33.83
	3788	C02	IPP	C	2	3.668	-3.126	81.578	1.00	33.83
10	3789	C05	IPP	C	2	1.513	-4.452	81.609	1.00	33.83
	3790	C09	IPP	C	2	1.487	-1.841	81.385	1.00	33.83
	3791	C12	IPP	C	2	1.887	-0.699	82.354	1.00	33.83
	3792	O14	IPP	C	2	-0.767	2.198	82.197	1.00	33.83
	3793	P15	IPP	C	2	0.246	1.188	81.498	1.00	33.83
15	3794	O16	IPP	C	2	-0.425	0.460	80.333	1.00	33.83
	3795	O17	IPP	C	2	0.736	0.134	82.638	1.00	33.83
	3796	O18	IPP	C	2	1.498	2.051	81.154	1.00	33.83
	3797	P19	IPP	C	2	-1.027	3.757	81.972	1.00	33.83
	3798	O20	IPP	C	2	-0.542	4.097	80.558	1.00	33.83
20	3799	O21	IPP	C	2	-2.512	4.040	82.143	1.00	33.83
	3800	O22	IPP	C	2	-0.165	4.429	83.060	1.00	33.83
	3801	OH2	WAT	W	1	12.965	-11.206	62.097	1.00	33.83
	3802	OH2	WAT	W	2	11.962	-27.690	81.314	1.00	33.83
	3803	OH2	WAT	W	3	2.139	4.914	78.332	1.00	33.83
25	3804	OH2	WAT	W	4	14.094	-9.399	58.598	1.00	33.83
	3805	OH2	WAT	W	5	12.062	14.669	72.584	1.00	33.83

END

Table IIA. Interatomic distances in the native UPPS structure

FROM	TO	DISTANCE, Angstrom		27CE	71N	3.956
			45	27C	27O	1.230
5	27N	27CA	1.470	27C	28N	1.328
	27N	27CB	2.442	27C	27CA	1.515
	27N	27C	2.480	27C	28CA	2.451
	27N	27CG	2.947	27C	27N	2.480
	27N	28N	3.122	27C	27CB	2.501
10	27N	70O	3.142	27C	28C	3.406
	27N	27O	3.285	27C	28CB	3.563
	27CA	27N	1.470	27C	28O	3.753
	27CA	27C	1.515	27C	27CG	3.873
	27CA	27CB	1.531	27O	27C	1.230
15	27CA	27O	2.394	27O	28N	2.255
	27CA	28N	2.404	27O	27CA	2.394
	27CA	27CG	2.545	27O	27CB	2.749
	27CA	28CA	3.793	27O	28CA	2.816
	27CA	70O	3.988	27O	27N	3.285
20	27CB	27CG	1.526	27O	72N	3.332
	27CB	27CA	1.531	27O	72CA	3.576
	27CB	27N	2.442	27O	28C	3.674
	27CB	27C	2.501	27O	72CB	3.836
	27CB	27O	2.749	28N	27C	1.328
25	27CB	27SD	2.828	28N	28CA	1.456
	27CB	27CE	3.129	28N	27O	2.255
	27CB	28N	3.678	28N	28CB	2.396
	27CB	70O	3.850	28N	27CA	2.404
	27CG	27CB	1.526	28N	28C	2.490
30	27CG	27SD	1.817	28N	28O	2.808
	27CG	27CA	2.545	28N	27N	3.122
	27CG	27CE	2.831	28N	28CG	3.615
	27CG	27N	2.947	28N	29N	3.640
	27CG	27C	3.873	28N	27CB	3.678
35	27SD	27CG	1.817	28CA	28N	1.456
	27SD	27CE	1.863	28CA	28CB	1.524
	27SD	27CB	2.828	28CA	28C	1.546
	27CE	27SD	1.863	28CA	28O	2.410
	27CE	27CG	2.831	28CA	27C	2.451
40	27CE	27CB	3.129	28CA	29N	2.466
	27CE	70O	3.804	28CA	28CG	2.518
	27CE	71CA	3.877	28CA	27O	2.816
	27CE	70C	3.929	28CA	28OD1	3.045

	28CA	28OD2	3.384		28C	27C	3.406
	28CA	27CA	3.793	45	28C	28CG	3.411
	28CA	29CA	3.824		28C	28OD1	3.456
	28CA	72CD1	3.860		28C	29C	3.518
5	28CB	28CG	1.490		28C	27O	3.674
	28CB	28CA	1.524		28C	30N	3.732
	28CB	28OD2	2.338	50	28O	28C	1.228
	28CB	28OD1	2.356		28O	29N	2.239
	28CB	28N	2.396		28O	28CA	2.410
10	28CB	28C	2.500		28O	29CA	2.711
	28CB	28O	3.169		28O	28N	2.808
	28CB	29N	3.287	55	28O	28CB	3.169
	28CB	27C	3.563		28O	29C	3.724
	28CG	28OD1	1.240		28O	27C	3.753
15	28CG	28OD2	1.244		29N	28C	1.331
	28CG	28CB	1.490		29N	29CA	1.458
	28CG	28CA	2.518	60	29N	28O	2.239
	28CG	72CD1	3.356		29N	28CA	2.466
	28CG	28C	3.411		29N	29C	2.585
20	28CG	72CE1	3.411		29N	30N	2.897
	28CG	28N	3.615		29N	28CB	3.287
	28CG	29N	3.697	65	29N	28OD1	3.296
	28OD1	28CG	1.240		29N	28N	3.640
	28OD1	28OD2	2.190		29N	29O	3.691
25	28OD1	28CB	2.356		29N	28CG	3.697
	28OD1	72CE1	2.694		29CA	29N	1.458
	28OD1	28CA	3.045	70	29CA	29C	1.520
	28OD1	72CD1	3.057		29CA	29O	2.380
	28OD1	29N	3.296		29CA	28C	2.410
30	28OD1	28C	3.456		29CA	30N	2.454
	28OD1	72CZ	3.710		29CA	28O	2.711
	28OD2	28CG	1.244	75	29CA	30CA	3.802
	28OD2	28OD1	2.190		29CA	28CA	3.824
	28OD2	28CB	2.338		29C	29O	1.234
35	28OD2	28CA	3.384		29C	30N	1.333
	28OD2	72CD1	3.624		29C	29CA	1.520
	28OD2	72CE1	3.724	80	29C	30CA	2.408
	28C	28O	1.228		29C	29N	2.585
	28C	29N	1.331		29C	30C	2.963
40	28C	28CA	1.546		29C	31N	3.163
	28C	29CA	2.410		29C	28C	3.518
	28C	28N	2.490	85	29C	30CB	3.696
	28C	28CB	2.500		29C	28O	3.724

	29C	30ND2	3.761		30CB	300	3.224
	29C	300	3.854	45	30CB	45CD2	3.655
	290	29C	1.234		30CB	29C	3.696
	290	30N	2.247		30CG	30OD1	1.229
5	290	29CA	2.380		30CG	30ND2	1.311
	290	30CA	2.717		30CG	30CB	1.496
	290	30C	2.845	50	30CG	30CA	2.502
	290	31N	3.224		30CG	30N	2.971
	290	300	3.391		30CG	30C	3.825
10	290	32N	3.461		30CG	45CD2	3.961
	290	29N	3.691		30OD1	30CG	1.229
	290	32C	3.973	55	30OD1	30ND2	2.230
	30N	29C	1.333		30OD1	30CB	2.380
	30N	30CA	1.452		30OD1	45CD2	3.392
15	30N	290	2.247		30OD1	30CA	3.656
	30N	30CB	2.444		30OD1	45CA	3.772
	30N	29CA	2.454	60	30ND2	30CG	1.311
	30N	30C	2.470		30ND2	30OD1	2.230
	30N	30ND2	2.764		30ND2	30CB	2.380
20	30N	31N	2.805		30ND2	30CA	2.652
	30N	29N	2.897		30ND2	30N	2.764
	30N	30CG	2.971	65	30ND2	29C	3.761
	30N	300	3.526		30C	300	1.229
	30N	28C	3.732		30C	31N	1.336
25	30CA	30N	1.452		30C	30CA	1.527
	30CA	30CB	1.518		30C	31CA	2.435
	30CA	30C	1.527	70	30C	30N	2.470
	30CA	300	2.391		30C	30CB	2.480
	30CA	29C	2.408		30C	290	2.845
30	30CA	31N	2.442		30C	29C	2.963
	30CA	30CG	2.502		30C	31C	3.116
	30CA	30ND2	2.652	75	30C	32N	3.583
	30CA	290	2.717		30C	30CG	3.825
	30CA	30OD1	3.656		30C	310	3.839
35	30CA	29CA	3.802		300	30C	1.229
	30CA	31CA	3.812		300	31N	2.256
	30CB	30CG	1.496	80	300	30CA	2.391
	30CB	30CA	1.518		300	31CA	2.775
	30CB	30OD1	2.380		300	31C	3.111
40	30CB	30ND2	2.380		300	30CB	3.224
	30CB	30N	2.444		300	290	3.391
	30CB	30C	2.480	85	300	310	3.441
	30CB	31N	3.172		300	30N	3.526

	300	32N	3.804		32N	31CA	2.431
	300	29C	3.854	45	32N	32C	2.438
	31N	30C	1.336		32N	32CB	2.466
	31N	31CA	1.454		32N	31N	2.938
5	31N	300	2.256		32N	32CG	3.309
	31N	30CA	2.442		32N	290	3.461
	31N	31C	2.491	50	32N	320	3.504
	31N	30N	2.805		32N	30C	3.583
	31N	32N	2.938		32N	300	3.804
10	31N	29C	3.163		32CA	32N	1.457
	31N	30CB	3.172		32CA	32C	1.531
	31N	290	3.224	55	32CA	32CB	1.534
	31N	310	3.471		32CA	320	2.397
15	31CA	31N	1.454		32CA	31C	2.434
	31CA	31C	1.515		32CA	32CG	2.585
	31CA	310	2.378		32CA	310	2.775
	31CA	32N	2.431	60	32CA	31CA	3.803
	31CA	30C	2.435		32CA	32CD	3.927
	31CA	300	2.775		32CB	32CG	1.531
20	31CA	32CA	3.803		32CB	32CA	1.534
	31CA	30CA	3.812		32CB	32N	2.466
	31C	310	1.230	65	32CB	32C	2.495
	31C	32N	1.331		32CB	32CD	2.539
	31C	31CA	1.515		32CB	32NE	3.067
25	31C	32CA	2.434		32CB	320	3.244
	31C	31N	2.491		32CB	31C	3.727
	31C	32C	2.939	70	32CG	32CB	1.531
	31C	300	3.111		32CG	32CD	1.535
	31C	30C	3.116		32CG	32NE	2.519
30	31C	32CB	3.727		32CG	32CA	2.585
	31C	320	3.847		32CG	32N	3.309
	310	31C	1.230	75	32CG	32CZ	3.766
	310	32N	2.253		32CG	32C	3.838
	310	31CA	2.378		32CD	32NE	1.467
35	310	32CA	2.775		32CD	32CG	1.535
	310	32C	2.870		32CD	32CZ	2.476
	310	320	3.433	80	32CD	32CB	2.539
	310	300	3.441		32CD	32NH1	2.829
	310	31N	3.471		32CD	32NH2	3.686
40	310	30C	3.839		32CD	32CA	3.927
	32N	31C	1.331		32NE	32CZ	1.336
	32N	32CA	1.457	85	32NE	32CD	1.467
	32N	310	2.253		32NE	32NH1	2.311



	32NE	32NH2	2.314		45CA	45ND1	3.589
	32NE	32CG	2.519	45	45CA	30OD1	3.772
	32NE	32CB	3.067		45CB	45CG	1.497
	32CZ	32NH2	1.329		45CB	45CA	1.532
5	32CZ	32NH1	1.329		45CB	45N	2.449
	32CZ	32NE	1.336		45CB	45ND1	2.527
	32CZ	32CD	2.476	50	45CB	45C	2.535
	32CZ	32CG	3.766		45CB	45CD2	2.596
	32NH1	32CZ	1.329		45CB	45O	3.264
10	32NH1	32NH2	2.292		45CB	45CE1	3.631
	32NH1	32NE	2.311		45CB	45NE2	3.673
	32NH1	32CD	2.829	55	45CG	45CD2	1.356
	32NH2	32CZ	1.329		45CG	45ND1	1.379
	32NH2	32NH1	2.292		45CG	45CB	1.497
15	32NH2	32NE	2.314		45CG	45NE2	2.200
	32NH2	32CD	3.686		45CG	45CE1	2.206
	32C	32O	1.226	60	45CG	45CA	2.520
	32C	32CA	1.531		45CG	45N	2.975
	32C	32N	2.438		45CG	45C	3.865
20	32C	32CB	2.495		45CD2	45CG	1.356
	32C	31O	2.870		45CD2	45NE2	1.376
	32C	31C	2.939	65	45CD2	45ND1	2.185
	32C	32CG	3.838		45CD2	45CE1	2.195
	32C	29O	3.973		45CD2	45CB	2.596
25	32O	32C	1.226		45CD2	45CA	3.208
	32O	32CA	2.397		45CD2	30OD1	3.392
	32O	32CB	3.244	70	45CD2	30CB	3.655
	32O	31O	3.433		45CD2	45N	3.660
	32O	32N	3.504		45CD2	30CG	3.961
30	32O	31C	3.847		45ND1	45CE1	1.322
	45N	45CA	1.457		45ND1	45CG	1.379
	45N	45C	2.445	75	45ND1	45NE2	2.145
	45N	45CB	2.449		45ND1	45CD2	2.185
	45N	45CG	2.975		45ND1	45CB	2.527
35	45N	45O	3.510		45ND1	45CA	3.589
	45N	45ND1	3.612		45ND1	45N	3.612
	45N	45CD2	3.660	80	45CE1	45NE2	1.322
	45CA	45N	1.457		45CE1	45ND1	1.322
	45CA	45C	1.515		45CE1	45CD2	2.195
40	45CA	45CB	1.532		45CE1	45CG	2.206
	45CA	45O	2.382		45CE1	45CB	3.631
	45CA	45CG	2.520	85	45NE2	45CE1	1.322
	45CA	45CD2	3.208		45NE2	45CD2	1.376

	45NE2	45ND1	2.145		48O	49CA	2.787
	45NE2	45CG	2.200	45	48O	52N	2.961
	45NE2	45CB	3.673		48O	49C	2.992
	45C	45O	1.219		48O	48N	3.474
5	45C	45CA	1.515		48O	49O	3.497
	45C	45N	2.445		48O	52CB	3.661
	45C	45CB	2.535	50	48O	52CA	3.871
	45C	48N	3.564		49N	48C	1.339
	45C	45CG	3.865		49N	49CA	1.467
10	45O	45C	1.219		49N	48O	2.266
	45O	45CA	2.382		49N	48CA	2.435
	45O	49N	2.958	55	49N	49C	2.446
	45O	48N	3.126		49N	49CB	2.492
	45O	45CB	3.264		49N	48N	2.721
15	45O	45N	3.510		49N	45O	2.958
	45O	48CA	3.519		49N	49CG	3.422
	45O	48C	3.661	60	49N	49O	3.509
	45O	49CB	3.852		49CA	49N	1.467
	45O	49CA	3.942		49CA	49C	1.533
20	48N	48CA	1.449		49CA	49CB	1.539
	48N	48C	2.409		49CA	49O	2.409
	48N	49N	2.721	65	49CA	48C	2.446
	48N	45O	3.126		49CA	49CG	2.603
	48N	48O	3.474		49CA	48O	2.787
25	48N	45C	3.564		49CA	48CA	3.814
	48CA	48N	1.449		49CA	45O	3.942
	48CA	48C	1.513	70	49CB	49CG	1.527
	48CA	48O	2.379		49CB	49CA	1.539
	48CA	49N	2.435		49CB	49N	2.492
30	48CA	45O	3.519		49CB	49C	2.502
	48CA	49CA	3.814		49CB	49SD	2.839
	48C	48O	1.235	75	49CB	49O	3.272
	48C	49N	1.339		49CB	49CE	3.332
	48C	48CA	1.513		49CB	48C	3.755
35	48C	48N	2.409		49CB	45O	3.852
	48C	49CA	2.446		49CG	49CB	1.527
	48C	49C	3.014	80	49CG	49SD	1.852
	48C	45O	3.661		49CG	49CA	2.603
	48C	49CB	3.755		49CG	49CE	2.722
40	48C	49O	3.882		49CG	49N	3.422
	48O	48C	1.235		49CG	49C	3.813
	48O	49N	2.266	85	49SD	49CE	1.728
	48O	48CA	2.379		49SD	49CG	1.852

	49SD	49CB	2.839		52CB	52CD1	2.516
	49CE	49SD	1.728	45	52CB	52CD2	2.530
	49CE	49CG	2.722		52CB	52O	3.325
	49CE	49CB	3.332		52CB	49O	3.590
5	49C	49O	1.232		52CB	48O	3.661
	49C	49CA	1.533		52CG	52CD1	1.528
	49C	49N	2.446	50	52CG	52CD2	1.531
	49C	49CB	2.502		52CG	52CB	1.545
	49C	48O	2.992		52CG	52CA	2.602
10	49C	48C	3.014		52CG	52C	3.070
	49C	52N	3.736		52CG	52O	3.399
	49C	49CG	3.813	55	52CG	52N	3.887
	49O	49C	1.232		52CD1	52CG	1.528
	49O	49CA	2.409		52CD1	52CD2	2.502
15	49O	49CB	3.272		52CD1	52CB	2.516
	49O	52N	3.272		52CD1	52CA	3.017
	49O	48O	3.497	60	52CD1	52O	3.563
	49O	49N	3.509		52CD1	52C	3.612
	49O	52CB	3.590		52CD2	52CG	1.531
20	49O	52CA	3.712		52CD2	52CD1	2.502
	49O	52C	3.774		52CD2	52CB	2.530
	49O	48C	3.882	65	52CD2	52CA	3.936
	52N	52CA	1.462		52C	52O	1.227
	52N	52C	2.431		52C	52CA	1.519
25	52N	52CB	2.493		52C	52N	2.431
	52N	48O	2.961		52C	52CB	2.510
	52N	49O	3.272	70	52C	52CG	3.070
	52N	52O	3.446		52C	52CD1	3.612
	52N	49C	3.736		52C	49O	3.774
30	52N	52CG	3.887		52O	52C	1.227
	52CA	52N	1.462		52O	52CA	2.385
	52CA	52C	1.519	75	52O	52CB	3.325
	52CA	52CB	1.544		52O	52CG	3.399
	52CA	52O	2.385		52O	52N	3.446
35	52CA	52CG	2.602		52O	52CD1	3.563
	52CA	52CD1	3.017		70N	70CA	1.453
	52CA	49O	3.712	80	70N	70CB	2.386
	52CA	48O	3.871		70N	70C	2.439
	52CA	52CD2	3.936		70N	70O	2.904
40	52CB	52CA	1.544		70N	71N	3.442
	52CB	52CG	1.545		70N	70CG	3.785
	52CB	52N	2.493	85	70CA	70N	1.453
	52CB	52C	2.510		70CA	70CB	1.517

	70CA	70C	1.519		70CE1	70CD2	2.772
	70CA	70O	2.393	45	70CE1	70CB	3.808
	70CA	71N	2.421		70CD2	70CE2	1.380
	70CA	70CG	2.582		70CD2	70CG	1.392
5	70CA	70CD1	3.068		70CD2	70CD1	2.387
	70CA	70CD2	3.793		70CD2	70CZ	2.394
	70CA	71CA	3.804	50	70CD2	70CB	2.510
	70CB	70CG	1.502		70CD2	70CE1	2.772
	70CB	70CA	1.517		70CD2	70OH	3.639
10	70CB	70N	2.386		70CD2	70CA	3.793
	70CB	70C	2.487		70CE2	70CD2	1.380
	70CB	70CD2	2.510	55	70CE2	70CZ	1.385
	70CB	70CD1	2.521		70CE2	70OH	2.380
	70CB	70O	2.952		70CE2	70CE1	2.396
15	70CB	71N	3.466		70CE2	70CG	2.414
	70CB	70CE2	3.780		70CE2	70CD1	2.760
	70CB	70CE1	3.808	60	70CE2	70CB	3.780
	70CG	70CD1	1.391		70CZ	70OH	1.367
	70CG	70CD2	1.392		70CZ	70CE1	1.376
20	70CG	70CB	1.502		70CZ	70CE2	1.385
	70CG	70CE2	2.414		70CZ	70CD1	2.394
	70CG	70CE1	2.432	65	70CZ	70CD2	2.394
	70CG	70CA	2.582		70CZ	70CG	2.791
	70CG	70CZ	2.791		70OH	70CZ	1.367
25	70CG	70C	3.132		70OH	70CE1	2.371
	70CG	70O	3.664		70OH	70CE2	2.380
	70CG	71N	3.713	70	70OH	70CD2	3.639
	70CG	70N	3.785		70OH	70CD1	3.644
	70CD1	70CG	1.391		70C	70O	1.238
30	70CD1	70CE1	1.400		70C	71N	1.321
	70CD1	70CD2	2.387		70C	70CA	1.519
	70CD1	70CZ	2.394	75	70C	71CA	2.436
	70CD1	70CB	2.521		70C	70N	2.439
	70CD1	70CE2	2.760		70C	70CB	2.487
35	70CD1	70CA	3.068		70C	71C	3.127
	70CD1	70C	3.613		70C	70CG	3.132
	70CD1	70OH	3.644	80	70C	72N	3.541
	70CD1	71N	3.740		70C	70CD1	3.613
	70CE1	70CZ	1.376		70C	71CB	3.684
40	70CE1	70CD1	1.400		70C	71O	3.882
	70CE1	70OH	2.371		70C	27CE	3.929
	70CE1	70CE2	2.396	85	70O	70C	1.238
	70CE1	70CG	2.432		70O	71N	2.251

	700	70CA	2.393		71C	72CA	2.475
	700	71CA	2.782	45	71C	71CB	2.505
	700	70N	2.904		71C	71N	2.507
	700	70CB	2.952		71C	70C	3.127
5	700	72N	3.044		71C	700	3.133
	700	71C	3.133		71C	72CB	3.251
	700	27N	3.142	50	710	71C	1.236
	700	70CG	3.664		710	72N	2.274
	700	27CE	3.804		710	71CA	2.415
10	700	27CB	3.850		710	72CA	2.843
	700	27CA	3.988		710	71CB	2.849
	71N	70C	1.321	55	710	71N	3.137
	71N	71CA	1.462		710	72CB	3.448
	71N	700	2.251		710	70C	3.882
15	71N	70CA	2.421		72N	71C	1.342
	71N	71CB	2.434		72N	72CA	1.470
	71N	71C	2.507	60	72N	710	2.274
	71N	710	3.137		72N	72CB	2.456
	71N	72N	3.354		72N	71CA	2.459
20	71N	70N	3.442		72N	700	3.044
	71N	70CB	3.466		72N	270	3.332
	71N	70CG	3.713	65	72N	71N	3.354
	71N	70CD1	3.740		72N	70C	3.541
	71N	27CE	3.956		72N	71CB	3.608
25	71CA	71N	1.462		72N	72CG	3.820
	71CA	71CB	1.517		72CA	72N	1.470
	71CA	71C	1.549	70	72CA	72CB	1.536
	71CA	710	2.415		72CA	71C	2.475
	71CA	70C	2.436		72CA	72CG	2.554
30	71CA	72N	2.459		72CA	710	2.843
	71CA	700	2.782		72CA	72CD2	3.379
	71CA	70CA	3.804	75	72CA	72CD1	3.398
	71CA	72CA	3.860		72CA	270	3.576
	71CA	27CE	3.877		72CA	71CA	3.860
35	71CB	71CA	1.517		72CB	72CG	1.507
	71CB	71N	2.434		72CB	72CA	1.536
	71CB	71C	2.505	80	72CB	72N	2.456
	71CB	710	2.849		72CB	72CD2	2.513
	71CB	72N	3.608		72CB	72CD1	2.518
40	71CB	70C	3.684		72CB	71C	3.251
	71C	710	1.236		72CB	710	3.448
	71C	72N	1.342	85	72CB	72CE2	3.802
	71C	71CA	1.549		72CB	72CE1	3.806

	72CB	270	3.836		72CZ	72CE1	1.384
	72CG	72CD2	1.387	45	72CZ	72CD2	2.406
	72CG	72CD1	1.388		72CZ	72CD1	2.410
	72CG	72CB	1.507		72CZ	72CG	2.799
5	72CG	72CE2	2.420		72CZ	28OD1	3.710
	72CG	72CE1	2.421		72C	72CA	1.526
	72CG	72CA	2.554	50	72C	72N	2.477
	72CG	72CZ	2.799		72C	72CB	2.499
	72CG	72N	3.820		72C	710	2.651
10	72CD1	72CG	1.388		72C	71C	2.881
	72CD1	72CE1	1.398		72C	72CG	3.042
	72CD1	72CD2	2.388	55	72C	72CD2	3.243
	72CD1	72CZ	2.410		72O	72CA	2.410
	72CD1	72CB	2.518		72O	72CB	3.415
15	72CD1	72CE2	2.769		72O	72N	3.450
	72CD1	28OD1	3.057		72O	72CG	3.541
	72CD1	28CG	3.356	60	72O	72CD2	3.581
	72CD1	72CA	3.398		72O	710	3.734
	72CD1	28OD2	3.624		72O	71C	3.950
20	72CD1	28CA	3.860		90CD1	45CB	3.755
	72CD2	72CG	1.387		90CD2	49CE	3.288
	72CD2	72CE2	1.396	65	90O	49SD	3.899
	72CD2	72CD1	2.388		94N	49SD	3.988
	72CD2	72CZ	2.406		94CA	49SD	3.982
25	72CD2	72CB	2.513		143CE2	52CD2	3.572
	72CD2	72CE1	2.767		143CZ	52CD2	3.734
	72CD2	72CA	3.379	70	200NE	28OD2	3.552
	72CE1	72CZ	1.384		200CZ	28OD2	3.594
	72CE1	72CD1	1.398		200NH2	28OD2	2.807
30	72CE1	72CE2	2.392		200NH2	28CG	3.947
	72CE1	72CG	2.421		208O	70CE2	3.609
	72CE1	28OD1	2.694	75	208O	70OH	3.637
	72CE1	72CD2	2.767				
	72CE1	28CG	3.411				
35	72CE1	28OD2	3.724				
	72CE1	72CB	3.806				
	72CE2	72CZ	1.381				
	72CE2	72CD2	1.396				
	72CE2	72CE1	2.392				
40	72CE2	72CG	2.420				
	72CE2	72CD1	2.769				
	72CE2	72CB	3.802				
	72CZ	72CE2	1.381				

Table IIB

Interatomic distances in the active  
site of UPPS in complex with FPP

5	FROM	TO			
	DISTANCE, Angstrom				
	1C1	79NH1	3.600		
	1C1	79NH2	3.700	50	
	101	27O	3.689		
10	1C2	30OD1	3.734		
	1C2	45NE2	3.829		
	1C2	79NH1	3.943	55	
	1C3	71O	3.693		
	1C4	71O	3.205		
15	1C4	71C	3.901		
	1C5	71O	3.250		
	1C5	45CD2	3.935	60	
	1C6	30OD1	3.590		
	1C6	71O	3.792		
20	1C7	71O	3.815		
	1C10	49N	3.149		
	1C10	45O	3.182		
	1C10	48C	3.455	65	
	1C10	48CA	3.529		
25	1C10	30OD1	3.732		
	1C10	49CA	3.898		
	1C11	90CD1	3.926	70	
	1C13	143CE2	3.797		
	1C14	143CE2	3.506		
30	1C14	143CZ	3.626		
	1C14	143CD2	3.943		
	1C14	91CG	3.966		
	1C14	91CA	3.973		
	1C15	49SD	3.501		
35	1C15	94CG	3.603		
	1C15	94CB	3.631		
	1C15	94CD1	3.657		
	1C15	49CG	3.786		
	1C15	90O	3.878		
40	1PA	79NH2	3.866		
	101A	79NH2	3.513		
	101A	45CE1	3.716		

101A	79NH1	3.816
101A	31N	3.871
102A	79NH2	3.383
102A	28OD2	3.815
103A	29N	3.119
103A	30N	3.133
103A	31N	3.539
103A	29C	3.628
103A	30CB	3.710
103A	29CA	3.773
103A	30CA	3.821
1PB	29N	3.332
1PB	29CA	3.751
1PB	29C	3.892
1PB	30N	3.917
1PB	31N	3.953
101B	28OD2	3.279
101B	29N	3.303
101B	28CG	3.959
103B	29CA	3.054
103B	32N	3.066
103B	32CB	3.174
103B	29C	3.179
103B	29N	3.239
103B	29O	3.525
103B	30N	3.683
103B	31N	3.695
103B	32CA	3.724

Table IIC. Interatomic distances in the active site of UPPS in complex with IPP

5	FROM	TO			1017	28OD2	3.512
	DISTANCE, Angstrom				1017	28CG	3.928
	1C01	70O	3.809	35	1018	28OD2	2.364
	1C02	28OD2	3.216		1018	28CG	3.315
	1C02	27O	3.687	40	1018	247NH2	3.318
10	1C02	28CB	3.980		1018	28OD1	3.896
	1C05	71O	2.963		1P19	208OG	3.381
	1C05	70O	3.179	45	1P19	250CA	3.746
	1C05	71C	3.316		1P19	206NH1	3.934
	1C05	72N	3.740		1P19	247O	3.982
15	1C05	70C	3.796		1P19	206CD	3.996
	1C05	72CA	3.902		1020	208OG	2.922
	1C05	76ND2	3.926	50	1020	250N	3.251
	1C09	70CD2	3.339		1020	250CA	3.346
	1C09	70CE2	3.717		1020	217CE2	3.424
20	1C09	70CG	3.726		1020	208CB	3.573
	1C12	70CE2	3.543	55	1020	247O	3.929
	1C12	70CD2	3.700		1021	206NH1	2.419
	1014	200NH2	3.012		1021	206CD	2.885
	1014	208OG	3.176		1021	206CZ	3.136
25	1014	208CB	3.901		1021	206NE	3.301
	1P15	28OD2	3.515		1021	208OG	3.619
	1P15	200NH2	3.785	60	1021	200NH2	3.888
	1016	76ND2	3.221		1022	250CA	2.964
	1016	76OD1	3.395		1022	247NE	3.080
30	1016	76CG	3.703		1022	247O	3.568
	1016	250CA	3.833		1022	247CZ	3.603
	1016	73OG	3.895	65	1022	247CG	3.609
	1017	200NH2	3.277		1022	250C	3.669
					1022	247CD	3.708
					1022	250N	3.789
					1022	247NH2	3.794
					1022	250O	3.945

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Table IIIA

Interatomic angle between residues in the active site of the native UPPS

	ATOM1	ATOM2	ATOM3	ANGLE, degree
	27CA	27N	27CB	36.380
75	27CA	27N	27C	34.390



	27CA	27N	27CG	59.730
	27CA	27N	28N	48.110
	27CA	27N	700	114.81
	27CA	27N	27O	41.610
5	27CB	27N	27C	61.060
	27CB	27N	27CG	31.140
	27CB	27N	28N	81.760
	27CB	27N	700	86.200
	27CB	27N	27O	55.020
10	27C	27N	27CG	90.640
	27C	27N	28N	24.120
	27C	27N	700	105.55
	27C	27N	27O	18.750
	27CG	27N	28N	107.82
15	27CG	27N	700	86.660
	27CG	27N	27O	86.150
	28N	27N	700	122.16
	28N	27N	27O	41.130
	700	27N	27O	87.110
20	27N	27CA	27C	112.36
	27N	27CA	27CB	108.92
	27N	27CA	27O	114.32
	27N	27CA	28N	104.81
	27N	27CA	27CG	90.350
25	27N	27CA	28CA	106.75
	27N	27CA	700	45.650
	27C	27CA	27CB	110.35
	27C	27CA	27O	26.110
	27C	27CA	28N	29.970
30	27C	27CA	27CG	143.84
	27C	27CA	28CA	21.730
	27C	27CA	700	99.510
	27CB	27CA	27O	85.940
	27CB	27CA	28N	137.21
35	27CB	27CA	27CG	33.580
	27CB	27CA	28CA	130.36
	27CB	27CA	700	73.670
	27O	27CA	28N	56.090
	27O	27CA	27CG	119.32
40	27O	27CA	28CA	47.840
	27O	27CA	700	83.930
	28N	27CA	27CG	164.74
	28N	27CA	28CA	8.280

	28N	27CA	700	115.89
	27CG	27CA	28CA	161.71
	27CG	27CA	700	76.000
	28CA	27CA	700	111.21
5	27CG	27CB	27CA	112.71
	27CG	27CB	27N	93.000
	27CG	27CB	27C	147.22
	27CG	27CB	27O	171.19
	27CG	27CB	27SD	35.510
10	27CG	27CB	27CE	64.550
	27CG	27CB	28N	136.98
	27CG	27CB	700	91.600
	27CA	27CB	27N	34.700
	27CA	27CB	27C	34.610
15	27CA	27CB	27O	60.300
	27CA	27CB	27SD	147.93
	27CA	27CB	27CE	148.37
	27CA	27CB	28N	26.360
	27CA	27CB	700	83.880
20	27N	27CB	27C	60.210
	27N	27CB	27O	78.260
	27N	27CB	27SD	121.10
	27N	27CB	27CE	114.61
	27N	27CB	28N	57.150
25	27N	27CB	700	54.530
	27C	27CB	27O	26.560
	27C	27CB	27SD	177.03
	27C	27CB	27CE	141.31
	27C	27CB	28N	11.650
30	27C	27CB	700	87.400
	27O	27CB	27SD	150.53
	27O	27CB	27CE	118.05
	27O	27CB	28N	37.710
	27O	27CB	700	82.510
35	27SD	27CB	27CE	36.000
	27SD	27CB	28N	171.28
	27SD	27CB	700	91.440
	27CE	27CB	28N	152.38
	27CE	27CB	700	65.120
40	28N	27CB	700	93.470
	27CB	27CG	27SD	115.29
	27CB	27CG	27CA	33.710
	27CB	27CG	27CE	86.330

	27CB	27CG	27N	55.860
	27CB	27CG	27C	20.460
	27SD	27CG	27CA	148.72
	27SD	27CG	27CE	40.300
5	27SD	27CG	27N	148.35
	27SD	27CG	27C	135.74
	27CA	27CG	27CE	113.74
	27CA	27CG	27N	29.920
	27CA	27CG	27C	13.340
10	27CE	27CG	27N	108.96
	27CE	27CG	27C	103.84
	27N	27CG	27C	39.820
	27CG	27SD	27CE	100.58
	27CG	27SD	27CB	29.200
15	27CE	27SD	27CB	80.830
	27SD	27CE	27CG	39.120
	27SD	27CE	27CB	63.170
	27SD	27CE	700	112.50
	27SD	27CE	71CA	151.28
20	27SD	27CE	70C	125.18
	27SD	27CE	71N	144.45
	27CG	27CE	27CB	29.120
	27CG	27CE	700	76.540
	27CG	27CE	71CA	112.15
25	27CG	27CE	70C	92.940
	27CG	27CE	71N	110.19
	27CB	27CE	700	66.630
	27CB	27CE	71CA	89.780
	27CB	27CE	70C	84.950
30	27CB	27CE	71N	96.340
	700	27CE	71CA	42.450
	700	27CE	70C	18.330
	700	27CE	71N	33.650
	71CA	27CE	70C	36.360
35	71CA	27CE	71N	21.480
	70C	27CE	71N	19.290
	270	27C	28N	123.65
	270	27C	27CA	121.05
	270	27C	28CA	93.890
40	270	27C	27N	120.82
	270	27C	27CB	88.040
	270	27C	28C	92.660
	270	27C	28CB	106.86

	270	27C	280	106.26
	270	27C	27CG	100.06
	28N	27C	27CA	115.29
	28N	27C	28CA	29.780
5	28N	27C	27N	106.14
	28N	27C	27CB	146.02
	28N	27C	28C	37.660
	28N	27C	28CB	22.870
	28N	27C	280	36.990
10	28N	27C	27CG	135.19
	27CA	27C	28CA	145.05
	27CA	27C	27N	33.240
	27CA	27C	27CB	35.040
	27CA	27C	28C	139.44
15	27CA	27C	28CB	129.53
	27CA	27C	280	120.75
	27CA	27C	27CG	22.820
	28CA	27C	27N	128.73
	28CA	27C	27CB	168.13
20	28CA	27C	28C	24.300
	28CA	27C	28CB	20.290
	28CA	27C	280	39.070
	28CA	27C	27CG	163.41
	27N	27C	27CB	58.730
25	27N	27C	28C	143.49
	27N	27C	28CB	108.49
	27N	27C	280	132.89
	27N	27C	27CG	49.540
	27CB	27C	28C	143.99
30	27CB	27C	28CB	164.54
	27CB	27C	280	129.27
	27CB	27C	27CG	12.320
	28C	27C	28CB	41.960
	28C	27C	280	18.970
35	28C	27C	27CG	144.47
	28CB	27C	280	51.260
	28CB	27C	27CG	152.23
	280	27C	27CG	126.78
	27C	270	28N	29.360
40	27C	270	27CA	32.830
	27C	270	27CB	65.400
	27C	270	28CA	60.270
	27C	270	27N	40.420

	27C	27O	72N	119.25
	27C	27O	72CA	115.84
	27C	27O	28C	67.810
	27C	27O	72CB	133.62
5	28N	27O	27CA	62.190
	28N	27O	27CB	94.090
	28N	27O	28CA	30.930
	28N	27O	27N	65.570
	28N	27O	72N	123.25
10	28N	27O	72CA	107.43
	28N	27O	28C	41.640
	28N	27O	72CB	115.21
	27CA	27O	27CB	33.760
	27CA	27O	28CA	93.110
15	27CA	27O	27N	24.070
	27CA	27O	72N	106.33
	27CA	27O	72CA	117.49
	27CA	27O	28C	98.190
	27CA	27O	72CB	141.08
20	27CB	27O	28CA	124.52
	27CB	27O	27N	46.720
	27CB	27O	72N	98.900
	27CB	27O	72CA	120.62
	27CB	27O	28C	121.57
25	27CB	27O	72CB	137.19
	28CA	27O	27N	93.240
	28CA	27O	72N	116.21
	28CA	27O	72CA	93.160
	28CA	27O	28C	23.060
30	28CA	27O	72CB	91.060
	27N	27O	72N	84.810
	27N	27O	72CA	93.480
	27N	27O	28C	106.96
	27N	27O	72CB	117.07
35	72N	27O	72CA	24.250
	72N	27O	28C	134.35
	72N	27O	72CB	39.290
	72CA	27O	28C	110.11
	72CA	27O	72CB	23.590
40	28C	27O	72CB	100.52
	27C	28N	28CA	123.27
	27C	28N	27O	26.990
	27C	28N	28CB	144.68

	27C	28N	27CA	34.730
	27C	28N	28C	123.32
	27C	28N	28O	126.47
	27C	28N	27N	49.740
5	27C	28N	28CG	128.18
	27C	28N	29N	114.65
	27C	28N	27CB	22.340
	28CA	28N	27O	96.310
10	28CA	28N	28CB	37.450
	28CA	28N	27CA	157.96
	28CA	28N	28C	35.130
	28CA	28N	28O	59.120
	28CA	28N	27N	150.28
15	28CA	28N	28CG	32.800
	28CA	28N	29N	28.800
	28CA	28N	27CB	143.49
	27O	28N	28CB	123.25
	27O	28N	27CA	61.720
	27O	28N	28C	101.36
20	27O	28N	28O	114.28
	27O	28N	27N	73.310
	27O	28N	28CG	106.86
	27O	28N	29N	90.580
	27O	28N	27CB	48.200
25	28CB	28N	27CA	153.91
	28CB	28N	28C	61.510
	28CB	28N	28O	74.560
	28CB	28N	27N	126.83
	28CB	28N	28CG	16.730
30	28CB	28N	29N	62.020
	28CB	28N	27CB	163.11
	27CA	28N	28C	144.55
	27CA	28N	28O	129.18
	27CA	28N	27N	27.080
35	27CA	28N	28CG	147.04
	27CA	28N	29N	142.51
	27CA	28N	27CB	16.430
	28C	28N	28O	25.920
	28C	28N	27N	171.56
40	28C	28N	28CG	64.910
	28C	28N	29N	12.790
	28C	28N	27CB	130.53
	28O	28N	27N	150.57

	28O	28N	28CG	83.730
	28O	28N	29N	37.940
	28O	28N	27CB	121.55
	27N	28N	28CG	122.57
5	27N	28N	29N	163.88
	27N	28N	27CB	41.090
	28CG	28N	29N	61.280
	28CG	28N	27CB	148.65
	29N	28N	27CB	126.52
10	28N	28CA	28CB	107.02
	28N	28CA	28C	112.05
	28N	28CA	28O	89.640
	28N	28CA	27C	26.940
	28N	28CA	29N	134.67
15	28N	28CA	28CG	128.94
	28N	28CA	27O	52.760
	28N	28CA	28OD1	152.34
	28N	28CA	28OD2	113.57
	28N	28CA	27CA	13.760
20	28N	28CA	29CA	127.71
	28N	28CA	72CD1	129.63
	28CB	28CA	28C	109.05
	28CB	28CA	28O	105.11
	28CB	28CA	27C	125.81
25	28CB	28CA	29N	108.67
	28CB	28CA	28CG	32.900
	28CB	28CA	27O	139.28
	28CB	28CA	28OD1	49.370
	28CB	28CA	28OD2	36.310
30	28CB	28CA	27CA	116.48
	28CB	28CA	29CA	108.66
	28CB	28CA	72CD1	91.900
	28C	28CA	28O	26.130
	28C	28CA	27C	114.99
35	28C	28CA	29N	28.520
	28C	28CA	28CG	111.90
	28C	28CA	27O	111.43
	28C	28CA	28OD1	91.730
	28C	28CA	28OD2	129.48
40	28C	28CA	27CA	114.99
	28C	28CA	29CA	18.660
	28C	28CA	72CD1	104.41
	28O	28CA	27C	101.07

	280	28CA	29N	54.660
	280	28CA	28CG	122.89
	280	28CA	270	109.10
	280	28CA	28OD1	109.04
5	280	28CA	28OD2	138.00
	280	28CA	27CA	96.260
	280	28CA	29CA	44.780
	280	28CA	72CD1	130.51
	27C	28CA	29N	125.15
10	27C	28CA	28CG	133.04
	27C	28CA	270	25.830
	27C	28CA	28OD1	149.66
	27C	28CA	28OD2	115.49
	27C	28CA	27CA	13.230
15	27C	28CA	29CA	123.17
	27C	28CA	72CD1	105.64
	29N	28CA	28CG	95.780
	29N	28CA	270	108.87
	29N	28CA	28OD1	72.600
20	29N	28CA	28OD2	111.76
	29N	28CA	27CA	131.70
	29N	28CA	29CA	9.900
	29N	28CA	72CD1	75.920
	28CG	28CA	270	127.43
25	28CG	28CA	28OD1	23.400
	28CG	28CA	28OD2	17.580
	28CG	28CA	27CA	131.69
	28CG	28CA	29CA	101.05
	28CG	28CA	72CD1	59.120
30	270	28CA	28OD1	132.28
	270	28CA	28OD2	112.81
	270	28CA	27CA	39.060
	270	28CA	29CA	111.06
	270	28CA	72CD1	82.410
35	28OD1	28CA	28OD2	39.380
	28OD1	28CA	27CA	153.28
	28OD1	28CA	29CA	78.560
	28OD1	28CA	72CD1	50.890
	28OD2	28CA	27CA	114.54
40	28OD2	28CA	29CA	117.93
	28OD2	28CA	72CD1	59.590
	27CA	28CA	29CA	127.25
	27CA	28CA	72CD1	117.24



	29CA	28CA	72CD1	85.820
	28CG	28CB	28CA	113.35
	28CG	28CB	28OD2	28.210
	28CG	28CB	28OD1	27.410
5	28CG	28CB	28N	135.71
	28CG	28CB	28C	115.15
	28CG	28CB	28O	133.29
	28CG	28CB	29N	93.780
	28CG	28CB	27C	123.45
10	28CA	28CB	28OD2	120.99
	28CA	28CB	28OD1	101.24
	28CA	28CB	28N	35.530
	28CA	28CB	28C	35.780
	28CA	28CB	28O	47.240
15	28CA	28CB	29N	45.280
	28CA	28CB	27C	33.900
	28OD2	28CB	28OD1	55.620
	28OD2	28CB	28N	124.28
	28OD2	28CB	28C	138.72
20	28OD2	28CB	28O	159.46
	28OD2	28CB	29N	118.99
	28OD2	28CB	27C	112.73
	28OD1	28CB	28N	134.80
	28OD1	28CB	28C	90.710
25	28OD1	28CB	28O	106.63
	28OD1	28CB	29N	69.220
	28OD1	28CB	27C	126.18
	28N	28CB	28C	61.110
	28N	28CB	28O	58.660
30	28N	28CB	29N	77.910
	28N	28CB	27C	12.440
	28C	28CB	28O	21.080
	28C	28CB	29N	21.570
	28C	28CB	27C	65.640
35	28O	28CB	29N	40.530
	28O	28CB	27C	67.460
	29N	28CB	27C	79.030
	28OD1	28CG	28OD2	123.68
	28OD1	28CG	28CB	119.02
40	28OD1	28CG	28CA	102.89
	28OD1	28CG	72CD1	65.440
	28OD1	28CG	28C	81.670
	28OD1	28CG	72CE1	45.630

	28OD1	28CG	28N	121.14
	28OD1	28CG	29N	61.710
	28OD2	28CG	28CB	117.30
	28OD2	28CG	28CA	124.73
5	28OD2	28CG	72CD1	92.190
	28OD2	28CG	28C	149.60
	28OD2	28CG	72CE1	94.670
	28OD2	28CG	28N	108.81
	28OD2	28CG	29N	157.61
10	28CB	28CG	28CA	33.750
	28CB	28CG	72CD1	114.38
	28CB	28CG	28C	41.560
	28CB	28CG	72CE1	131.88
	28CB	28CG	28N	27.570
15	28CB	28CG	29N	62.520
	28CA	28CG	72CD1	80.800
	28CA	28CG	28C	24.870
	28CA	28CG	72CE1	98.780
	28CA	28CG	28N	18.260
20	28CA	28CG	29N	41.560
	72CD1	28CG	28C	83.390
	72CD1	28CG	72CE1	23.830
	72CD1	28CG	28N	89.660
	72CD1	28CG	29N	69.760
25	28C	28CG	72CE1	93.160
	28C	28CG	28N	41.390
	28C	28CG	29N	21.080
	72CE1	28CG	28N	111.07
	72CE1	28CG	29N	74.320
30	28N	28CG	29N	59.690
	28CG	28OD1	28OD2	28.200
	28CG	28OD1	28CB	33.570
	28CG	28OD1	72CE1	115.15
	28CG	28OD1	28CA	53.710
35	28CG	28OD1	72CD1	92.900
	28CG	28OD1	29N	98.940
	28CG	28OD1	28C	77.530
	28CG	28OD1	72CZ	114.77
	28OD2	28OD1	28CB	61.770
40	28OD2	28OD1	72CE1	98.870
	28OD2	28OD1	28CA	78.700
	28OD2	28OD1	72CD1	85.680
	28OD2	28OD1	29N	123.95

	28OD2	28OD1	28C	104.36
	28OD2	28OD1	72CZ	92.370
	28CB	28OD1	72CE1	128.09
	28CB	28OD1	28CA	29.390
5	28CB	28OD1	72CD1	100.88
	28CB	28OD1	29N	68.830
	28CB	28OD1	28C	46.320
	28CB	28OD1	72CZ	137.45
	72CE1	28OD1	28CA	104.36
10	72CE1	28OD1	72CD1	27.220
	72CE1	28OD1	29N	91.190
	72CE1	28OD1	28C	106.70
	72CE1	28OD1	72CZ	17.090
	28CA	28OD1	72CD1	78.500
15	28CA	28OD1	29N	45.550
	28CA	28OD1	28C	26.560
	28CA	28OD1	72CZ	118.77
	72CD1	28OD1	29N	78.970
	72CD1	28OD1	28C	87.210
20	72CD1	28OD1	72CZ	40.290
	29N	28OD1	28C	22.570
	29N	28OD1	72CZ	107.81
	28C	28OD1	72CZ	123.75
	28CG	28OD2	28OD1	28.120
25	28CG	28OD2	28CB	34.490
	28CG	28OD2	28CA	37.690
	28CG	28OD2	72CD1	67.750
	28CG	28OD2	72CE1	65.900
	28OD1	28OD2	28CB	62.620
30	28OD1	28OD2	28CA	61.920
	28OD1	28OD2	72CD1	57.260
	28OD1	28OD2	72CE1	45.610
	28CB	28OD2	28CA	22.700
	28CB	28OD2	72CD1	86.670
35	28CB	28OD2	72CE1	94.290
	28CA	28OD2	72CD1	66.750
	28CA	28OD2	72CE1	79.190
	72CD1	28OD2	72CE1	21.880
	28O	28C	29N	122.03
40	28O	28C	28CA	120.19
	28O	28C	29CA	90.290
	28O	28C	28N	91.640
	28O	28C	28CB	111.86

	28O	28C	27C	96.690
	28O	28C	28CG	131.90
	28O	28C	28OD1	139.06
5	28O	28C	29C	89.870
	28O	28C	27O	110.57
	28O	28C	30N	98.730
	29N	28C	28CA	117.78
	29N	28C	29CA	31.750
10	29N	28C	28N	142.75
	29N	28C	28CB	114.75
	29N	28C	27C	128.76
	29N	28C	28CG	91.670
	29N	28C	28OD1	71.910
15	29N	28C	29C	37.100
	29N	28C	27O	109.27
	29N	28C	30N	42.660
	28CA	28C	29CA	149.50
	28CA	28C	28N	32.820
20	28CA	28C	28CB	35.180
	28CA	28C	27C	40.710
	28CA	28C	28CG	43.230
	28CA	28C	28OD1	61.710
	28CA	28C	29C	144.76
25	28CA	28C	27O	45.510
	28CA	28C	30N	126.41
	29CA	28C	28N	164.06
	29CA	28C	28CB	135.61
	29CA	28C	27C	145.15
30	29CA	28C	28CG	116.00
	29CA	28C	28OD1	95.230
	29CA	28C	29C	20.590
	29CA	28C	27O	128.30
	29CA	28C	30N	40.330
35	28N	28C	28CB	57.390
	28N	28C	27C	19.020
	28N	28C	28CG	73.700
	28N	28C	28OD1	93.660
	28N	28C	29C	143.57
40	28N	28C	27O	37.000
	28N	28C	30N	123.80
	28CB	28C	27C	72.390
	28CB	28C	28CG	23.290
	28CB	28C	28OD1	42.970

	28CB	28C	29C	151.53
	28CB	28C	27O	80.610
	28CB	28C	30N	149.41
5	27C	28C	28CG	83.910
	27C	28C	28OD1	101.30
	27C	28C	29C	124.95
	27C	28C	27O	19.530
	27C	28C	30N	104.83
10	28CG	28C	28OD1	20.800
	28CG	28C	29C	128.73
	28CG	28C	27O	84.850
	28CG	28C	30N	127.77
	28OD1	28C	29C	108.58
	28OD1	28C	27O	97.440
15	28OD1	28C	30N	111.48
	29C	28C	27O	109.67
	29C	28C	30N	20.910
	27O	28C	30N	88.790
20	28C	28O	29N	30.260
	28C	28O	28CA	33.680
	28C	28O	29CA	62.770
	28C	28O	28N	62.440
	28C	28O	28CB	47.070
	28C	28O	29C	70.870
25	28C	28O	27C	64.340
	29N	28O	28CA	63.940
	29N	28O	29CA	32.520
	29N	28O	28N	91.600
	29N	28O	28CB	72.570
30	29N	28O	29C	42.980
	29N	28O	27C	89.830
	28CA	28O	29CA	96.440
	28CA	28O	28N	31.240
	28CA	28O	28CB	27.650
35	28CA	28O	29C	102.81
	28CA	28O	27C	39.860
	29CA	28O	28N	123.14
	29CA	28O	28CB	101.00
	29CA	28O	29C	20.550
40	29CA	28O	27C	117.68
	28N	28O	28CB	46.780
	28N	28O	29C	121.50
	28N	28O	27C	16.540

	28CB	28O	29C	115.55
	28CB	28O	27C	61.280
	29C	28O	27C	110.43
5	28C	29N	29CA	119.54
	28C	29N	28O	27.710
	28C	29N	28CA	33.700
	28C	29N	29C	124.80
	28C	29N	30N	119.21
	28C	29N	28CB	43.680
10	28C	29N	28OD1	85.520
	28C	29N	28N	24.470
	28C	29N	29O	124.97
	28C	29N	28CG	67.240
	29CA	29N	28O	91.840
15	29CA	29N	28CA	153.19
	29CA	29N	29C	30.470
	29CA	29N	30N	57.840
	29CA	29N	28CB	143.85
	29CA	29N	28OD1	130.87
20	29CA	29N	28N	140.42
	29CA	29N	29O	20.390
	29CA	29N	28CG	145.23
	28O	29N	28CA	61.410
	28O	29N	29C	100.82
25	28O	29N	30N	105.29
	28O	29N	28CB	66.900
	28O	29N	28OD1	105.70
	28O	29N	28N	50.460
	28O	29N	29O	98.780
30	28O	29N	28CG	90.190
	28CA	29N	29C	148.72
	28CA	29N	30N	127.48
	28CA	29N	28CB	26.040
	28CA	29N	28OD1	61.840
35	28CA	29N	28N	16.530
	28CA	29N	29O	154.26
	28CA	29N	28CG	42.650
	29C	29N	30N	27.380
	29C	29N	28CB	167.69
40	29C	29N	28OD1	148.53
	29C	29N	28N	132.65
	29C	29N	29O	10.120
	29C	29N	28CG	167.76

	30N	29N	28CB	153.45
	30N	29N	28OD1	147.27
	30N	29N	28N	114.75
	30N	29N	29O	37.500
5	30N	29N	28CG	153.02
	28CB	29N	28OD1	41.940
	28CB	29N	28N	40.060
	28CB	29N	29O	162.27
	28CB	29N	28CG	23.710
10	28OD1	29N	28N	78.310
	28OD1	29N	29O	143.62
	28OD1	29N	28CG	19.360
	28N	29N	29O	137.73
	28N	29N	28CG	59.030
15	29O	29N	28CG	162.19
	29N	29CA	29C	120.43
	29N	29CA	29O	147.28
	29N	29CA	28C	28.710
	29N	29CA	30N	91.970
20	29N	29CA	28O	55.640
	29N	29CA	30CA	102.08
	29N	29CA	28CA	16.910
	29C	29CA	29O	26.900
	29C	29CA	28C	125.53
25	29C	29CA	30N	28.490
	29C	29CA	28O	120.71
	29C	29CA	30CA	18.360
	29C	29CA	28CA	125.32
	29O	29CA	28C	146.41
30	29O	29CA	30N	55.390
	29O	29CA	28O	129.18
	29O	29CA	30CA	45.260
	29O	29CA	28CA	150.37
	28C	29CA	30N	100.21
35	28C	29CA	28O	26.940
	28C	29CA	30CA	109.44
	28C	29CA	28CA	11.840
	30N	29CA	28O	105.06
	30N	29CA	30CA	10.130
40	30N	29CA	28CA	97.730
	28O	29CA	30CA	111.26
	28O	29CA	28CA	38.780
	30CA	29CA	28CA	107.63

	290	29C	30N	122.23
	290	29C	29CA	119.22
	290	29C	30CA	90.610
	290	29C	29N	148.27
5	290	29C	30C	72.390
	290	29C	31N	81.660
	290	29C	28C	145.21
	290	29C	30CB	106.09
	290	29C	28O	128.94
10	290	29C	30ND2	114.58
	290	29C	30O	59.110
	30N	29C	29CA	118.55
	30N	29C	30CA	31.620
	30N	29C	29N	89.480
15	30N	29C	30C	55.670
	30N	29C	31N	62.350
	30N	29C	28C	88.620
	30N	29C	30CB	16.150
	30N	29C	28O	96.860
20	30N	29C	30ND2	34.300
	30N	29C	30O	65.850
	29CA	29C	30CA	150.17
	29CA	29C	29N	29.100
	29CA	29C	30C	154.01
25	29CA	29C	31N	129.42
	29CA	29C	28C	33.880
	29CA	29C	30CB	134.69
	29CA	29C	28O	38.750
	29CA	29C	30ND2	114.59
30	29CA	29C	30O	163.18
	30CA	29C	29N	121.08
	30CA	29C	30C	30.880
	30CA	29C	31N	49.750
	30CA	29C	28C	118.92
35	30CA	29C	30CB	15.480
	30CA	29C	28O	122.44
	30CA	29C	30ND2	44.530
	30CA	29C	30O	36.420
	29N	29C	30C	134.46
40	29N	29C	31N	116.51
	29N	29C	28C	18.100
	29N	29C	30CB	105.61
	29N	29C	28O	36.200



	29N	29C	30ND2	91.810
	29N	29C	300	148.84
	30C	29C	31N	24.920
	30C	29C	28C	142.20
5	30C	29C	30CB	41.950
	30C	29C	280	152.26
	30C	29C	30ND2	75.400
	30C	29C	300	14.380
	31N	29C	28C	130.82
10	31N	29C	30CB	54.430
	31N	29C	280	149.26
	31N	29C	30ND2	91.600
	31N	29C	300	35.810
	28C	29C	30CB	104.20
15	28C	29C	280	19.260
	28C	29C	30ND2	80.950
	28C	29C	300	154.43
	30CB	29C	280	110.33
	30CB	29C	30ND2	37.220
20	30CB	29C	300	50.510
	280	29C	30ND2	78.810
	280	29C	300	156.96
	30ND2	29C	300	78.520
	29C	290	30N	30.100
25	29C	290	29CA	33.880
	29C	290	30CA	62.390
	29C	290	30C	83.190
	29C	290	31N	76.100
	29C	290	300	102.69
30	29C	290	32N	109.56
	29C	290	29N	21.600
	29C	290	32C	146.61
	30N	290	29CA	63.980
	30N	290	30CA	32.290
35	30N	290	30C	56.600
	30N	290	31N	58.480
	30N	290	300	74.320
	30N	290	32N	106.90
	30N	290	29N	51.700
40	30N	290	32C	139.48
	29CA	290	30CA	96.270
	29CA	290	30C	113.67
	29CA	290	31N	98.860

	29CA	290	30O	134.07
	29CA	290	32N	106.33
	29CA	290	29N	12.320
	29CA	290	32C	130.82
5	30CA	290	30C	31.760
	30CA	290	31N	47.590
	30CA	290	30O	44.420
	30CA	290	32N	98.540
	30CA	290	29N	83.970
10	30CA	290	32C	116.67
	30C	290	31N	24.420
	30C	290	30O	20.410
	30C	290	32N	68.450
	30C	290	29N	102.30
15	30C	290	32C	85.980
	31N	290	30O	39.770
	31N	290	32N	51.990
	31N	290	29N	89.920
	31N	290	32C	81.050
20	30O	290	32N	67.440
	30O	290	29N	122.54
	30O	290	32C	72.860
	32N	290	29N	107.39
	32N	290	32C	37.500
25	29N	290	32C	137.88
	29C	30N	30CA	119.61
	29C	30N	29O	27.670
	29C	30N	30CB	155.13
	29C	30N	29CA	32.960
30	29C	30N	30C	97.880
	29C	30N	30ND2	129.93
	29C	30N	31N	92.760
	29C	30N	29N	63.130
	29C	30N	30CG	154.93
35	29C	30N	30O	93.970
	29C	30N	28C	70.460
	30CA	30N	29O	91.950
	30CA	30N	30CB	35.520
	30CA	30N	29CA	152.57
40	30CA	30N	30C	34.960
	30CA	30N	30ND2	70.210
	30CA	30N	31N	60.460
	30CA	30N	29N	176.68

	30CA	30N	30CG	57.170
	30CA	30N	300	30.530
	30CA	30N	28C	162.37
	290	30N	30CB	127.47
5	290	30N	29CA	60.630
	290	30N	30C	73.990
	290	30N	30ND2	123.38
	290	30N	31N	78.450
	290	30N	29N	90.800
10	290	30N	30CG	138.42
	290	30N	300	67.810
	290	30N	28C	97.020
	30CB	30N	29CA	171.88
	30CB	30N	30C	60.600
15	30CB	30N	30ND2	53.970
	30CB	30N	31N	74.000
	30CB	30N	29N	141.69
	30CB	30N	30CG	30.100
	30CB	30N	300	62.310
20	30CB	30N	28C	133.31
	29CA	30N	30C	125.63
	29CA	30N	30ND2	123.82
	29CA	30N	31N	109.21
	29CA	30N	29N	30.190
25	29CA	30N	30CG	145.25
	29CA	30N	300	125.03
	29CA	30N	28C	39.460
	30C	30N	30ND2	105.12
	30C	30N	31N	28.440
30	30C	30N	29N	144.78
	30C	30N	30CG	88.830
	30C	30N	300	12.250
	30C	30N	28C	162.66
	30ND2	30N	31N	126.86
35	30ND2	30N	29N	109.72
	30ND2	30N	30CG	26.110
	30ND2	30N	300	99.330
	30ND2	30N	28C	92.200
	31N	30N	29N	118.36
40	31N	30N	30CG	103.99
	31N	30N	300	39.730
	31N	30N	28C	136.29
	29N	30N	30CG	121.32

	29N	30N	300	150.40
	29N	30N	28C	18.130
	30CG	30N	300	87.520
	30CG	30N	28C	107.18
5	300	30N	28C	164.36
	30N	30CA	30CB	110.71
	30N	30CA	30C	112.03
	30N	30CA	300	131.50
	30N	30CA	29C	28.760
10	30N	30CA	31N	88.380
	30N	30CA	30CG	93.640
	30N	30CA	30ND2	78.770
	30N	30CA	290	55.760
	30N	30CA	30OD1	97.290
15	30N	30CA	29CA	17.300
	30N	30CA	31CA	96.000
	30CB	30CA	30C	109.05
	30CB	30CA	300	109.06
	30CB	30CA	29C	139.47
20	30CB	30CA	31N	104.02
	30CB	30CA	30CG	33.600
	30CB	30CA	30ND2	62.890
	30CB	30CA	290	166.48
	30CB	30CA	30OD1	25.650
25	30CB	30CA	29CA	128.00
	30CB	30CA	31CA	105.80
	30C	30CA	300	26.410
	30C	30CA	29C	95.100
	30C	30CA	31N	29.210
30	30C	30CA	30CG	142.26
	30C	30CA	30ND2	168.84
	30C	30CA	290	78.730
	30C	30CA	30OD1	134.55
	30C	30CA	29CA	101.94
35	30C	30CA	31CA	20.100
	300	30CA	29C	106.87
	300	30CA	31N	55.620
	300	30CA	30CG	134.40
	300	30CA	30ND2	145.73
40	300	30CA	290	82.910
	300	30CA	30OD1	129.50
	300	30CA	29CA	116.83
	300	30CA	31CA	46.510

	29C	30CA	31N	81.430
	29C	30CA	30CG	118.36
	29C	30CA	30ND2	95.920
	29C	30CA	29O	27.000
5	29C	30CA	30OD1	123.63
	29C	30CA	29CA	11.470
	29C	30CA	31CA	85.860
	31N	30CA	30CG	134.14
	31N	30CA	30ND2	155.92
10	31N	30CA	29O	77.160
	31N	30CA	30OD1	126.87
	31N	30CA	29CA	83.830
	31N	30CA	31CA	9.120
	30CG	30CA	30ND2	29.300
15	30CG	30CA	29O	138.81
	30CG	30CA	30OD1	8.000
	30CG	30CA	29CA	108.76
	30CG	30CA	31CA	138.10
	30ND2	30CA	29O	110.79
20	30ND2	30CA	30OD1	37.290
	30ND2	30CA	29CA	89.220
	30ND2	30CA	31CA	163.85
	29O	30CA	30OD1	145.98
	29O	30CA	29CA	38.470
25	29O	30CA	31CA	77.550
	30OD1	30CA	29CA	113.33
	30OD1	30CA	31CA	130.32
	29CA	30CA	31CA	89.710
	30CG	30CB	30CA	112.22
30	30CG	30CB	30OD1	26.140
	30CG	30CB	30ND2	29.720
	30CG	30CB	30N	94.860
	30CG	30CB	30C	147.37
	30CG	30CB	31N	152.68
35	30CG	30CB	30O	143.17
	30CG	30CB	45CD2	90.510
	30CG	30CB	29C	99.810
	30CA	30CB	30OD1	138.33
	30CA	30CB	30ND2	82.530
40	30CA	30CB	30N	33.760
	30CA	30CB	30C	35.600
	30CA	30CB	31N	48.310
	30CA	30CB	30O	44.510

	30CA	30CB	45CD2	156.51
	30CA	30CB	29C	25.040
	30OD1	30CB	30ND2	55.860
5	30OD1	30CB	30N	116.48
	30OD1	30CB	30C	173.05
	30OD1	30CB	31N	161.44
	30OD1	30CB	300	157.21
	30OD1	30CB	45CD2	64.420
10	30OD1	30CB	29C	123.04
	30ND2	30CB	30N	69.900
	30ND2	30CB	30C	117.72
	30ND2	30CB	31N	126.99
	30ND2	30CB	300	117.84
	30ND2	30CB	45CD2	120.16
15	30ND2	30CB	29C	72.880
	30N	30CB	30C	60.230
	30N	30CB	31N	58.220
	30N	30CB	300	75.530
	30N	30CB	45CD2	143.63
20	30N	30CB	29C	8.720
	30C	30CB	31N	23.510
	30C	30CB	300	19.910
	30C	30CB	45CD2	122.11
	30C	30CB	29C	53.020
25	31N	30CB	300	41.290
	31N	30CB	45CD2	108.35
	31N	30CB	29C	54.210
	300	30CB	45CD2	118.45
	300	30CB	29C	67.300
30	45CD2	30CB	29C	149.57
	30OD1	30CG	30ND2	122.71
	30OD1	30CG	30CB	121.44
	30OD1	30CG	30CA	155.54
	30OD1	30CG	30N	152.61
35	30OD1	30CG	30C	141.79
	30OD1	30CG	45CD2	54.230
	30ND2	30CG	30CB	115.85
	30ND2	30CG	30CA	81.700
	30ND2	30CG	30N	68.090
40	30ND2	30CG	30C	95.470
	30ND2	30CG	45CD2	175.41
	30CB	30CG	30CA	34.170
	30CB	30CG	30N	55.040

	30CB	30CG	30C	20.460
	30CB	30CG	45CD2	67.310
	30CA	30CG	30N	29.190
	30CA	30CG	30C	14.140
5	30CA	30CG	45CD2	101.31
	30N	30CG	30C	40.220
	30N	30CG	45CD2	112.99
	30C	30CG	45CD2	87.760
	30CG	30OD1	30ND2	29.660
10	30CG	30OD1	30CB	32.420
	30CG	30OD1	45CD2	108.68
	30CG	30OD1	30CA	16.460
	30CG	30OD1	45CA	107.38
	30ND2	30OD1	30CB	62.080
15	30ND2	30OD1	45CD2	138.23
	30ND2	30OD1	30CA	46.090
	30ND2	30OD1	45CA	123.53
	30CB	30OD1	45CD2	76.330
	30CB	30OD1	30CA	16.030
20	30CB	30OD1	45CA	86.380
	45CD2	30OD1	30CA	92.220
	45CD2	30OD1	45CA	52.870
	30CA	30OD1	45CA	97.680
	30CG	30ND2	30OD1	27.630
25	30CG	30ND2	30CB	34.430
	30CG	30ND2	30CA	69.000
	30CG	30ND2	30N	85.800
	30CG	30ND2	29C	101.18
	30OD1	30ND2	30CB	62.060
30	30OD1	30ND2	30CA	96.620
	30OD1	30ND2	30N	109.98
	30OD1	30ND2	29C	125.74
	30CB	30ND2	30CA	34.590
	30CB	30ND2	30N	56.130
35	30CB	30ND2	29C	69.900
	30CA	30ND2	30N	31.020
	30CA	30ND2	29C	39.550
	30N	30ND2	29C	15.760
	30O	30C	31N	123.08
40	30O	30C	30CA	120.03
	30O	30C	31CA	92.500
	30O	30C	30N	142.51
	30O	30C	30CB	116.68

	300	30C	290	105.73
	300	30C	29C	128.83
	300	30C	31C	78.390
	300	30C	32N	90.790
5	300	30C	30CG	116.60
	300	30C	310	62.180
	31N	30C	30CA	116.88
	31N	30C	31CA	30.580
	31N	30C	30N	89.840
10	31N	30C	30CB	108.74
	31N	30C	290	93.910
	31N	30C	29C	85.950
	31N	30C	31C	50.540
	31N	30C	32N	51.260
15	31N	30C	30CG	114.95
	31N	30C	310	64.140
	30CA	30C	31CA	147.46
	30CA	30C	30N	33.020
	30CA	30C	30CB	35.360
20	30CA	30C	290	69.500
	30CA	30C	29C	54.020
	30CA	30C	31C	151.01
	30CA	30C	32N	129.67
	30CA	30C	30CG	23.600
25	30CA	30C	310	161.89
	31CA	30C	30N	118.61
	31CA	30C	30CB	130.91
	31CA	30C	290	104.32
	31CA	30C	29C	107.30
30	31CA	30C	31C	28.450
	31CA	30C	32N	42.540
	31CA	30C	30CG	140.74
	31CA	30C	310	36.590
	30N	30C	30CB	59.170
35	30N	30C	290	49.410
	30N	30C	29C	26.450
	30N	30C	31C	118.85
	30N	30C	32N	98.490
	30N	30C	30CG	50.950
40	30N	30C	310	133.57
	30CB	30C	290	104.22
	30CB	30C	29C	85.030
	30CB	30C	31C	158.64



	30CB	30C	32N	152.48
	30CB	30C	30CG	12.170
	30CB	30C	31O	162.52
5	29O	30C	29C	24.420
	29O	30C	31C	84.470
	29O	30C	32N	63.960
	29O	30C	30CG	93.020
	29O	30C	31O	92.450
10	29C	30C	31C	97.110
	29C	30C	32N	75.660
	29C	30C	30CG	75.610
	29C	30C	31O	109.46
	31C	30C	32N	21.500
15	31C	30C	30CG	164.83
	31C	30C	31O	16.550
	32N	30C	30CG	148.93
	32N	30C	31O	35.130
	30CG	30C	31O	174.51
20	30C	300	31N	29.760
	30C	300	30CA	33.560
	30C	300	31CA	61.240
	30C	300	31C	78.850
	30C	300	30CB	43.410
25	30C	300	29O	53.850
	30C	300	31O	99.410
	30C	300	30N	25.240
	30C	300	32N	70.370
	30C	300	29C	36.790
30	31N	300	30CA	63.320
	31N	300	31CA	31.480
	31N	300	31C	52.400
	31N	300	30CB	68.120
	31N	300	29O	66.140
	31N	300	31O	71.660
35	31N	300	30N	52.660
	31N	300	32N	50.450
	31N	300	29C	55.140
	30CA	300	31CA	94.800
40	30CA	300	31C	109.50
	30CA	300	30CB	26.430
	30CA	300	29O	52.670
	30CA	300	31O	130.30
	30CA	300	30N	17.970

5	30CA	300	32N	96.210
	30CA	300	29C	36.710
	31CA	300	31C	29.120
	31CA	300	30CB	96.070
	31CA	300	290	84.670
10	31CA	300	310	43.350
	31CA	300	30N	83.140
	31CA	300	32N	39.630
	31CA	300	29C	80.440
	31C	300	30CB	120.49
15	31C	300	290	76.060
	31C	300	310	20.860
	31C	300	30N	92.960
	31C	300	32N	19.020
	31C	300	29C	80.980
20	30CB	300	290	78.960
	30CB	300	310	139.22
	30CB	300	30N	42.160
	30CB	300	32N	113.76
	30CB	300	29C	62.190
25	290	300	310	91.030
	290	300	30N	37.860
	290	300	32N	57.170
	290	300	29C	18.190
	310	300	30N	113.40
30	310	300	32N	35.790
	310	300	29C	99.540
	30N	300	32N	78.500
	30N	300	29C	20.180
	32N	300	29C	63.760
35	30C	31N	31CA	121.54
	30C	31N	300	27.160
	30C	31N	30CA	33.900
	30C	31N	31C	104.99
	30C	31N	30N	61.710
40	30C	31N	32N	107.97
	30C	31N	29C	69.130
	30C	31N	30CB	47.750
	30C	31N	290	61.660
	30C	31N	310	95.590
	31CA	31N	300	94.380
	31CA	31N	30CA	155.43
	31CA	31N	31C	33.750

	31CA	31N	30N	163.31
	31CA	31N	32N	55.530
	31CA	31N	29C	138.46
	31CA	31N	30CB	147.89
5	31CA	31N	29O	121.80
	31CA	31N	31O	32.550
	30O	31N	30CA	61.060
	30O	31N	31C	81.750
	30O	31N	30N	87.610
10	30O	31N	32N	93.250
	30O	31N	29C	89.050
	30O	31N	30CB	70.590
	30O	31N	29O	74.090
	30O	31N	31O	70.250
15	30CA	31N	31C	132.39
	30CA	31N	30N	31.160
	30CA	31N	32N	121.81
	30CA	31N	29C	48.820
	30CA	31N	30CB	27.660
20	30CA	31N	29O	55.240
	30CA	31N	31O	127.00
	31C	31N	30N	130.99
	31C	31N	32N	26.800
	31C	31N	29C	106.84
25	31C	31N	30CB	152.25
	31C	31N	29O	88.200
	31C	31N	31O	14.520
	30N	31N	32N	107.85
	30N	31N	29C	24.880
30	30N	31N	30CB	47.780
	30N	31N	29O	43.070
	30N	31N	31O	135.94
	32N	31N	29C	82.970
	32N	31N	30CB	149.45
35	32N	31N	29O	68.170
	32N	31N	31O	40.090
	29C	31N	30CB	71.370
	29C	31N	29O	22.240
	29C	31N	31O	114.32
40	30CB	31N	29O	82.270
	30CB	31N	31O	140.26
	29O	31N	31O	93.370
	31N	31CA	31C	114.05

	31N	31CA	31O	128.25
	31N	31CA	32N	94.940
	31N	31CA	30C	27.880
	31N	31CA	30O	54.140
5	31N	31CA	32CA	100.77
	31N	31CA	30CA	15.440
	31C	31CA	31O	26.710
	31C	31CA	32N	29.160
	31C	31CA	30C	101.61
10	31C	31CA	30O	87.840
	31C	31CA	32CA	19.930
	31C	31CA	30CA	107.84
	31O	31CA	32N	55.860
	31O	31CA	30C	105.79
15	31O	31CA	30O	83.420
	31O	31CA	32CA	46.640
	31O	31CA	30CA	116.27
	32N	31CA	30C	94.840
	32N	31CA	30O	93.650
20	32N	31CA	32CA	9.260
	32N	31CA	30CA	95.310
	30C	31CA	30O	26.250
	30C	31CA	32CA	96.610
	30C	31CA	30CA	12.440
25	30O	31CA	32CA	91.250
	30O	31CA	30CA	38.700
	32CA	31CA	30CA	98.990
	31O	31C	32N	123.15
	31O	31C	31CA	119.67
30	31O	31C	32CA	92.510
	31O	31C	31N	134.95
	31O	31C	32C	74.640
	31O	31C	30O	94.880
	31O	31C	30C	117.27
35	31O	31C	32CB	108.24
	31O	31C	32O	61.430
	32N	31C	31CA	117.17
	32N	31C	32CA	30.680
	32N	31C	31N	95.680
40	32N	31C	32C	55.190
	32N	31C	30O	111.38
	32N	31C	30C	99.410
	32N	31C	32CB	15.030

	32N	31C	32O	65.220
	31CA	31C	32CA	147.82
	31CA	31C	31N	32.200
	31CA	31C	32C	151.85
5	31CA	31C	30O	63.040
	31CA	31C	30C	49.950
	31CA	31C	32CB	132.08
	31CA	31C	32O	161.58
	32CA	31C	31N	122.49
10	32CA	31C	32C	31.340
	32CA	31C	30O	117.61
	32CA	31C	30C	117.02
	32CA	31C	32CB	15.750
	32CA	31C	32O	36.890
15	31N	31C	32C	120.12
	31N	31C	30O	45.850
	31N	31C	30C	24.470
	31N	31C	32CB	108.34
	31N	31C	32O	132.40
20	32C	31C	30O	93.190
	32C	31C	30C	102.41
	32C	31C	32CB	41.910
	32C	31C	32O	14.090
	30O	31C	30C	22.760
25	30O	31C	32CB	114.13
	30O	31C	32O	98.730
	30C	31C	32CB	107.45
	30C	31C	32O	112.07
	32CB	31C	32O	50.690
30	31C	31O	32N	29.650
	31C	31O	31CA	33.620
	31C	31O	32CA	61.210
	31C	31O	32C	80.950
	31C	31O	32O	100.23
35	31C	31O	30O	64.260
	31C	31O	31N	30.520
	31C	31O	30C	46.190
	32N	31O	31CA	63.270
	32N	31O	32CA	31.570
40	32N	31O	32C	55.260
	32N	31O	32O	72.760
	32N	31O	30O	80.920
	32N	31O	31N	57.120

	32N	31O	30C	66.230
	31CA	31O	32CA	94.830
	31CA	31O	32C	111.03
	31CA	31O	32O	131.02
5	31CA	31O	30O	53.230
	31CA	31O	31N	19.200
	31CA	31O	30C	37.620
	32CA	31O	32C	31.410
	32CA	31O	32O	43.840
10	32CA	31O	30O	99.290
	32CA	31O	31N	86.720
	32CA	31O	30C	90.250
	32C	31O	32O	19.990
	32C	31O	30O	87.840
15	32C	31O	31N	95.500
	32C	31O	30C	88.220
	32O	31O	30O	100.93
	32O	31O	31N	115.06
	32O	31O	30C	105.40
20	30O	31O	31N	38.090
	30O	31O	30C	18.410
	31N	31O	30C	20.270
	31C	32N	32CA	121.54
	31C	32N	31O	27.200
25	31C	32N	31CA	33.670
	31C	32N	32C	98.180
	31C	32N	32CB	156.92
	31C	32N	31N	57.520
	31C	32N	32CG	153.52
30	31C	32N	29O	104.71
	31C	32N	32O	94.600
	31C	32N	30C	59.080
	31C	32N	30O	49.600
	32CA	32N	31O	94.370
35	32CA	32N	31CA	155.18
	32CA	32N	32C	36.320
	32CA	32N	32CB	35.500
	32CA	32N	31N	157.09
	32CA	32N	32CG	48.480
40	32CA	32N	29O	102.03
	32CA	32N	32O	32.040
	32CA	32N	30C	136.41
	32CA	32N	30O	122.95

	310	32N	31CA	60.870
	310	32N	32C	75.320
	310	32N	32CB	129.85
	310	32N	31N	82.780
5	310	32N	32CG	133.06
	310	32N	290	115.44
	310	32N	320	69.350
	310	32N	30C	78.640
	310	32N	300	63.290
10	31CA	32N	32C	125.80
	31CA	32N	32CB	168.95
	31CA	32N	31N	29.530
	31CA	32N	32CG	151.44
	31CA	32N	290	88.480
15	31CA	32N	320	125.80
	31CA	32N	30C	42.620
	31CA	32N	300	46.720
	32C	32N	32CB	61.170
	32C	32N	31N	122.11
20	32C	32N	32CG	82.280
	32C	32N	290	82.700
	32C	32N	320	11.910
	32C	32N	30C	101.56
	32C	32N	300	86.660
25	32CB	32N	31N	140.79
	32CB	32N	32CG	25.840
	32CB	32N	290	83.900
	32CB	32N	320	63.040
	32CB	32N	30C	131.25
30	32CB	32N	300	131.78
	31N	32N	32CG	143.06
	31N	32N	290	59.840
	31N	32N	320	129.20
	31N	32N	30C	20.780
35	31N	32N	300	36.300
	32CG	32N	290	101.62
	32CG	32N	320	80.410
	32CG	32N	30C	147.03
	32CG	32N	300	155.75
40	290	32N	320	94.600
	290	32N	30C	47.590
	290	32N	300	55.390
	320	32N	30C	109.54

	32O	32N	300	92.920
	30C	32N	300	18.840
	32N	32CA	32C	109.35
	32N	32CA	32CB	111.02
5	32N	32CA	32O	129.14
	32N	32CA	31C	27.780
	32N	32CA	32CG	106.55
	32N	32CA	31O	54.050
	32N	32CA	31CA	15.570
10	32N	32CA	32CD	105.36
	32C	32CA	32CB	109.02
	32C	32CA	32O	26.200
	32C	32CA	31C	92.860
	32C	32CA	32CG	136.13
15	32C	32CA	31O	77.720
	32C	32CA	31CA	99.800
	32C	32CA	32CD	127.84
	32CB	32CA	32O	109.26
	32CB	32CA	31C	138.74
20	32CB	32CA	32CG	32.450
	32CB	32CA	31O	164.98
	32CB	32CA	31CA	126.49
	32CB	32CA	32CD	19.890
	32O	32CA	31C	105.54
25	32O	32CA	32CG	124.05
	32O	32CA	31O	82.830
	32O	32CA	31CA	115.83
	32O	32CA	32CD	122.48
	31C	32CA	32CG	129.49
30	31C	32CA	31O	26.280
	31C	32CA	31CA	12.250
	31C	32CA	32CD	131.65
	32CG	32CA	31O	145.52
	32CG	32CA	31CA	120.06
35	32CG	32CA	32CD	13.440
	31O	32CA	31CA	38.530
	31O	32CA	32CD	153.77
	31CA	32CA	32CD	120.38
	32CG	32CB	32CA	115.02
40	32CG	32CB	32N	109.57
	32CG	32CB	32C	143.75
	32CG	32CB	32CD	34.150
	32CG	32CB	32NE	54.870



	32CG	32CB	32O	130.87
	32CG	32CB	31C	112.55
	32CA	32CB	32N	33.480
	32CA	32CB	32C	35.450
5	32CA	32CB	32CD	148.24
	32CA	32CB	32NE	161.45
	32CA	32CB	32O	44.220
	32CA	32CB	31C	25.510
	32N	32CB	32C	58.870
10	32N	32CB	32CD	130.02
	32N	32CB	32NE	157.91
	32N	32CB	32O	74.310
	32N	32CB	31C	8.050
	32C	32CB	32CD	169.75
15	32C	32CB	32NE	143.17
	32C	32CB	32O	19.650
	32C	32CB	31C	51.900
	32CD	32CB	32NE	28.390
	32CD	32CB	32O	150.28
20	32CD	32CB	31C	136.44
	32NE	32CB	32O	127.38
	32NE	32CB	31C	164.81
	32O	32CB	31C	66.560
	32CB	32CG	32CD	111.80
25	32CB	32CG	32NE	95.320
	32CB	32CG	32CA	32.520
	32CB	32CG	32N	44.590
	32CB	32CG	32CZ	94.360
	32CB	32CG	32C	22.610
30	32CD	32CG	32NE	32.100
	32CD	32CG	32CA	143.52
	32CD	32CG	32N	135.66
	32CD	32CG	32CZ	25.790
	32CD	32CG	32C	133.10
35	32NE	32CG	32CA	125.96
	32NE	32CG	32N	137.03
	32NE	32CG	32CZ	8.900
	32NE	32CG	32C	110.60
	32CA	32CG	32N	24.970
40	32CA	32CG	32CZ	126.39
	32CA	32CG	32C	16.050
	32N	32CG	32CZ	132.81
	32N	32CG	32C	39.010

	32CZ	32CG	32C	112.09
	32NE	32CD	32CG	114.11
	32NE	32CD	32CZ	26.540
	32NE	32CD	32CB	96.240
5	32NE	32CD	32NH1	54.560
	32NE	32CD	32NH2	16.130
	32NE	32CD	32CA	105.65
	32CG	32CD	32CZ	138.57
	32CG	32CD	32CB	34.050
10	32CG	32CD	32NH1	159.55
	32CG	32CD	32NH2	129.25
	32CG	32CD	32CA	23.040
	32CZ	32CD	32CB	112.59
	32CZ	32CD	32NH1	28.030
15	32CZ	32CD	32NH2	10.410
	32CZ	32CD	32CA	123.99
	32CB	32CD	32NH1	125.78
	32CB	32CD	32NH2	106.62
	32CB	32CD	32CA	11.860
20	32NH1	32CD	32NH2	38.430
	32NH1	32CD	32CA	137.27
	32NH2	32CD	32CA	117.35
	32CZ	32NE	32CD	124.08
	32CZ	32NE	32NH1	29.780
25	32CZ	32NE	32NH2	29.640
	32CZ	32NE	32CG	154.12
	32CZ	32NE	32CB	139.34
	32CD	32NE	32NH1	94.300
	32CD	32NE	32NH2	153.72
30	32CD	32NE	32CG	33.790
	32CD	32NE	32CB	55.370
	32NH1	32NE	32NH2	59.420
	32NH1	32NE	32CG	125.76
	32NH1	32NE	32CB	124.83
35	32NH2	32NE	32CG	168.08
	32NH2	32NE	32CB	138.50
	32CG	32NE	32CB	29.800
	32NH2	32CZ	32NH1	119.18
	32NH2	32CZ	32NE	120.54
40	32NH2	32CZ	32CD	149.91
	32NH2	32CZ	32CG	135.63
	32NH1	32CZ	32NE	120.28
	32NH1	32CZ	32CD	90.900

	32NH1	32CZ	32CG	104.70
	32NE	32CZ	32CD	29.380
	32NE	32CZ	32CG	16.970
	32CD	32CZ	32CG	15.640
5	32CZ	32NH1	32NH2	30.400
	32CZ	32NH1	32NE	29.940
	32CZ	32NH1	32CD	61.070
	32NH2	32NH1	32NE	60.340
10	32NH2	32NH1	32CD	91.470
	32NE	32NH1	32CD	31.130
	32CZ	32NH2	32NH1	30.420
	32CZ	32NH2	32NE	29.820
	32CZ	32NH2	32CD	19.680
	32NH1	32NH2	32NE	60.240
15	32NH1	32NH2	32CD	50.090
	32NE	32NH2	32CD	10.140
	32O	32C	32CA	120.36
	32O	32C	32N	143.86
	32O	32C	32CB	117.16
20	32O	32C	31O	106.87
	32O	32C	31C	130.20
	32O	32C	32CG	109.42
	32O	32C	29O	156.25
	32CA	32C	32N	34.330
25	32CA	32C	32CB	35.530
	32CA	32C	31O	70.870
	32CA	32C	31C	55.810
	32CA	32C	32CG	27.830
	32CA	32C	29O	80.940
30	32N	32C	32CB	59.960
	32N	32C	31O	49.410
	32N	32C	31C	26.640
	32N	32C	32CG	58.700
	32N	32C	29O	59.800
35	32CB	32C	31O	105.44
	32CB	32C	31C	86.190
	32CB	32C	32CG	13.640
	32CB	32C	29O	73.110
	31O	32C	31C	24.410
40	31O	32C	32CG	98.470
	31O	32C	29O	89.350
	31C	32C	32CG	82.980
	31C	32C	29O	69.110

	32CG	32C	290	84.420
	32C	320	32CA	33.440
	32C	320	32CB	43.190
	32C	320	310	53.140
5	32C	320	32N	24.230
	32C	320	31C	35.710
	32CA	320	32CB	26.510
	32CA	320	310	53.330
	32CA	320	32N	18.820
10	32CA	320	31C	37.570
	32CB	320	310	79.570
	32CB	320	32N	42.650
	32CB	320	31C	62.750
	310	320	32N	37.890
15	310	320	31C	18.340
	32N	320	31C	20.180
	45CA	45N	45C	35.410
	45CA	45N	45CB	35.970
	45CA	45N	45CG	57.760
20	45CA	45N	45O	31.000
	45CA	45N	45ND1	77.420
	45CA	45N	45CD2	60.650
	45C	45N	45CB	62.400
	45C	45N	45CG	90.430
25	45C	45N	45O	11.620
	45C	45N	45ND1	106.60
	45C	45N	45CD2	96.040
	45CB	45N	45CG	30.090
	45CB	45N	45O	63.510
30	45CB	45N	45ND1	44.300
	45CB	45N	45CD2	45.110
	45CG	45N	45O	88.630
	45CG	45N	45ND1	21.500
	45CG	45N	45CD2	20.440
35	45O	45N	45ND1	107.35
	45O	45N	45CD2	90.420
	45ND1	45N	45CD2	34.960
	45N	45CA	45C	110.71
	45N	45CA	45CB	110.04
40	45N	45CA	45O	130.63
	45N	45CA	45CG	92.950
	45N	45CA	45CD2	96.020
	45N	45CA	45ND1	79.230

	45N	45CA	300D1	102.51
	45C	45CA	45CB	112.68
	45C	45CA	45O	26.040
	45C	45CA	45CG	145.56
5	45C	45CA	45CD2	153.21
	45C	45CA	45ND1	144.96
	45C	45CA	300D1	115.68
	45CB	45CA	45O	111.13
	45CB	45CA	45CG	33.260
10	45CB	45CA	45CD2	53.130
	45CB	45CA	45ND1	36.450
	45CB	45CA	300D1	104.60
	45O	45CA	45CG	136.10
	45O	45CA	45CD2	130.56
15	45O	45CA	45ND1	147.24
	45O	45CA	300D1	92.340
	45CG	45CA	45CD2	23.730
	45CG	45CA	45ND1	16.650
	45CG	45CA	300D1	81.150
20	45CD2	45CA	45ND1	36.970
	45CD2	45CA	300D1	57.490
	45ND1	45CA	300D1	93.340
	45CG	45CB	45CA	112.60
	45CG	45CB	45N	94.770
25	45CG	45CB	45ND1	27.280
	45CG	45CB	45C	145.67
	45CG	45CB	45CD2	23.270
	45CG	45CB	45O	142.79
	45CG	45CB	45CE1	13.750
30	45CG	45CB	45NE2	7.790
	45CA	45CB	45N	33.990
	45CA	45CB	45ND1	122.45
	45CA	45CB	45C	33.450
	45CA	45CB	45CD2	98.710
35	45CA	45CB	45O	42.910
	45CA	45CB	45CE1	116.52
	45CA	45CB	45NE2	106.57
	45N	45CB	45ND1	93.090
	45N	45CB	45C	58.720
40	45N	45CB	45CD2	92.950
	45N	45CB	45O	74.290
	45N	45CB	45CE1	92.170
	45N	45CB	45NE2	92.100

	45ND1	45CB	45C	151.55
	45ND1	45CB	45CD2	50.470
	45ND1	45CB	45O	164.62
	45ND1	45CB	45CE1	13.790
5	45ND1	45CB	45NE2	34.610
	45C	45CB	45CD2	127.91
	45C	45CB	45O	19.560
	45C	45CB	45CE1	149.49
	45C	45CB	45NE2	138.98
10	45CD2	45CB	45O	120.15
	45CD2	45CB	45CE1	36.740
	45CD2	45CB	45NE2	15.920
	45O	45CB	45CE1	153.86
	45O	45CB	45NE2	135.00
15	45CE1	45CB	45NE2	20.840
	45CD2	45CG	45ND1	106.01
	45CD2	45CG	45CB	130.89
	45CD2	45CG	45NE2	36.670
	45CD2	45CG	45CE1	71.600
20	45CD2	45CG	45CA	107.89
	45CD2	45CG	45N	109.57
	45CD2	45CG	45C	115.29
	45ND1	45CG	45CB	122.88
	45ND1	45CG	45NE2	69.340
25	45ND1	45CG	45CE1	34.420
	45ND1	45CG	45CA	131.79
	45ND1	45CG	45N	106.27
	45ND1	45CG	45C	132.76
	45CB	45CG	45NE2	166.91
30	45CB	45CG	45CE1	156.97
	45CB	45CG	45CA	34.140
	45CB	45CG	45N	55.140
	45CB	45CG	45C	21.710
	45NE2	45CG	45CE1	34.920
35	45NE2	45CG	45CA	135.17
	45NE2	45CG	45N	119.59
	45NE2	45CG	45C	146.62
	45CE1	45CG	45CA	146.63
	45CE1	45CG	45N	117.91
40	45CE1	45CG	45C	156.80
	45CA	45CG	45N	29.290
	45CA	45CG	45C	12.800
	45N	45CG	45C	39.250

	45CG	45CD2	45NE2	107.24
	45CG	45CD2	45ND1	37.350
	45CG	45CD2	45CE1	72.490
	45CG	45CD2	45CB	25.840
5	45CG	45CD2	45CA	48.370
	45CG	45CD2	30OD1	117.87
	45CG	45CD2	30CB	117.20
	45CG	45CD2	45N	49.990
	45CG	45CD2	30CG	120.03
10	45NE2	45CD2	45ND1	69.890
	45NE2	45CD2	45CE1	34.750
	45NE2	45CD2	45CB	132.90
	45NE2	45CD2	45CA	141.09
	45NE2	45CD2	30OD1	126.04
15	45NE2	45CD2	30CB	94.760
	45NE2	45CD2	45N	118.90
	45NE2	45CD2	30CG	112.54
	45ND1	45CD2	45CE1	35.150
	45ND1	45CD2	45CB	63.110
20	45ND1	45CD2	45CA	81.050
	45ND1	45CD2	30OD1	146.78
	45ND1	45CD2	30CB	120.56
	45ND1	45CD2	45N	71.340
	45ND1	45CD2	30CG	137.77
25	45CE1	45CD2	45CB	98.210
	45CE1	45CD2	45CA	112.51
	45CE1	45CD2	30OD1	150.32
	45CE1	45CD2	30CB	111.11
	45CE1	45CD2	45N	95.890
30	45CE1	45CD2	30CG	133.23
	45CB	45CD2	45CA	28.160
	45CB	45CD2	30OD1	94.020
	45CB	45CD2	30CB	105.83
	45CB	45CD2	45N	41.950
35	45CB	45CD2	30CG	100.29
	45CA	45CD2	30OD1	69.640
	45CA	45CD2	30CB	77.970
	45CA	45CD2	45N	23.330
	45CA	45CD2	30CG	72.900
40	30OD1	45CD2	30CB	39.260
	30OD1	45CD2	45N	75.610
	30OD1	45CD2	30CG	17.090
	30CB	45CD2	45N	67.700

	30CB	45CD2	30CG	22.180
	45N	45CD2	30CG	71.680
	45CE1	45ND1	45CG	109.46
	45CE1	45ND1	45NE2	35.790
5	45CE1	45ND1	45CD2	72.830
	45CE1	45ND1	45CB	139.12
	45CE1	45ND1	45CA	128.17
	45CE1	45ND1	45N	121.97
	45CG	45ND1	45NE2	73.670
10	45CG	45ND1	45CD2	36.640
	45CG	45ND1	45CB	29.840
	45CG	45ND1	45CA	31.560
	45CG	45ND1	45N	52.230
	45NE2	45ND1	45CD2	37.030
15	45NE2	45ND1	45CB	103.39
	45NE2	45ND1	45CA	95.840
	45NE2	45ND1	45N	99.290
	45CD2	45ND1	45CB	66.410
	45CD2	45ND1	45CA	61.990
20	45CD2	45ND1	45N	73.700
	45CB	45ND1	45CA	21.110
	45CB	45ND1	45N	42.610
	45CA	45ND1	45N	23.350
	45NE2	45CE1	45ND1	108.40
25	45NE2	45CE1	45CD2	36.370
	45NE2	45CE1	45CG	72.280
	45NE2	45CE1	45CB	81.380
	45ND1	45CE1	45CD2	72.030
	45ND1	45CE1	45CG	36.120
30	45ND1	45CE1	45CB	27.090
	45CD2	45CE1	45CG	35.910
	45CD2	45CE1	45CB	45.040
	45CG	45CE1	45CB	9.280
	45CE1	45NE2	45CD2	108.88
35	45CE1	45NE2	45ND1	35.810
	45CE1	45NE2	45CG	72.800
	45CE1	45NE2	45CB	77.770
	45CD2	45NE2	45ND1	73.070
	45CD2	45NE2	45CG	36.090
40	45CD2	45NE2	45CB	31.180
	45ND1	45NE2	45CG	36.990
	45ND1	45NE2	45CB	42.000
	45CG	45NE2	45CB	5.290



	450	45C	45CA	120.88
	450	45C	45N	144.55
	450	45C	45CB	116.29
	450	45C	48N	59.440
5	450	45C	45CG	116.81
	45CA	45C	45N	33.880
	45CA	45C	45CB	33.870
	45CA	45C	48N	105.56
	45CA	45C	45CG	21.630
10	45N	45C	45CB	58.880
	45N	45C	48N	97.930
	45N	45C	45CG	50.330
	45CB	45C	48N	135.29
	45CB	45C	45CG	12.620
15	48N	45C	45CG	123.54
	45C	450	45CA	33.070
	45C	450	49N	151.39
	45C	450	48N	100.94
	45C	450	45CB	44.150
20	45C	450	45N	23.830
	45C	450	48CA	117.88
	45C	450	48C	140.93
	45C	450	49CB	145.57
	45C	450	49CA	159.39
25	45CA	450	49N	146.88
	45CA	450	48N	99.460
	45CA	450	45CB	25.960
	45CA	450	45N	18.370
	45CA	450	48CA	104.05
30	45CA	450	48C	127.00
	45CA	450	49CB	171.68
	45CA	450	49CA	163.08
	49N	450	48N	53.030
	49N	450	45CB	157.31
35	49N	450	45N	139.95
	49N	450	48CA	43.090
	49N	450	48C	19.950
	49N	450	49CB	40.320
	49N	450	49CA	18.350
40	48N	450	45CB	124.49
	48N	450	45N	87.380
	48N	450	48CA	24.280
	48N	450	48C	40.620

	48N	45O	49CB	88.850
	48N	45O	49CA	70.540
	45CB	45O	45N	42.200
5	45CB	45O	48CA	123.39
	45CB	45O	48C	141.10
	45CB	45O	49CB	145.86
	45CB	45O	49CA	155.67
	45N	45O	48CA	98.390
	45N	45O	48C	122.61
10	45N	45O	49CB	165.95
	45N	45O	49CA	157.92
	48CA	45O	48C	24.220
	48CA	45O	49CB	83.390
	48CA	45O	49CA	61.180
15	48C	45O	49CB	59.910
	48C	45O	49CA	37.310
	49CB	45O	49CA	22.740
	48CA	48N	48C	36.480
	48CA	48N	49N	63.070
20	48CA	48N	45O	93.220
	48CA	48N	48O	32.330
	48CA	48N	45C	107.30
	48C	48N	49N	29.480
	48C	48N	45O	81.700
25	48C	48N	48O	12.410
	48C	48N	45C	101.11
	49N	48N	45O	60.320
	49N	48N	48O	40.670
	49N	48N	45C	79.480
30	45O	48N	48O	93.900
	45O	48N	45C	19.610
	48O	48N	45C	113.14
	48N	48CA	48C	108.79
	48N	48CA	48O	128.65
35	48N	48CA	49N	84.880
	48N	48CA	45O	62.500
	48N	48CA	49CA	92.330
	48C	48CA	48O	26.840
	48C	48CA	49N	29.300
40	48C	48CA	45O	83.150
	48C	48CA	49CA	19.890
	48O	48CA	49N	56.140
	48O	48CA	45O	108.36

	48O	48CA	49CA	46.710
	49N	48CA	45O	56.090
	49N	48CA	49CA	9.430
	45O	48CA	49CA	64.890
5	48O	48C	49N	123.25
	48O	48C	48CA	119.60
	48O	48C	48N	142.82
	48O	48C	49CA	92.400
	48O	48C	49C	77.160
10	48O	48C	45O	158.07
	48O	48C	49CB	107.61
	48O	48C	49O	62.950
	49N	48C	48CA	117.14
	49N	48C	48N	88.270
15	49N	48C	49CA	30.850
	49N	48C	49C	52.700
	49N	48C	45O	48.910
	49N	48C	49CB	15.740
	49N	48C	49O	64.070
20	48CA	48C	48N	34.730
	48CA	48C	49CA	147.97
	48CA	48C	49C	149.29
	48CA	48C	45O	72.630
	48CA	48C	49CB	132.78
25	48CA	48C	49O	158.92
	48N	48C	49CA	116.79
	48N	48C	49C	116.29
	48N	48C	45O	57.670
	48N	48C	49CB	103.52
30	48N	48C	49O	129.63
	49CA	48C	49C	30.400
	49CA	48C	45O	77.590
	49CA	48C	49CB	15.360
	49CA	48C	49O	36.590
35	49C	48C	45O	101.29
	49C	48C	49CB	41.610
	49C	48C	49O	14.690
	45O	48C	49CB	62.570
	45O	48C	49O	112.91
40	49CB	48C	49O	50.700
	48C	48O	49N	29.620
	48C	48O	48CA	33.560
	48C	48O	49CA	61.300

	48C	48O	52N	152.10
	48C	48O	49C	79.110
	48C	48O	48N	24.770
	48C	48O	49O	98.710
5	48C	48O	52CB	144.86
	48C	48O	52CA	158.77
	49N	48O	48CA	63.180
	49N	48O	49CA	31.680
	49N	48O	52N	131.03
10	49N	48O	49C	53.300
	49N	48O	48N	51.490
	49N	48O	49O	71.410
	49N	48O	52CB	117.10
	49N	48O	52CA	129.65
15	48CA	48O	49CA	94.860
	48CA	48O	52N	149.04
	48CA	48O	49C	108.83
	48CA	48O	48N	19.010
	48CA	48O	49O	128.77
20	48CA	48O	52CB	165.82
	48CA	48O	52CA	165.56
	49CA	48O	52N	102.95
	49CA	48O	49C	30.500
	49CA	48O	48N	81.880
25	49CA	48O	49O	43.260
	49CA	48O	52CB	86.590
	49CA	48O	52CA	98.140
	52N	48O	49C	77.730
	52N	48O	48N	140.98
30	52N	48O	49O	60.200
	52N	48O	52CB	42.620
	52N	48O	52CA	19.450
	49C	48O	48N	90.800
	49C	48O	49O	20.000
35	49C	48O	52CB	79.260
	49C	48O	52CA	80.050
	48N	48O	49O	110.46
	48N	48O	52CB	168.46
	48N	48O	52CA	159.96
40	49O	48O	52CB	60.150
	49O	48O	52CA	60.240
	52CB	48O	52CA	23.440
	48C	49N	49CA	121.24

	48C	49N	48O	27.130
	48C	49N	48CA	33.560
	48C	49N	49C	101.49
	48C	49N	49CB	155.88
5	48C	49N	48N	62.250
	48C	49N	45O	111.14
	48C	49N	49CG	146.47
	48C	49N	49O	95.860
	49CA	49N	48O	94.120
10	49CA	49N	48CA	154.78
	49CA	49N	49C	36.270
	49CA	49N	49CB	34.930
	49CA	49N	48N	160.92
	49CA	49N	45O	122.27
15	49CA	49N	49CG	45.130
	49CA	49N	49O	32.710
	48O	49N	48CA	60.680
	48O	49N	49C	78.740
	48O	49N	49CB	128.86
20	48O	49N	48N	87.840
	48O	49N	45O	134.73
	48O	49N	49CG	126.47
	48O	49N	49O	70.850
	48CA	49N	49C	127.76
25	48CA	49N	49CB	170.15
	48CA	49N	48N	32.050
	48CA	49N	45O	80.820
	48CA	49N	49CG	151.39
	48CA	49N	49O	126.10
30	49C	49N	49CB	60.860
	49C	49N	48N	126.57
	49C	49N	45O	146.51
	49C	49N	49CG	79.150
	49C	49N	49O	12.200
35	49CB	49N	48N	140.85
	49CB	49N	45O	89.520
	49CB	49N	49CG	23.940
	49CB	49N	49O	63.430
	48N	49N	45O	66.650
40	48N	49N	49CG	142.91
	48N	49N	49O	133.25
	45O	49N	49CG	77.820
	45O	49N	49O	152.81

	49CG	49N	49O	77.780
	49N	49CA	49C	109.24
	49N	49CA	49CB	111.98
	49N	49CA	49O	128.08
5	49N	49CA	48C	27.910
	49N	49CA	49CG	111.32
	49N	49CA	48O	54.200
	49N	49CA	48CA	15.790
	49N	49CA	45O	39.390
10	49C	49CA	49CB	109.06
	49C	49CA	49O	26.050
	49C	49CA	48C	95.730
	49C	49CA	49CG	132.71
	49C	49CA	48O	82.190
15	49C	49CA	48CA	101.41
	49C	49CA	45O	137.56
	49CB	49CA	49O	109.97
	49CB	49CA	48C	139.72
	49CB	49CA	49CG	31.740
20	49CB	49CA	48O	165.37
	49CB	49CA	48CA	127.74
	49CB	49CA	45O	75.350
	49O	49CA	48C	106.16
	49O	49CA	49CG	120.47
25	49O	49CA	48O	84.290
	49O	49CA	48CA	115.68
	49O	49CA	45O	163.33
	48C	49CA	49CG	131.14
	48C	49CA	48O	26.290
30	48C	49CA	48CA	12.140
	48C	49CA	45O	65.100
	49CG	49CA	48O	142.54
	49CG	49CA	48CA	123.44
	49CG	49CA	45O	72.630
35	48O	49CA	48CA	38.430
	48O	49CA	45O	90.040
	48CA	49CA	45O	53.930
	49CG	49CB	49CA	116.24
	49CG	49CB	49N	114.58
40	49CG	49CB	49C	141.15
	49CG	49CB	49SD	36.600
	49CG	49CB	49O	126.24
	49CG	49CB	49CE	53.680

	49CG	49CB	48C	114.27
	49CG	49CB	450	85.220
	49CA	49CB	49N	33.090
	49CA	49CB	49C	35.390
5	49CA	49CB	49SD	148.81
	49CA	49CB	490	43.790
	49CA	49CB	49CE	162.24
	49CA	49CB	48C	24.910
	49CA	49CB	450	81.910
10	49N	49CB	49C	58.660
	49N	49CB	49SD	148.76
	49N	49CB	490	73.620
	49N	49CB	49CE	132.71
	49N	49CB	48C	8.380
15	49N	49CB	450	50.170
	49C	49CB	49SD	147.78
	49C	49CB	490	19.360
	49C	49CB	49CE	161.28
	49C	49CB	48C	53.120
20	49C	49CB	450	107.23
	49SD	49CB	490	129.07
	49SD	49CB	49CE	31.240
	49SD	49CB	48C	150.42
	49SD	49CB	450	104.41
25	490	49CB	49CE	153.30
	490	49CB	48C	66.660
	490	49CB	450	123.72
	49CE	49CB	48C	139.97
	49CE	49CB	450	82.570
30	48C	49CB	450	57.520
	49CB	49CG	49SD	113.95
	49CB	49CG	49CA	32.020
	49CB	49CG	49CE	99.440
	49CB	49CG	49N	41.480
35	49CB	49CG	49C	24.300
	49SD	49CG	49CA	142.90
	49SD	49CG	49CE	38.850
	49SD	49CG	49N	152.35
	49SD	49CG	49C	126.30
40	49CA	49CG	49CE	129.70
	49CA	49CG	49N	23.540
	49CA	49CG	49C	17.180
	49CE	49CG	49N	120.53

	49CE	49CG	49C	122.67
	49N	49CG	49C	39.050
	49CE	49SD	49CG	98.910
	49CE	49SD	49CB	90.350
5	49CG	49SD	49CB	29.450
	49SD	49CE	49CG	42.240
	49SD	49CE	49CB	58.410
	49CG	49CE	49CB	26.880
	49O	49C	49CA	120.82
10	49O	49C	49N	142.98
	49O	49C	49CB	118.34
	49O	49C	48O	103.81
	49O	49C	48C	126.98
	49O	49C	52N	58.820
15	49O	49C	49CG	107.87
	49CA	49C	49N	34.490
	49CA	49C	49CB	35.550
	49CA	49C	48O	67.310
	49CA	49C	48C	53.870
20	49CA	49C	52N	110.05
	49CA	49C	49CG	30.110
	49N	49C	49CB	60.480
	49N	49C	48O	47.960
	49N	49C	48C	25.810
25	49N	49C	52N	98.720
	49N	49C	49CG	61.800
	49CB	49C	48O	102.42
	49CB	49C	48C	85.270
	49CB	49C	52N	142.85
30	49CB	49C	49CG	14.550
	48O	49C	48C	23.740
	48O	49C	52N	50.760
	48O	49C	49CG	96.450
	48C	49C	52N	73.810
35	48C	49C	49CG	83.800
	52N	49C	49CG	129.66
	49C	49O	49CA	33.120
	49C	49O	49CB	42.300
	49C	49O	52N	102.39
40	49C	49O	48O	56.180
	49C	49O	49N	24.820
	49C	49O	52CB	115.92
	49C	49O	52CA	120.50



	49C	490	52C	141.89
	49C	490	48C	38.330
	49CA	490	49CB	26.240
	49CA	490	52N	103.66
5	49CA	490	48O	52.450
	49CA	490	49N	19.220
	49CA	490	52CB	94.190
	49CA	490	52CA	110.37
	49CA	490	52C	132.79
10	49CA	490	48C	37.250
	49CB	490	52N	129.79
	49CB	490	48O	78.650
	49CB	490	49N	42.950
	49CB	490	52CB	111.70
15	49CB	490	52CA	132.78
	49CB	490	52C	150.79
	49CB	490	48C	62.640
	52N	490	48O	51.750
	52N	490	49N	89.230
20	52N	490	52CB	42.290
	52N	490	52CA	23.070
	52N	490	52C	39.550
	52N	490	48C	69.220
	48O	490	49N	37.740
25	48O	490	52CB	62.180
	48O	490	52CA	64.870
	48O	490	52C	87.820
	48O	490	48C	18.340
	49N	490	52CB	92.020
30	49N	490	52CA	101.56
	49N	490	52C	124.93
	49N	490	48C	20.070
	52CB	490	52CA	24.340
	52CB	490	52C	39.750
35	52CB	490	48C	78.350
	52CA	490	52C	23.400
	52CA	490	48C	83.190
	52C	490	48C	106.15
	52CA	52N	52C	36.160
40	52CA	52N	52CB	35.020
	52CA	52N	48O	118.11
	52CA	52N	49O	95.590
	52CA	52N	52O	34.260

	52CA	52N	49C	110.60
	52CA	52N	52CG	22.800
	52C	52N	52CB	61.280
	52C	52N	480	138.59
5	52C	52N	490	81.420
	52C	52N	520	13.660
	52C	52N	49C	100.20
	52C	52N	52CG	52.160
	52CB	52N	480	83.850
10	52CB	52N	490	75.680
	52CB	52N	520	65.820
	52CB	52N	49C	84.150
	52CB	52N	52CG	12.280
	480	52N	490	68.050
15	480	52N	520	148.48
	480	52N	49C	51.510
	480	52N	52CG	95.630
	490	52N	520	95.050
	490	52N	49C	18.790
20	490	52N	52CG	83.320
	520	52N	49C	113.83
	520	52N	52CG	54.830
	49C	52N	52CG	94.170
	52N	52CA	52C	109.25
25	52N	52CA	52CB	112.09
	52N	52CA	520	125.56
	52N	52CA	52CG	144.63
	52N	52CA	52CD1	150.46
	52N	52CA	490	61.340
30	52N	52CA	480	42.440
	52N	52CA	52CD2	131.15
	52C	52CA	52CB	110.05
	52C	52CA	520	26.420
	52C	52CA	52CG	92.510
35	52C	52CA	52CD1	100.27
	52C	52CA	490	80.610
	52C	52CA	480	134.08
	52C	52CA	52CD2	101.02
	52CB	52CA	520	113.90
40	52CB	52CA	52CG	32.610
	52CB	52CA	52CD1	56.390
	52CB	52CA	490	73.420
	52CB	52CA	480	70.630

	52CB	52CA	52CD2	19.210
	52O	52CA	52CG	85.830
	52O	52CA	52CD1	81.620
	52O	52CA	49O	106.77
5	52O	52CA	48O	160.23
	52O	52CA	52CD2	98.070
	52CG	52CA	52CD1	30.440
	52CG	52CA	49O	96.880
	52CG	52CA	48O	102.57
10	52CG	52CA	52CD2	13.480
	52CD1	52CA	49O	127.05
	52CD1	52CA	48O	114.61
	52CD1	52CA	52CD2	39.470
	49O	52CA	48O	54.890
15	49O	52CA	52CD2	87.930
	48O	52CA	52CD2	89.170
	52CA	52CB	52CG	114.81
	52CA	52CB	52N	32.900
	52CA	52CB	52C	34.650
20	52CA	52CB	52CD1	92.870
	52CA	52CB	52CD2	149.21
	52CA	52CB	52O	40.980
	52CA	52CB	49O	82.240
	52CA	52CB	48O	85.930
25	52CG	52CB	52N	147.64
	52CG	52CB	52C	95.470
	52CG	52CB	52CD1	34.840
	52CG	52CB	52CD2	34.490
	52CG	52CB	52O	79.430
30	52CG	52CB	49O	133.14
	52CG	52CB	48O	156.22
	52N	52CB	52C	58.130
	52N	52CB	52CD1	120.49
	52N	52CB	52CD2	176.02
35	52N	52CB	52O	71.010
	52N	52CB	49O	62.030
	52N	52CB	48O	53.530
	52C	52CB	52CD1	91.890
	52C	52CB	52CD2	125.58
40	52C	52CB	52O	18.270
	52C	52CB	49O	74.080
	52C	52CB	48O	108.30
	52CD1	52CB	52CD2	59.460

	52CD1	52CB	52O	73.720
	52CD1	52CB	490	161.73
	52CD1	52CB	480	139.85
	52CD2	52CB	52O	112.23
5	52CD2	52CB	490	119.44
	52CD2	52CB	480	123.55
	52O	52CB	490	91.500
	52O	52CB	480	123.93
	490	52CB	480	57.670
10	52CD1	52CG	52CD2	109.75
	52CD1	52CG	52CB	109.89
	52CD1	52CG	52CA	89.960
	52CD1	52CG	52C	97.850
	52CD1	52CG	52O	83.370
15	52CD1	52CG	52N	97.080
	52CD2	52CG	52CB	110.66
	52CD2	52CG	52CA	143.17
	52CD2	52CG	52C	152.23
	52CD2	52CG	52O	162.30
20	52CD2	52CG	52N	130.60
	52CB	52CG	52CA	32.590
	52CB	52CG	52C	54.470
	52CB	52CG	52O	74.040
	52CB	52CG	52N	20.080
25	52CA	52CG	52C	29.630
	52CA	52CG	52O	44.400
	52CA	52CG	52N	12.570
	52C	52CG	52O	21.080
	52C	52CG	52N	38.700
30	52O	52CG	52N	55.970
	52CG	52CD1	52CD2	35.160
	52CG	52CD1	52CB	35.270
	52CG	52CD1	52CA	59.600
	52CG	52CD1	52O	71.410
35	52CG	52CD1	52C	57.360
	52CD2	52CD1	52CB	60.550
	52CD2	52CD1	52CA	90.490
	52CD2	52CD1	52O	105.83
	52CD2	52CD1	52C	92.480
40	52CB	52CD1	52CA	30.740
	52CB	52CD1	52O	63.610
	52CB	52CD1	52C	43.990
	52CA	52CD1	52O	41.470

	52CA	52CD1	52C	24.450
	52O	52CD1	52C	19.680
	52CG	52CD2	52CD1	35.090
	52CG	52CD2	52CB	34.850
5	52CG	52CD2	52CA	23.350
	52CD1	52CD2	52CB	59.990
	52CD1	52CD2	52CA	50.040
	52CB	52CD2	52CA	11.580
	52O	52C	52CA	120.16
10	52O	52C	52N	138.43
	52O	52C	52CB	121.83
	52O	52C	52CG	94.760
	52O	52C	52CD1	77.910
	52O	52C	49O	162.23
15	52CA	52C	52N	34.590
	52CA	52C	52CB	35.300
	52CA	52C	52CG	57.870
	52CA	52C	52CD1	55.280
	52CA	52C	49O	75.990
20	52N	52C	52CB	60.600
	52N	52C	52CG	89.150
	52N	52C	52CD1	89.870
	52N	52C	49O	59.020
	52CB	52C	52CG	30.060
25	52CB	52C	52CD1	44.120
	52CB	52C	49O	66.170
	52CG	52C	52CD1	24.790
	52CG	52C	49O	88.000
	52CD1	52C	49O	109.46
30	52C	52O	52CA	33.420
	52C	52O	52CB	39.900
	52C	52O	52CG	64.160
	52C	52O	52N	27.900
	52C	52O	52CD1	82.410
35	52CA	52O	52CB	25.130
	52CA	52O	52CG	49.770
	52CA	52O	52N	20.180
	52CA	52O	52CD1	56.910
	52CB	52O	52CG	26.530
40	52CB	52O	52N	43.170
	52CB	52O	52CD1	42.670
	52CG	52O	52N	69.200
	52CG	52O	52CD1	25.220

	52N	52O	52CD1	76.680
	70CA	70N	70CB	37.460
	70CA	70N	70C	35.750
	70CA	70N	70O	55.180
5	70CA	70N	71N	35.970
	70CA	70N	70CG	27.370
	70CB	70N	70C	62.020
	70CB	70N	70O	67.000
	70CB	70N	71N	70.330
10	70CB	70N	70CG	10.490
	70C	70N	70O	24.900
	70C	70N	71N	17.080
	70C	70N	70CG	55.470
	70O	70N	71N	40.450
15	70O	70N	70CG	64.880
	71N	70N	70CG	61.620
	70N	70CA	70CB	106.91
	70N	70CA	70C	110.27
	70N	70CA	70O	94.920
20	70N	70CA	71N	123.39
	70N	70CA	70CG	137.63
	70N	70CA	70CD1	150.73
	70N	70CA	70CD2	130.99
	70N	70CA	71CA	120.25
25	70CB	70CA	70C	109.97
	70CB	70CA	70O	95.430
	70CB	70CA	71N	121.60
	70CB	70CA	70CG	31.050
	70CB	70CA	70CD1	54.880
30	70CB	70CA	70CD2	25.460
	70CB	70CA	71CA	118.53
	70C	70CA	70O	26.590
	70C	70CA	71N	29.160
	70C	70CA	70CG	96.100
35	70C	70CA	70CD1	98.220
	70C	70CA	70CD2	90.820
	70C	70CA	71CA	20.220
	70O	70CA	71N	55.750
	70O	70CA	70CG	94.790
40	70O	70CA	70CD1	108.55
	70O	70CA	70CD2	84.990
	70O	70CA	71CA	46.810
	71N	70CA	70CG	95.770

	71N	70CA	70CD1	85.040
	71N	70CA	70CD2	96.710
	71N	70CA	71CA	8.940
	70CG	70CA	70CD1	26.790
5	70CG	70CA	70CD2	12.590
	70CG	70CA	71CA	95.830
	70CD1	70CA	70CD2	38.940
	70CD1	70CA	71CA	88.910
	70CD2	70CA	71CA	94.810
10	70CG	70CB	70CA	117.56
	70CG	70CB	70N	152.70
	70CG	70CB	70C	100.55
	70CG	70CB	70CD2	28.640
	70CG	70CB	70CD1	28.170
15	70CG	70CB	70O	106.07
	70CG	70CB	71N	87.340
	70CG	70CB	70CE2	19.310
	70CG	70CB	70CE1	18.640
	70CA	70CB	70N	35.640
20	70CA	70CB	70C	35.040
	70CA	70CB	70CD2	139.47
	70CA	70CB	70CD1	95.650
	70CA	70CB	70O	53.800
	70CA	70CB	71N	36.510
25	70CA	70CB	70CE2	134.74
	70CA	70CB	70CE1	105.29
	70N	70CB	70C	60.030
	70N	70CB	70CD2	168.48
	70N	70CB	70CD1	127.04
30	70N	70CB	70O	64.910
	70N	70CB	71N	69.250
	70N	70CB	70CE2	170.05
	70N	70CB	70CE1	137.27
	70C	70CB	70CD2	110.54
35	70C	70CB	70CD1	92.340
	70C	70CB	70O	24.450
	70C	70CB	71N	17.380
	70C	70CB	70CE2	110.50
	70C	70CB	70CE1	98.260
40	70CD2	70CB	70CD1	56.640
	70CD2	70CB	70O	103.72
	70CD2	70CB	71N	103.59
	70CD2	70CB	70CE2	10.040

	70CD2	70CB	70CE1	46.680
	70CD1	70CB	700	108.56
	70CD1	70CB	71N	75.480
	70CD1	70CB	70CE2	46.880
5	70CD1	70CB	70CE1	10.230
	700	70CB	71N	40.070
	700	70CB	70CE2	107.98
	700	70CB	70CE1	111.25
	71N	70CB	70CE2	100.81
10	71N	70CB	70CE1	82.170
	70CE2	70CB	70CE1	36.820
	70CD1	70CG	70CD2	118.06
	70CD1	70CG	70CB	121.18
	70CD1	70CG	70CE2	88.760
15	70CD1	70CG	70CE1	29.500
	70CD1	70CG	70CA	96.460
	70CD1	70CG	70CZ	59.020
	70CD1	70CG	70C	98.630
	70CD1	70CG	700	115.86
20	70CD1	70CG	71N	80.340
	70CD1	70CG	70N	106.78
	70CD2	70CG	70CB	120.20
	70CD2	70CG	70CE2	29.310
	70CD2	70CG	70CE1	88.570
25	70CD2	70CG	70CA	143.55
	70CD2	70CG	70CZ	59.050
	70CD2	70CG	70C	125.91
	70CD2	70CG	700	108.07
	70CD2	70CG	71N	130.21
30	70CD2	70CG	70N	135.15
	70CB	70CG	70CE2	148.81
	70CB	70CG	70CE1	149.97
	70CB	70CG	70CA	31.380
	70CB	70CG	70CZ	171.65
35	70CB	70CG	70C	51.310
	70CB	70CG	700	50.730
	70CB	70CG	71N	68.810
	70CB	70CG	70N	16.810
	70CE2	70CG	70CE1	59.270
40	70CE2	70CG	70CA	167.45
	70CE2	70CG	70CZ	29.740
	70CE2	70CG	70C	139.06
	70CE2	70CG	700	126.97



	70CE2	70CG	71N	130.33
	70CE2	70CG	70N	164.45
	70CE1	70CG	70CA	125.33
	70CE1	70CG	70CZ	29.530
5	70CE1	70CG	70C	120.26
	70CE1	70CG	70O	132.40
	70CE1	70CG	71N	100.25
	70CE1	70CG	70N	136.28
	70CA	70CG	70CZ	153.44
10	70CA	70CG	70C	28.840
	70CA	70CG	70O	40.600
	70CA	70CG	71N	40.450
	70CA	70CG	70N	15.000
	70CZ	70CG	70C	136.67
15	70CZ	70CG	70O	137.52
	70CZ	70CG	71N	118.53
	70CZ	70CG	70N	165.80
	70C	70CG	70O	18.990
	70C	70CG	71N	20.040
20	70C	70CG	70N	39.910
	70O	70CG	71N	35.520
	70O	70CG	70N	45.860
	71N	70CG	70N	54.640
	70CG	70CD1	70CE1	121.21
25	70CG	70CD1	70CD2	30.980
	70CG	70CD1	70CZ	91.090
	70CG	70CD1	70CB	30.650
	70CG	70CD1	70CE2	60.970
	70CG	70CD1	70CA	56.760
30	70CG	70CD1	70C	58.990
	70CG	70CD1	70OH	101.71
	70CG	70CD1	71N	78.140
	70CE1	70CD1	70CD2	90.240
	70CE1	70CD1	70CZ	30.130
35	70CE1	70CD1	70CB	151.11
	70CE1	70CD1	70CE2	60.240
	70CE1	70CD1	70CA	170.56
	70CE1	70CD1	70C	146.02
	70CE1	70CD1	70OH	19.540
40	70CE1	70CD1	71N	131.69
	70CD2	70CD1	70CZ	60.120
	70CD2	70CD1	70CB	61.440
	70CD2	70CD1	70CE2	30.000

	70CD2	70CD1	70CA	87.180
	70CD2	70CD1	70C	83.720
	70CD2	70CD1	70OH	70.760
	70CD2	70CD1	71N	98.740
5	70CZ	70CD1	70CB	121.24
	70CZ	70CD1	70CE2	30.120
	70CZ	70CD1	70CA	146.25
	70CZ	70CD1	70C	131.84
	70CZ	70CD1	70OH	10.700
10	70CZ	70CD1	71N	131.06
	70CB	70CD1	70CE2	91.290
	70CB	70CD1	70CA	29.480
	70CB	70CD1	70C	43.450
	70CB	70CD1	70OH	131.64
15	70CB	70CD1	71N	63.770
	70CE2	70CD1	70CA	116.79
	70CE2	70CD1	70C	108.68
	70CE2	70CD1	70OH	40.770
	70CE2	70CD1	71N	117.73
20	70CA	70CD1	70C	24.590
	70CA	70CD1	70OH	156.75
	70CA	70CD1	71N	40.160
	70C	70CD1	70OH	139.51
	70C	70CD1	71N	20.610
25	70OH	70CD1	71N	134.22
	70CZ	70CE1	70CD1	119.14
	70CZ	70CE1	70OH	30.030
	70CZ	70CE1	70CE2	29.880
	70CZ	70CE1	70CG	89.850
30	70CZ	70CE1	70CD2	59.730
	70CZ	70CE1	70CB	100.75
	70CD1	70CE1	70OH	149.06
	70CD1	70CE1	70CE2	89.270
	70CD1	70CE1	70CG	29.290
35	70CD1	70CE1	70CD2	59.420
	70CD1	70CE1	70CB	18.660
	70OH	70CE1	70CE2	59.890
	70OH	70CE1	70CG	119.81
	70OH	70CE1	70CD2	89.720
40	70OH	70CE1	70CB	130.48
	70CE2	70CE1	70CG	59.990
	70CE2	70CE1	70CD2	29.850
	70CE2	70CE1	70CB	70.960

	70CG	70CE1	70CD2	30.130
	70CG	70CE1	70CB	11.390
	70CD2	70CE1	70CB	41.200
	70CE2	70CD2	70CG	121.11
5	70CE2	70CD2	70CD1	90.150
	70CE2	70CD2	70CZ	30.070
	70CE2	70CD2	70CB	151.47
	70CE2	70CD2	70CE1	59.810
	70CE2	70CD2	70OH	19.220
10	70CE2	70CD2	70CA	143.09
	70CG	70CD2	70CD1	30.960
	70CG	70CD2	70CZ	91.040
	70CG	70CD2	70CB	31.150
	70CG	70CD2	70CE1	61.300
15	70CG	70CD2	70OH	101.91
	70CG	70CD2	70CA	23.850
	70CD1	70CD2	70CZ	60.090
	70CD1	70CD2	70CB	61.930
	70CD1	70CD2	70CE1	30.340
20	70CD1	70CD2	70OH	70.980
	70CD1	70CD2	70CA	53.880
	70CZ	70CD2	70CB	121.70
	70CZ	70CD2	70CE1	29.750
	70CZ	70CD2	70OH	10.950
25	70CZ	70CD2	70CA	113.46
	70CB	70CD2	70CE1	92.130
	70CB	70CD2	70OH	132.34
	70CB	70CD2	70CA	15.060
	70CE1	70CD2	70OH	40.660
30	70CE1	70CD2	70CA	83.920
	70OH	70CD2	70CA	124.41
	70CD2	70CE2	70CZ	119.98
	70CD2	70CE2	70OH	149.77
	70CD2	70CE2	70CE1	90.330
35	70CD2	70CE2	70CG	29.590
	70CD2	70CE2	70CD1	59.850
	70CD2	70CE2	70CB	18.490
	70CZ	70CE2	70OH	29.900
	70CZ	70CE2	70CE1	29.650
40	70CZ	70CE2	70CG	90.400
	70CZ	70CE2	70CD1	60.140
	70CZ	70CE2	70CB	101.79
	70OH	70CE2	70CE1	59.530

	700H	70CE2	70CG	120.21
	700H	70CE2	70CD1	89.990
	700H	70CE2	70CB	131.38
	70CE1	70CE2	70CG	60.750
5	70CE1	70CE2	70CD1	30.480
	70CE1	70CE2	70CB	72.220
	70CG	70CE2	70CD1	30.260
	70CG	70CE2	70CB	11.880
	70CD1	70CE2	70CB	41.820
10	700H	70CZ	70CE1	119.71
	700H	70CZ	70CE2	119.76
	700H	70CZ	70CD1	150.31
	700H	70CZ	70CD2	149.60
	700H	70CZ	70CG	176.52
15	70CE1	70CZ	70CE2	120.47
	70CE1	70CZ	70CD1	30.730
	70CE1	70CZ	70CD2	90.520
	70CE1	70CZ	70CG	60.620
	70CE2	70CZ	70CD1	89.750
20	70CE2	70CZ	70CD2	29.950
	70CE2	70CZ	70CG	59.860
	70CD1	70CZ	70CD2	59.800
	70CD1	70CZ	70CG	29.890
	70CD2	70CZ	70CG	29.910
25	70CZ	700H	70CE1	30.260
	70CZ	700H	70CE2	30.340
	70CZ	700H	70CD2	19.450
	70CZ	700H	70CD1	18.980
	70CE1	700H	70CE2	60.580
30	70CE1	700H	70CD2	49.620
	70CE1	700H	70CD1	11.390
	70CE2	700H	70CD2	11.010
	70CE2	700H	70CD1	49.240
	70CD2	700H	70CD1	38.260
35	700	70C	71N	123.14
	700	70C	70CA	120.09
	700	70C	71CA	92.570
	700	70C	70N	99.070
	700	70C	70CB	99.330
40	700	70C	71C	78.860
	700	70C	70CG	105.60
	700	70C	72N	56.760
	700	70C	70CD1	125.74

	700	70C	71CB	108.48
	700	70C	71O	90.870
	700	70C	27CE	75.140
	71N	70C	70CA	116.77
5	71N	70C	71CA	30.570
	71N	70C	70N	130.09
	71N	70C	70CB	128.41
	71N	70C	71C	50.660
	71N	70C	70CG	105.64
10	71N	70C	72N	71.070
	71N	70C	70CD1	85.130
	71N	70C	71CB	15.220
	71N	70C	71O	47.160
	71N	70C	27CE	81.520
15	70CA	70C	71CA	147.33
	70CA	70C	70N	33.980
	70CA	70C	70CB	34.980
	70CA	70C	71C	149.00
	70CA	70C	70CG	55.070
20	70CA	70C	72N	156.37
	70CA	70C	70CD1	57.190
	70CA	70C	71CB	131.27
	70CA	70C	71O	132.91
	70CA	70C	27CE	115.72
25	71CA	70C	70N	149.80
	71CA	70C	70CB	147.07
	71CA	70C	71C	29.080
	71CA	70C	70CG	118.97
	71CA	70C	72N	43.930
30	71CA	70C	70CD1	104.65
	71CA	70C	71CB	16.560
	71CA	70C	71O	36.650
	71CA	70C	27CE	70.660
	70N	70C	70CB	57.950
35	70N	70C	71C	177.02
	70N	70C	70CG	84.620
	70N	70C	72N	155.82
	70N	70C	70CD1	90.970
	70N	70C	71CB	137.64
40	70N	70C	71O	166.83
	70N	70C	27CE	85.480
	70CB	70C	71C	124.36
	70CB	70C	70CG	28.140

	70CB	70C	72N	121.93
	70CB	70C	70CD1	44.210
	70CB	70C	71CB	142.05
	70CB	70C	71O	112.09
5	70CB	70C	27CE	142.09
	71C	70C	70CG	97.990
	71C	70C	72N	22.120
	71C	70C	70CD1	91.980
	71C	70C	71CB	42.180
10	71C	70C	71O	16.150
	71C	70C	27CE	91.900
	70CG	70C	72N	101.82
	70CG	70C	70CD1	22.380
	70CG	70C	71CB	116.61
15	70CG	70C	71O	84.400
	70CG	70C	27CE	170.06
	72N	70C	70CD1	103.85
	72N	70C	71CB	59.890
	72N	70C	71O	35.310
20	72N	70C	27CE	86.930
	70CD1	70C	71CB	97.910
	70CD1	70C	71O	76.150
	70CD1	70C	27CE	159.11
	71CB	70C	71O	44.150
25	71CB	70C	27CE	71.800
	71O	70C	27CE	105.54
	70C	70O	71N	29.440
	70C	70O	70CA	33.310
	70C	70O	71CA	61.030
30	70C	70O	70N	56.030
	70C	70O	70CB	56.220
	70C	70O	72N	103.35
	70C	70O	71C	78.330
	70C	70O	27N	162.85
35	70C	70O	70CG	55.410
	70C	70O	27CE	86.530
	70C	70O	27CB	134.75
	70C	70O	27CA	157.10
	71N	70O	70CA	62.750
40	71N	70O	71CA	31.590
	71N	70O	70N	82.720
	71N	70O	70CB	82.340
	71N	70O	72N	77.000

	71N	700	71C	52.450
	71N	700	27N	157.23
	71N	700	70CG	73.420
	71N	700	27CE	76.870
5	71N	700	27CB	118.58
	71N	700	27CA	137.77
	70CA	700	71CA	94.340
	70CA	700	70N	29.900
	70CA	700	70CB	30.770
10	70CA	700	72N	131.80
	70CA	700	71C	108.22
	70CA	700	27N	134.37
	70CA	700	70CG	44.610
	70CA	700	27CE	98.600
15	70CA	700	27CB	137.96
	70CA	700	27CA	147.24
	71CA	700	70N	111.73
	71CA	700	70CB	110.81
	71CA	700	72N	49.690
20	71CA	700	71C	29.600
	71CA	700	27N	128.54
	71CA	700	70CG	95.550
	71CA	700	27CE	70.170
	71CA	700	27CB	95.820
25	71CA	700	27CA	109.66
	70N	700	70CB	48.090
	70N	700	72N	159.36
	70N	700	71C	134.32
	70N	700	27N	108.05
30	70N	700	70CG	69.260
	70N	700	27CE	82.110
	70N	700	27CB	109.82
	70N	700	27CA	117.61
	70CB	700	72N	124.02
35	70CB	700	71C	109.62
	70CB	700	27N	119.93
	70CB	700	70CG	23.200
	70CB	700	27CE	128.06
	70CB	700	27CB	149.98
40	70CB	700	27CA	139.34
	72N	700	71C	25.040
	72N	700	27N	92.310
	72N	700	70CG	100.85

	72N	700	27CE	96.810
	72N	700	27CB	83.640
	72N	700	27CA	80.850
	71C	700	27N	116.95
5	71C	700	70CG	87.670
	71C	700	27CE	94.180
	71C	700	27CB	100.37
	71C	700	27CA	103.44
	27N	700	70CG	128.88
10	27N	700	27CE	84.660
	27N	700	27CB	39.280
	27N	700	27CA	19.550
	70CG	700	27CE	140.73
	70CG	700	27CB	167.97
15	70CG	700	27CA	146.72
	27CE	700	27CB	48.260
	27CE	700	27CA	70.590
	27CB	700	27CA	22.440
	70C	71N	71CA	122.07
20	70C	71N	700	27.430
	70C	71N	70CA	34.070
	70C	71N	71CB	156.58
	70C	71N	71C	105.29
	70C	71N	710	114.85
25	70C	71N	72N	87.060
	70C	71N	70N	32.830
	70C	71N	70CB	34.210
	70C	71N	70CG	54.320
	70C	71N	70CD1	74.260
30	70C	71N	27CE	79.190
	71CA	71N	700	94.650
	71CA	71N	70CA	156.14
	71CA	71N	71CB	35.960
	71CA	71N	71C	34.730
35	71CA	71N	710	47.910
	71CA	71N	72N	41.570
	71CA	71N	70N	144.29
	71CA	71N	70CB	143.42
	71CA	71N	70CG	131.63
40	71CA	71N	70CD1	131.98
	71CA	71N	27CE	76.210
	700	71N	70CA	61.500
	700	71N	71CB	129.74



	700	71N	71C	82.170
	700	71N	71O	97.500
	700	71N	72N	62.170
	700	71N	70N	56.830
5	700	71N	70CB	57.590
	700	71N	70CG	71.060
	700	71N	70CD1	92.580
	700	71N	27CE	69.480
	70CA	71N	71CB	166.85
10	70CA	71N	71C	131.75
	70CA	71N	71O	129.72
	70CA	71N	72N	117.88
	70CA	71N	70N	20.640
	70CA	71N	70CB	21.890
15	70CA	71N	70CG	43.780
	70CA	71N	70CD1	54.810
	70CA	71N	27CE	94.230
	71CB	71N	71C	60.910
	71CB	71N	71O	59.960
20	71CB	71N	72N	75.260
	71CB	71N	70N	153.78
	71CB	71N	70CB	164.62
	71CB	71N	70CG	140.81
	71CB	71N	70CD1	124.74
25	71CB	71N	27CE	85.200
	71C	71N	71O	21.860
	71C	71N	72N	20.690
	71C	71N	70N	138.03
	71C	71N	70CB	111.76
30	71C	71N	70CG	96.900
	71C	71N	70CD1	100.26
	71C	71N	27CE	101.90
	71O	71N	72N	40.850
	71O	71N	70N	145.40
35	71O	71N	70CB	107.84
	71O	71N	70CG	87.250
	71O	71N	70CD1	84.080
	71O	71N	27CE	122.09
	72N	71N	70N	118.89
40	72N	71N	70CB	101.86
	72N	71N	70CG	94.280
	72N	71N	70CD1	104.97
	72N	71N	27CE	89.110

	70N	71N	70CB	40.420
	70N	71N	70CG	63.740
	70N	71N	70CD1	75.300
	70N	71N	27CE	73.750
5	70CB	71N	70CG	23.840
	70CB	71N	70CD1	40.740
	70CB	71N	27CE	109.99
	70CG	71N	70CD1	21.520
	70CG	71N	27CE	133.04
10	70CD1	71N	27CE	149.03
	71N	71CA	71CB	109.56
	71N	71CA	71C	112.75
	71N	71CA	71O	105.38
	71N	71CA	70C	27.360
15	71N	71CA	72N	115.21
	71N	71CA	70O	53.760
	71N	71CA	70CA	14.920
	71N	71CA	72CA	115.46
	71N	71CA	27CE	82.300
20	71CB	71CA	71C	109.60
	71CB	71CA	71O	89.910
	71CB	71CA	70C	136.21
	71CB	71CA	72N	128.74
	71CB	71CA	70O	160.54
25	71CB	71CA	70CA	124.20
	71CB	71CA	72CA	123.62
	71CB	71CA	27CE	102.93
	71C	71CA	71O	26.360
	71C	71CA	70C	101.06
30	71C	71CA	72N	29.260
	71C	71CA	70O	87.880
	71C	71CA	70CA	106.58
	71C	71CA	72CA	20.910
	71C	71CA	27CE	135.72
35	71O	71CA	70C	106.32
	71O	71CA	72N	55.620
	71O	71CA	70O	103.70
	71O	71CA	70CA	106.14
	71O	71CA	72CA	47.270
40	71O	71CA	27CE	162.06
	70C	71CA	72N	92.660
	70C	71CA	70O	26.400
	70C	71CA	70CA	12.450

	70C	71CA	72CA	95.460
	70C	71CA	27CE	72.980
	72N	71CA	700	70.710
	72N	71CA	70CA	102.91
5	72N	71CA	72CA	8.350
	72N	71CA	27CE	106.47
	700	71CA	70CA	38.850
	700	71CA	72CA	75.600
	700	71CA	27CE	67.380
10	70CA	71CA	72CA	104.61
	70CA	71CA	27CE	77.110
	72CA	71CA	27CE	114.81
	71CA	71CB	71N	34.470
	71CA	71CB	71C	35.620
15	71CA	71CB	710	57.930
	71CA	71CB	72N	32.120
	71CA	71CB	70C	27.230
	71N	71CB	71C	61.000
	71N	71CB	710	72.360
20	71N	71CB	72N	64.020
	71N	71CB	70C	8.190
	71C	71CB	710	25.670
	71C	71CB	72N	14.610
	71C	71CB	70C	56.950
25	710	71CB	72N	39.060
	710	71CB	70C	71.620
	72N	71CB	70C	58.090
	710	71C	72N	123.77
	710	71C	71CA	119.82
30	710	71C	72CA	93.990
	710	71C	71CB	92.930
	710	71C	71N	109.08
	710	71C	70C	119.12
	710	71C	700	134.27
35	710	71C	72CB	88.520
	72N	71C	71CA	116.41
	72N	71C	72CA	29.780
	72N	71C	71CB	137.30
	72N	71C	71N	118.01
40	72N	71C	70C	96.550
	72N	71C	700	73.760
	72N	71C	72CB	43.410
	71CA	71C	72CA	146.18

	71CA	71C	71CB	34.780
	71CA	71C	71N	32.530
	71CA	71C	70C	49.860
	71CA	71C	700	62.520
5	71CA	71C	72CB	141.88
	72CA	71C	71CB	155.41
	72CA	71C	71N	139.72
	72CA	71C	70C	115.69
	72CA	71C	700	94.990
10	72CA	71C	72CB	27.030
	71CB	71C	71N	58.090
	71CB	71C	70C	80.870
	71CB	71C	700	96.960
	71CB	71C	72CB	129.92
15	71N	71C	70C	24.050
	71N	71C	700	45.370
	71N	71C	72CB	161.09
	70C	71C	700	22.810
	70C	71C	72CB	139.51
20	700	71C	72CB	116.94
	71C	710	72N	29.380
	71C	710	71CA	33.810
	71C	710	72CA	60.310
	71C	710	71CB	61.410
25	71C	710	71N	49.060
	71C	710	72CB	70.480
	71C	710	70C	44.730
	72N	710	71CA	63.190
	72N	710	72CA	30.930
30	72N	710	71CB	88.790
	72N	710	71N	74.700
	72N	710	72CB	45.310
	72N	710	70C	64.140
	71CA	710	72CA	94.120
35	71CA	710	71CB	32.160
	71CA	710	71N	26.700
	71CA	710	72CB	100.98
	71CA	710	70C	37.030
	72CA	710	71CB	117.50
40	72CA	710	71N	102.84
	72CA	710	72CB	26.060
	72CA	710	70C	88.620
	71CB	710	71N	47.680

	71CB	71O	72CB	111.77
	71CB	71O	70C	64.230
	71N	71O	72CB	119.19
	71N	71O	70C	17.990
5	72CB	71O	70C	109.31
	71C	72N	72CA	123.26
	71C	72N	71O	26.850
	71C	72N	72CB	114.53
	71C	72N	71CA	34.330
10	71C	72N	70O	81.190
	71C	72N	27O	146.86
	71C	72N	71N	41.300
	71C	72N	70C	61.330
	71C	72N	71CB	28.090
15	71C	72N	72CG	120.73
	72CA	72N	71O	96.410
	72CA	72N	72CB	36.130
	72CA	72N	71CA	157.59
	72CA	72N	70O	130.94
20	72CA	72N	27O	87.240
	72CA	72N	71N	149.24
	72CA	72N	70C	139.50
	72CA	72N	71CB	143.24
	72CA	72N	72CG	24.380
25	71O	72N	72CB	93.520
	71O	72N	71CA	61.190
	71O	72N	70O	99.610
	71O	72N	27O	166.12
	71O	72N	71N	64.450
30	71O	72N	70C	80.560
	71O	72N	71CB	52.140
	71O	72N	72CG	96.790
	72CB	72N	71CA	136.83
	72CB	72N	70O	163.29
35	72CB	72N	27O	81.510
	72CB	72N	71N	155.58
	72CB	72N	70C	172.50
	72CB	72N	71CB	117.74
	72CB	72N	72CG	12.020
40	71CA	72N	70O	59.600
	71CA	72N	27O	114.35
	71CA	72N	71N	23.230
	71CA	72N	70C	43.410

	71CA	72N	71CB	19.140
	71CA	72N	72CG	147.56
	700	72N	270	87.890
	700	72N	71N	40.840
5	700	72N	70C	19.890
	700	72N	71CB	78.740
	700	72N	72CG	152.63
	270	72N	71N	117.30
	270	72N	70C	105.29
10	270	72N	71CB	119.05
	270	72N	72CG	81.040
	71N	72N	70C	21.880
	71N	72N	71CB	40.720
	71N	72N	72CG	161.22
15	70C	72N	71CB	62.020
	70C	72N	72CG	163.70
	71CB	72N	72CG	128.46
	72N	72CA	72CB	109.52
	72N	72CA	71C	26.960
20	72N	72CA	72CG	141.87
	72N	72CA	71O	52.660
	72N	72CA	72CD2	146.65
	72N	72CA	72CD1	139.86
	72N	72CA	270	68.520
25	72N	72CA	71CA	14.060
	72CB	72CA	71C	105.89
	72CB	72CA	72CG	32.600
	72CB	72CA	71O	99.550
	72CB	72CA	72CD2	44.050
30	72CB	72CA	72CD1	43.570
	72CB	72CA	270	87.730
	72CB	72CA	71CA	107.84
	71C	72CA	72CG	135.26
	71C	72CA	71O	25.700
35	71C	72CA	72CD2	126.95
	71C	72CA	72CD1	148.66
	71C	72CA	270	94.770
	71C	72CA	71CA	12.900
	72CG	72CA	71O	119.79
40	72CG	72CA	72CD2	21.870
	72CG	72CA	72CD1	21.560
	72CG	72CA	270	97.590
	72CG	72CA	71CA	139.89

	710	72CA	72CD2	104.93
	710	72CA	72CD1	140.32
	710	72CA	270	119.83
	710	72CA	71CA	38.610
5	72CD2	72CA	72CD1	41.260
	72CD2	72CA	270	119.45
	72CD2	72CA	71CA	136.99
	72CD1	72CA	270	79.620
	72CD1	72CA	71CA	146.25
10	270	72CA	71CA	82.130
	72CG	72CB	72CA	114.08
	72CG	72CB	72N	148.14
	72CG	72CB	72CD2	28.400
	72CG	72CB	72CD1	28.260
15	72CG	72CB	71C	153.74
	72CG	72CB	710	137.43
	72CG	72CB	72CE2	18.460
	72CG	72CB	72CE1	18.190
	72CG	72CB	270	114.19
20	72CA	72CB	72N	34.350
	72CA	72CB	72CD2	110.80
	72CA	72CB	72CD1	111.57
	72CA	72CB	71C	47.080
	72CA	72CB	710	54.380
25	72CA	72CB	72CE2	112.85
	72CA	72CB	72CE1	113.46
	72CA	72CB	270	68.670
	72N	72CB	72CD2	140.56
	72N	72CB	72CD1	136.51
30	72N	72CB	71C	22.060
	72N	72CB	710	41.170
	72N	72CB	72CE2	145.55
	72N	72CB	72CE1	142.65
	72N	72CB	270	59.200
35	72CD2	72CB	72CD1	56.660
	72CD2	72CB	71C	130.98
	72CD2	72CB	710	111.11
	72CD2	72CB	72CE2	9.950
	72CD2	72CB	72CE1	46.590
40	72CD2	72CB	270	141.36
	72CD1	72CB	71C	157.53
	72CD1	72CB	710	159.45
	72CD1	72CB	72CE2	46.710

	72CD1	72CB	72CE1	10.080
	72CD1	72CB	270	86.740
	71C	72CB	710	20.990
	71C	72CB	72CE2	139.78
5	71C	72CB	72CE1	160.44
	71C	72CB	270	78.680
	710	72CB	72CE2	120.56
	710	72CB	72CE1	152.99
	710	72CB	270	99.520
10	72CE2	72CB	72CE1	36.640
	72CE2	72CB	270	132.04
	72CE1	72CB	270	96.610
	72CD2	72CG	72CD1	118.70
	72CD2	72CG	72CB	120.48
15	72CD2	72CG	72CE2	29.700
	72CD2	72CG	72CE1	88.910
	72CD2	72CG	72CA	114.81
	72CD2	72CG	72CZ	59.270
	72CD2	72CG	72N	120.43
20	72CD1	72CG	72CB	120.81
	72CD1	72CG	72CE2	89.010
	72CD1	72CG	72CE1	29.800
	72CD1	72CG	72CA	115.91
	72CD1	72CG	72CZ	59.430
25	72CD1	72CG	72N	117.10
	72CB	72CG	72CE2	150.17
	72CB	72CG	72CE1	150.61
	72CB	72CG	72CA	33.320
	72CB	72CG	72CZ	179.28
30	72CB	72CG	72N	19.840
	72CE2	72CG	72CE1	59.210
	72CE2	72CG	72CA	136.56
	72CE2	72CG	72CZ	29.580
	72CE2	72CG	72N	146.64
35	72CE1	72CG	72CA	137.55
	72CE1	72CG	72CZ	29.630
	72CE1	72CG	72N	143.84
	72CA	72CG	72CZ	147.36
	72CA	72CG	72N	13.750
40	72CZ	72CG	72N	160.86
	72CG	72CD1	72CE1	120.63
	72CG	72CD1	72CD2	30.630
	72CG	72CD1	72CZ	90.830



	72CG	72CD1	72CB	30.930
	72CG	72CD1	72CE2	60.910
	72CG	72CD1	28OD1	142.39
	72CG	72CD1	28CG	124.62
5	72CG	72CD1	72CA	42.530
	72CG	72CD1	28OD2	106.03
	72CG	72CD1	28CA	122.27
	72CE1	72CD1	72CD2	90.000
	72CE1	72CD1	72CZ	29.800
10	72CE1	72CD1	72CB	151.55
	72CE1	72CD1	72CE2	59.720
	72CE1	72CD1	28OD1	61.780
	72CE1	72CD1	28CG	80.270
	72CE1	72CD1	72CA	147.38
15	72CE1	72CD1	28OD2	83.110
	72CE1	72CD1	28CA	110.27
	72CD2	72CD1	72CZ	60.200
	72CD2	72CD1	72CB	61.560
	72CD2	72CD1	72CE2	30.280
20	72CD2	72CD1	28OD1	129.67
	72CD2	72CD1	28CG	123.86
	72CD2	72CD1	72CA	68.940
	72CD2	72CD1	28OD2	104.25
	72CD2	72CD1	28CA	145.48
25	72CZ	72CD1	72CB	121.76
	72CZ	72CD1	72CE2	29.920
	72CZ	72CD1	28OD1	84.600
	72CZ	72CD1	28CG	97.410
	72CZ	72CD1	72CA	123.48
30	72CZ	72CD1	28OD2	90.960
	72CZ	72CD1	28CA	135.19
	72CB	72CD1	72CE2	91.840
	72CB	72CD1	28OD1	136.58
	72CB	72CD1	28CG	115.00
35	72CB	72CD1	72CA	24.860
	72CB	72CD1	28OD2	103.47
	72CB	72CD1	28CA	95.310
	72CE2	72CD1	28OD1	108.17
	72CE2	72CD1	28CG	113.24
40	72CE2	72CD1	72CA	96.530
	72CE2	72CD1	28OD2	98.660
	72CE2	72CD1	28CA	152.31
	28OD1	72CD1	28CG	21.660

	28OD1	72CD1	72CA	112.55
	28OD1	72CD1	28OD2	37.060
	28OD1	72CD1	28CA	50.620
	28CG	72CD1	72CA	90.900
5	28CG	72CD1	28OD2	20.050
	28CG	72CD1	28CA	40.080
	72CA	72CD1	28OD2	78.630
	72CA	72CD1	28CA	79.860
	28OD2	72CD1	28CA	53.660
10	72CG	72CD2	72CE2	120.82
	72CG	72CD2	72CD1	30.660
	72CG	72CD2	72CZ	91.020
	72CG	72CD2	72CB	31.120
	72CG	72CD2	72CE1	61.010
15	72CG	72CD2	72CA	43.310
	72CE2	72CD2	72CD1	90.160
	72CE2	72CD2	72CZ	29.800
	72CE2	72CD2	72CB	151.94
	72CE2	72CD2	72CE1	59.810
20	72CE2	72CD2	72CA	147.84
	72CD1	72CD2	72CZ	60.360
	72CD1	72CD2	72CB	61.780
	72CD1	72CD2	72CE1	30.350
	72CD1	72CD2	72CA	69.800
25	72CZ	72CD2	72CB	122.14
	72CZ	72CD2	72CE1	30.010
	72CZ	72CD2	72CA	124.38
	72CB	72CD2	72CE1	92.130
	72CB	72CD2	72CA	25.150
30	72CE1	72CD2	72CA	97.470
	72CZ	72CE1	72CD1	120.06
	72CZ	72CE1	72CE2	30.110
	72CZ	72CE1	72CG	90.490
	72CZ	72CE1	28OD1	128.03
35	72CZ	72CE1	72CD2	60.410
	72CZ	72CE1	28CG	126.46
	72CZ	72CE1	28OD2	109.52
	72CZ	72CE1	72CB	101.69
	72CD1	72CE1	72CE2	89.950
40	72CD1	72CE1	72CG	29.570
	72CD1	72CE1	28OD1	91.000
	72CD1	72CE1	72CD2	59.650
	72CD1	72CE1	28CG	75.900

	72CD1	72CE1	28OD2	75.000
	72CD1	72CE1	72CB	18.370
	72CE2	72CE1	72CG	60.390
	72CE2	72CE1	28OD1	136.30
5	72CE2	72CE1	72CD2	30.310
	72CE2	72CE1	28CG	123.13
	72CE2	72CE1	28OD2	103.74
	72CE2	72CE1	72CB	71.590
	72CG	72CE1	28OD1	111.96
10	72CG	72CE1	72CD2	30.080
	72CG	72CE1	28CG	93.450
	72CG	72CE1	28OD2	83.970
	72CG	72CE1	72CB	11.210
	28OD1	72CE1	72CD2	129.34
15	28OD1	72CE1	28CG	19.220
	28OD1	72CE1	28OD2	35.520
	28OD1	72CE1	72CB	104.46
	72CD2	72CE1	28CG	110.49
	72CD2	72CE1	28OD2	94.360
20	72CD2	72CE1	72CB	41.280
	28CG	72CE1	28OD2	19.440
	28CG	72CE1	72CB	86.970
	28OD2	72CE1	72CB	80.590
	72CZ	72CE2	72CD2	120.05
25	72CZ	72CE2	72CE1	30.170
	72CZ	72CE2	72CG	90.570
	72CZ	72CE2	72CD1	60.490
	72CZ	72CE2	72CB	101.94
	72CD2	72CE2	72CE1	89.890
30	72CD2	72CE2	72CG	29.480
	72CD2	72CE2	72CD1	59.560
	72CD2	72CE2	72CB	18.120
	72CE1	72CE2	72CG	60.400
	72CE1	72CE2	72CD1	30.320
35	72CE1	72CE2	72CB	71.770
	72CG	72CE2	72CD1	30.080
	72CG	72CE2	72CB	11.370
	72CD1	72CE2	72CB	41.450
	72CE2	72CZ	72CE1	119.73
40	72CE2	72CZ	72CD2	30.150
	72CE2	72CZ	72CD1	89.590
	72CE2	72CZ	72CG	59.850
	72CE2	72CZ	28OD1	130.21

	72CE1	72CZ	72CD2	89.580
	72CE1	72CZ	72CD1	30.140
	72CE1	72CZ	72CG	59.870
	72CE1	72CZ	28OD1	34.880
5	72CD2	72CZ	72CD1	59.440
	72CD2	72CZ	72CG	29.700
	72CD2	72CZ	28OD1	105.62
	72CD1	72CZ	72CG	29.740
	72CD1	72CZ	28OD1	55.110
10	72CG	72CZ	28OD1	80.010

Table IIIB

Interatomic angle between residues in the active site of UPPS in complex with FPP

	ATOM1	ATOM2	ATOM3	ANGLE, degree
5	79NH1	1C1	79NH2	36.680
	30OD1	1C2	45NE2	73.500
	30OD1	1C2	79NH1	123.81
	45NE2	1C2	79NH1	54.230
10	71O	1C4	71C	16.510
	71O	1C5	45CD2	138.38
	30OD1	1C6	71O	158.04
	49N	1C10	45O	54.930
	49N	1C10	48C	22.570
15	49N	1C10	48CA	41.710
	49N	1C10	30OD1	112.37
	49N	1C10	49CA	20.490
	45O	1C10	48C	66.450
	45O	1C10	48CA	60.290
20	45O	1C10	30OD1	80.140
	45O	1C10	49CA	66.810
	48C	1C10	48CA	24.950
	48C	1C10	30OD1	98.690
	48C	1C10	49CA	38.030
25	48CA	1C10	30OD1	73.850
	48CA	1C10	49CA	60.970
	30OD1	1C10	49CA	132.86
	143CE2	1C14	143CZ	22.460
	143CE2	1C14	143CD2	20.550
30	143CE2	1C14	91CG	154.92
	143CE2	1C14	91CA	166.15
	143CZ	1C14	143CD2	36.950
	143CZ	1C14	91CG	161.83
	143CZ	1C14	91CA	143.89
35	143CD2	1C14	91CG	134.76
	143CD2	1C14	91CA	159.08
	91CG	1C14	91CA	34.360
	49SD	1C15	94CG	72.370
	49SD	1C15	94CB	63.260
40	49SD	1C15	94CD1	62.610
	49SD	1C15	49CG	28.760
	49SD	1C15	90O	60.290

	94CG	1C15	94CB	23.960
	94CG	1C15	94CD1	22.200
	94CG	1C15	49CG	80.380
	94CG	1C15	900	71.370
5	94CB	1C15	94CD1	40.410
	94CB	1C15	49CG	81.980
	94CB	1C15	900	47.420
	94CD1	1C15	49CG	61.840
	94CD1	1C15	900	84.480
10	49CG	1C15	900	89.040
	79NH2	101A	45CE1	104.86
	79NH2	101A	79NH1	36.270
	79NH2	101A	31N	161.20
	45CE1	101A	79NH1	69.380
15	45CE1	101A	31N	73.460
	79NH1	101A	31N	141.07
	79NH2	102A	28OD2	143.61
	29N	103A	30N	51.620
	29N	103A	31N	98.770
20	29N	103A	29C	42.330
	29N	103A	30CB	88.140
	29N	103A	29CA	21.740
	29N	103A	30CA	72.890
	30N	103A	31N	53.440
25	30N	103A	29C	21.050
	30N	103A	30CB	40.610
	30N	103A	29CA	39.740
	30N	103A	30CA	21.320
	31N	103A	29C	56.440
30	31N	103A	30CB	47.440
	31N	103A	29CA	78.530
	31N	103A	30CA	38.230
	29C	103A	30CB	60.250
	29C	103A	29CA	23.500
35	29C	103A	30CA	37.980
	30CB	103A	29CA	80.270
	30CB	103A	30CA	23.300
	29CA	103A	30CA	59.960
	29N	1PB	29CA	22.630
40	29N	1PB	29C	39.230
	29N	1PB	30N	43.180
	29N	1PB	31N	87.600
	29CA	1PB	29C	22.740

	29CA	1PB	30N	36.770
	29CA	1PB	31N	73.860
	29C	1PB	30N	19.570
	29C	1PB	31N	51.200
5	30N	1PB	31N	45.170
	28OD2	101B	29N	84.890
	28OD2	101B	28CG	16.680
	29N	101B	28CG	68.950
	29CA	103B	32N	96.470
10	29CA	103B	32CB	86.020
	29CA	103B	29C	28.020
	29CA	103B	29N	26.430
	29CA	103B	29O	41.610
	29CA	103B	30N	40.840
15	29CA	103B	31N	86.120
	29CA	103B	32CA	93.510
	32N	103B	32CB	45.930
	32N	103B	29C	74.560
	32N	103B	29N	119.84
20	32N	103B	29O	55.800
	32N	103B	30N	80.770
	32N	103B	31N	48.860
	32N	103B	32CA	22.120
	32CB	103B	29C	83.310
25	32CB	103B	29N	111.02
	32CB	103B	29O	65.280
	32CB	103B	30N	101.43
	32CB	103B	31N	92.340
	32CB	103B	32CA	23.970
30	29C	103B	29N	45.490
	29C	103B	29O	20.200
	29C	103B	30N	20.670
	29C	103B	31N	58.520
	29C	103B	32CA	79.800
35	29N	103B	29O	64.150
	29N	103B	30N	45.760
	29N	103B	31N	93.530
	29N	103B	32CA	119.86
	29O	103B	30N	36.150
40	29O	103B	31N	54.170
	29O	103B	32CA	59.600
	30N	103B	31N	48.360
	30N	103B	32CA	92.530

31N 103B 32CA 70.170

Table IIIC

Interatomic angle between residues in the active site of UPPS in complex  
with IPP

	ATOM1	ATOM2	ATOM3	ANGLE, degree
	28OD2	1C02	27O	87.520
	28OD2	1C02	28CB	36.210
	27O	1C02	28CB	61.460
10	71O	1C05	70O	72.200
	71O	1C05	71C	21.680
	71O	1C05	72N	37.100
	71O	1C05	70C	69.880
	71O	1C05	72CA	46.020
15	71O	1C05	76ND2	106.01
	70O	1C05	71C	62.240
	70O	1C05	72N	74.850
	70O	1C05	70C	17.710
	70O	1C05	72CA	96.890
20	70O	1C05	76ND2	166.88
	71C	1C05	72N	20.700
	71C	1C05	70C	54.260
	71C	1C05	72CA	38.940
	71C	1C05	76ND2	111.29
25	72N	1C05	70C	61.890
	72N	1C05	72CA	22.050
	72N	1C05	76ND2	95.800
	70C	1C05	72CA	83.310
	70C	1C05	76ND2	149.20
30	72CA	1C05	76ND2	73.940
	70CD2	1C09	70CE2	21.400
	70CD2	1C09	70CG	21.670
	70CE2	1C09	70CG	37.390
	70CE2	1C12	70CD2	21.540
35	200NH2	1O14	208OG	65.400
	200NH2	1O14	208CB	73.390
	208OG	1O14	208CB	19.950
	28OD2	1P15	200NH2	73.130
	76ND2	1O16	76OD1	39.750
40	76ND2	1O16	76CG	20.700
	76ND2	1O16	250CA	101.94
	76ND2	1O16	73OG	42.420



	760D1	1016	76CG	19.460
	760D1	1016	250CA	65.930
	760D1	1016	730G	64.870
	76CG	1016	250CA	82.090
5	76CG	1016	730G	49.850
	250CA	1016	730G	95.020
	200NH2	1017	280D2	79.710
	200NH2	1017	28CG	64.100
	280D2	1017	28CG	18.170
10	280D2	1018	28CG	16.510
	280D2	1018	247NH2	84.690
	280D2	1018	280D1	30.030
	28CG	1018	247NH2	88.990
	28CG	1018	280D1	17.610
15	247NH2	1018	280D1	77.660
	208OG	1P19	250CA	119.39
	208OG	1P19	206NH1	91.290
	208OG	1P19	247O	124.73
	208OG	1P19	206CD	51.730
20	250CA	1P19	206NH1	134.73
	250CA	1P19	247O	54.230
	250CA	1P19	206CD	138.68
	206NH1	1P19	247O	81.340
	206NH1	1P19	206CD	41.710
25	247O	1P19	206CD	95.200
	208OG	1020	250N	151.34
	208OG	1020	250CA	158.25
	208OG	1020	217CE2	77.450
	208OG	1020	208CB	22.490
30	208OG	1020	247O	144.34
	250N	1020	250CA	25.390
	250N	1020	217CE2	75.240
	250N	1020	208CB	131.25
	250N	1020	247O	53.360
35	250CA	1020	217CE2	97.310
	250CA	1020	208CB	136.92
	250CA	1020	247O	57.350
	217CE2	1020	208CB	64.610
	217CE2	1020	247O	103.98
40	208CB	1020	247O	160.34
	206NH1	1021	206CD	63.610
	206NH1	1021	206CZ	23.320
	206NH1	1021	206NE	44.300

	206NH1	1021	208OG	119.29
	206NH1	1021	200NH2	93.260
	206CD	1021	206CZ	48.080
	206CD	1021	206NE	26.130
5	206CD	1021	208OG	59.000
	206CD	1021	200NH2	72.680
	206CZ	1021	206NE	23.690
	206CZ	1021	208OG	107.07
	206CZ	1021	200NH2	101.44
10	206NE	1021	208OG	84.290
	206NE	1021	200NH2	92.980
	208OG	1021	200NH2	52.780
	250CA	1022	247NE	114.53
	250CA	1022	247O	64.620
15	250CA	1022	247CZ	128.51
	250CA	1022	247CG	95.540
	250CA	1022	250C	23.580
	250CA	1022	247CD	114.32
	250CA	1022	250N	20.550
20	250CA	1022	247NH2	120.77
	250CA	1022	250O	37.250
	247NE	1022	247O	86.700
	247NE	1022	247CZ	21.230
	247NE	1022	247CG	43.200
25	247NE	1022	250C	91.090
	247NE	1022	247CD	22.540
	247NE	1022	250N	124.46
	247NE	1022	247NH2	37.560
	247NE	1022	250O	82.000
30	247O	1022	247CZ	107.10
	247O	1022	247CG	44.460
	247O	1022	250C	57.580
	247O	1022	247CD	68.380
	247O	1022	250N	52.860
35	247O	1022	247NH2	123.53
	247O	1022	250O	41.550
	247CZ	1022	247CG	62.780
	247CZ	1022	250C	106.76
	247CZ	1022	247CD	39.430
40	247CZ	1022	250N	143.24
	247CZ	1022	247NH2	20.530
	247CZ	1022	250O	101.15
	247CG	1022	250C	75.970

5	247CG	1022	247CD	24.070
	247CG	1022	250N	92.820
	247CG	1022	247NH2	80.760
	247CG	1022	2500	58.790
	250C	1022	247CD	91.780
10	250C	1022	250N	37.390
	250C	1022	247NH2	104.02
	250C	1022	2500	18.310
	247CD	1022	250N	115.79
	247CD	1022	247NH2	58.770
15	247CD	1022	2500	77.290
	250N	1022	247NH2	140.47
	250N	1022	2500	42.510
	247NH2	1022	2500	105.05

## WHAT IS CLAIMED IS:

1. A composition comprising a UPPS in crystalline form.
2. The composition according to claim 1 wherein said UPPS is a dimer.
3. The composition of claim 1 wherein said UPPS is a *Streptococcus*
- 5 *pneumoniae* UPPS.
4. The composition according to claim 1 comprising a protein wherein defined by coordinates of Table IA, interatomic distances in Table IIA, or angles of active site residues listed in Table IIIA, in an essentially pure native form or a homolog thereof.
- 10 5. A prenyltransferase of claim 4 which is in its native crystalline form.
6. A prenyltransferase according to claims 4 or 5 wherein said prenyltransferase has an active site formed by the amino acids Arg247, Gly250, Arg206, Arg200, Ser208, Tyr217, Asp28, Tyr70, Ile26, Phe72, Asn76, Met27, Ala71 as ligands to IPP.
- 15 7. A prenyltransferase according to claims 4 or 5 wherein said prenyltransferase has an active site formed by the amino acids Asp28-Arg32, Arg79, Met27, His45, Gly48, Met49, Leu52, Ala71, Tyr70, Leu90, Pro91, Phe94, Phe149 as ligands to FPP.
8. A composition comprising the prenyltransferase of claim 4 in complex with
- 20 the substrate FPP wherein defined by coordinates of Table IB, interatomic distances in Table IIB, or angles of active site residues listed in Table IIIB.
9. A composition comprising the prenyltransferase of claim 4 in complex with the substrate IPP wherein defined by coordinates of Table IC, interatomic distances in Table IIC, or angles of active site residues listed in Table IIICB.
- 25 10. A heavy atom derivative of a *Streptococcus pneumoniae* UPPS crystal wherein the prenyltransferase comprises a protein having the coordinates listed in Tables IA-IC, IIA-IIC, or IIIA-IIIC.
11. A prenyltransferase according to claim 4 wherein said prenyltransferase is characterized by an  $\alpha+\beta$  fold with three layers,  $\alpha\beta\alpha$ , wherein the  $\beta$ -strands form a
- 30 six-strand parallel  $\beta$ -sheet and three  $\alpha$ -helices pack against one face of the sheet and three to four  $\alpha$ -helices located on the opposite face.

12. A composition comprising a *Streptococcus pneumoniae* UPPS in orthorhombic crystalline form having a space group of  $P2_12_12_1$ .
13. The composition according to claim 12 wherein the crystalline form has lattice constants of  $a = 59.6 \text{ \AA}$ ,  $b = 118.0 \text{ \AA}$ ,  $c = 178.2 \text{ \AA}$ .
- 5 14. The composition according to claim 12 wherein the crystalline form contains two 60 kDa dimers in an asymmetric unit.
15. A composition comprising a *Streptococcus pneumoniae* UPPS in orthorhombic crystalline form having a space group of  $I2_12_12_1$ .
- 10 16. A composition comprising a co-crystal of *Streptococcus pneumoniae* UPPS in complex with a substrate IPP in orthorhombic crystalline form having a space group selected from the group consisting of  $P2_12_12_1$  and  $I2_12_12_1$ .
17. A composition comprising a co-crystal of *Streptococcus pneumoniae* UPPS in complex with a substrate FPP in monoclinic crystalline form having a space group of  $P2_1$ .
- 15 18. The composition according to claim 17 wherein the crystalline form has lattice constants of  $a = 58.1 \text{ \AA}$ ,  $b = 44.6 \text{ \AA}$ ,  $c = 115.5 \text{ \AA}$ ,  $\beta = 98.7^\circ$ .
19. A process for determining a crystal structure form using the structural coordinates of a *Streptococcus pneumoniae* UPPS crystal or portions thereof, to determine a crystal form of a mutant, homologue, or co-complex of a binding pocket
- 20 or active site by molecular replacement.
20. A process of identifying an inhibitor compound capable of binding to and inhibiting the enzymatic activity of a *Streptococcus pneumoniae* UPPS said process comprising:
- a) introducing into a suitable computer program information defining an active
  - 25 site conformation of a UPPS molecule comprising a conformation defined by the coordinates and listed in Table IA, IIA, or IIIA wherein said program displays the three-dimensional structure thereof;
  - b) creating a three dimensional structure of a test compound in said computer program;
  - 30 c) displaying and superimposing a model of said test compound on a model of said active site;

- d) incorporating said test compound in a biological prenyltransferase activity assay for a prenyltransferase characterized by said active site; and
- e) determining whether said test compound inhibits enzymatic activity in said assay.

5        21. A process designing drugs useful for inhibiting UPPS activity using the atomic coordinates of a *Streptococcus pneumoniae* UPPS crystal to computationally evaluate a chemical entity for associating with a active site of a UPPS enzyme.

22. A method of modifying a test UPPS polypeptide comprising:

- 10        a) providing a test UPPS polypeptide sequence having a characteristic that is targeted for modification;
- b) aligning the test UPPS polypeptide sequence with at least one reference UPPS polypeptide sequence for which an X-ray structure is available, wherein the at least one reference UPPS polypeptide sequence has a characteristic that is desired for the test UPPS polypeptide;
- 15        c) building a three-dimensional model for the test UPPS polypeptide using the three-dimensional coordinates of the X-ray structure(s) of the at least one reference UPPS polypeptide and its sequence alignment with the test UPPS polypeptide sequence;
- d) examining the three-dimensional model of the test UPPS polypeptide for a  
20        difference in an amino acid residue as compared to the at least one reference polypeptide, wherein the residues are associated with the desired characteristic; and
- e) mutating an amino acid residue in the test UPPS polypeptide sequence located at a difference identified in step (d) to a residue associated with the desired characteristic, whereby the test UPPS polypeptide is modified.

25        23. A process of identifying an inhibitor compound capable of inhibiting the enzymatic activity of a *Streptococcus pneumoniae* UPPS according to claim 4, said process comprising:

- 30        a) carrying out an *in vitro* assay by introducing said compound in a biological prenyltransferase activity assay containing a prenyltransferase according to claim 4; and
- b) determining whether said test compound inhibits the enzymatic activity of the prenyltransferase in said assay.

24. A product of the process of claim 20 or 23 which is a peptide, peptidomimetic, or synthetic molecule and is useful for inhibiting a metallo-beta lactamase in treatment of bacterial infections in a mammal.

25. A product according to claim 24 wherein said product is a competitive or  
5 non-competitive inhibitor of the *Streptococcus pneumoniae* prenyltransferase.

26. A process designing drugs useful for inhibiting *Streptococcus pneumoniae* UPPS comprising using the atomic coordinates of a *Streptococcus pneumoniae* UPPS crystal or the atomic coordinates of a *Streptococcus pneumoniae* UPPS in complex with FPP or IPP to computationally evaluate a chemical entity for  
10 associating with the active site of a *Streptococcus pneumoniae* UPPS.

27. The process according to claim 26 comprising the step of using the structure coordinates of *Streptococcus pneumoniae* UPPS to identify an intermediate in a chemical reaction between a prenyltransferase and a compound that is a substrate or inhibitor of said prenyltransferase.

15 28. The process according to claims 26 or 27 wherein said structure coordinates comprise the coordinates listed in Tables IA-IC, IIA-IIC, or IIIA-IIIC.

Figure 1A

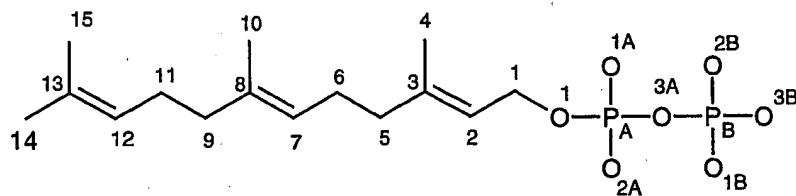


Figure 1B

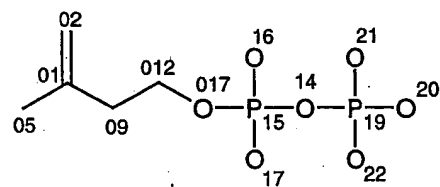




Figure 2A

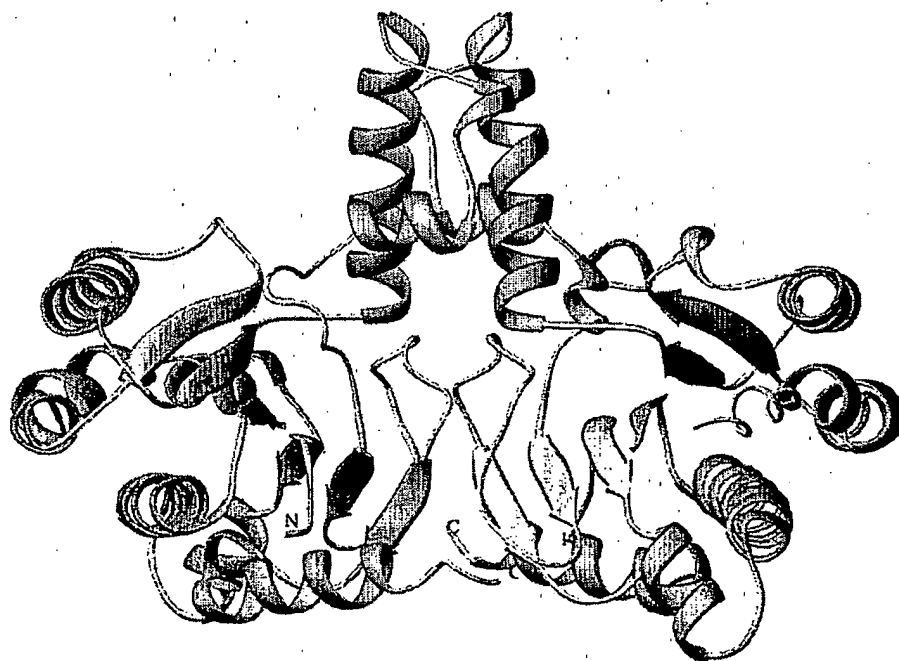


Figure 2B

**UPS ( *S. pneumoniae* )**

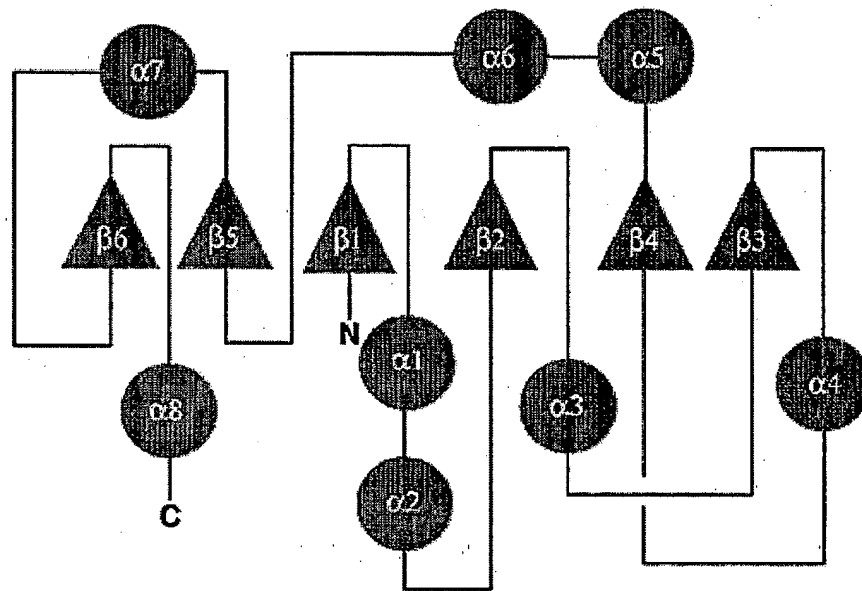


Figure 3A

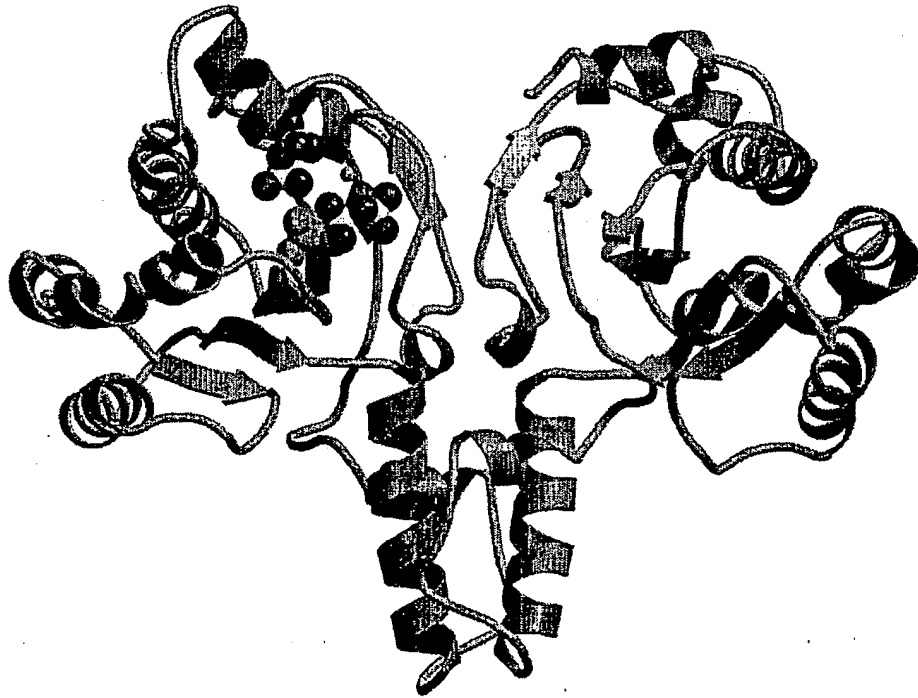


Figure 3B

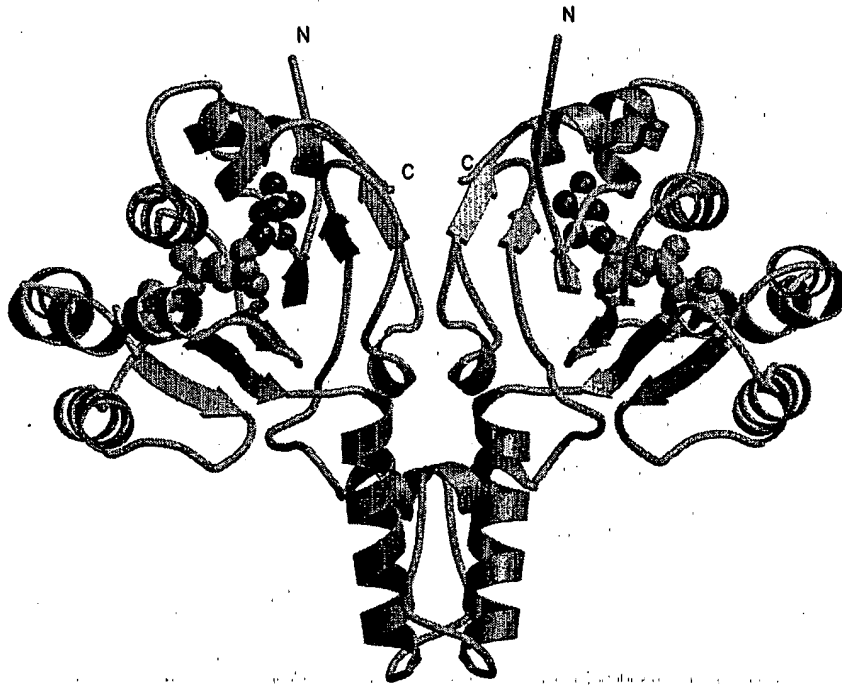


Figure 4A

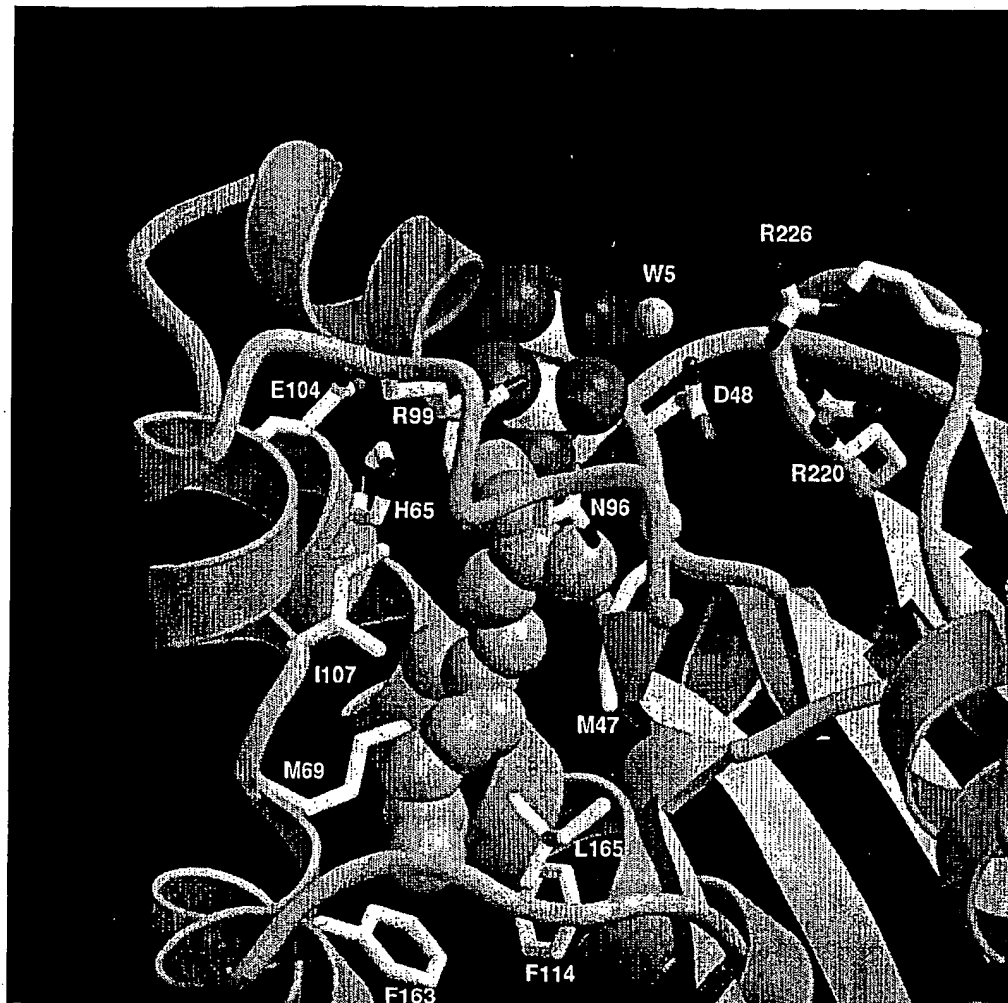
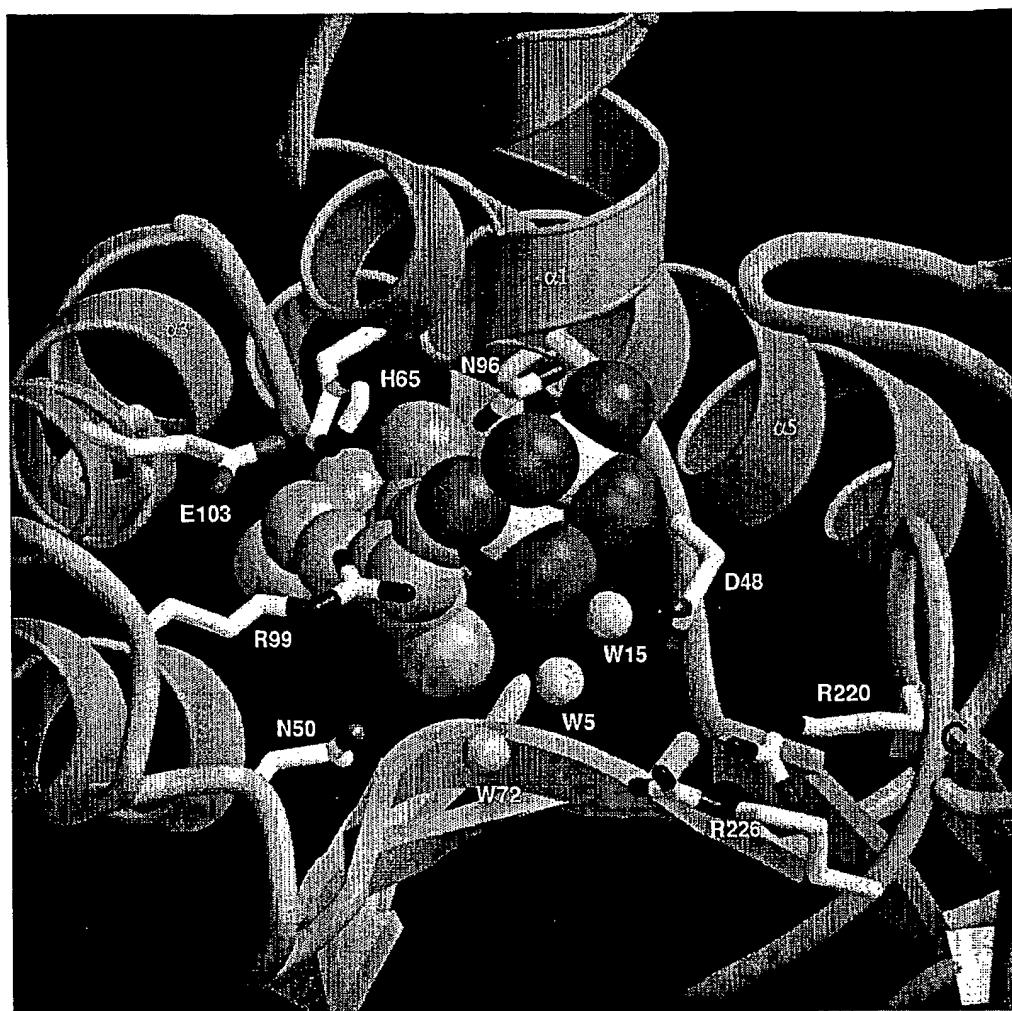
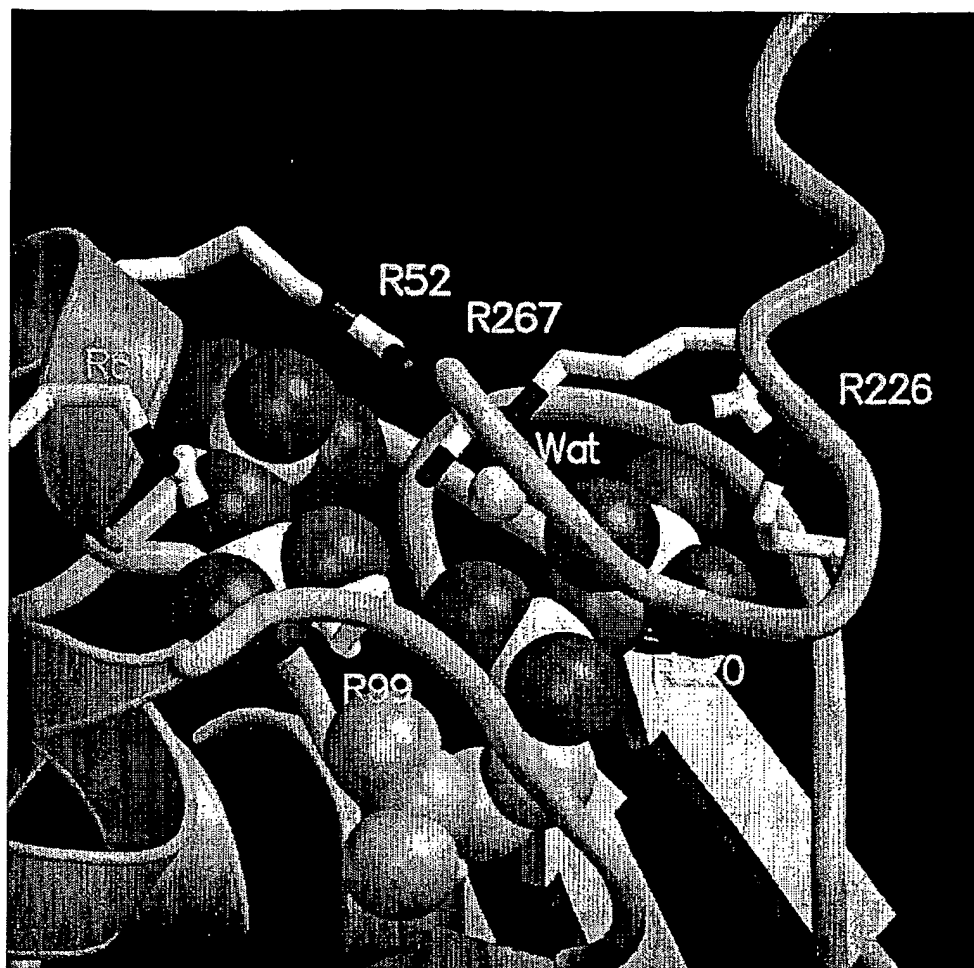


Figure 4B



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Figure 5



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698917InventoryList.txt

"InventoryList"

"PCT/US02/38715"

"20 Dec 2002"

- "1. DOE0901      Notification of Status of Requirements Under 35 U.S.C. 371"
- "2. ISA202      Notification of Receipt of Search Copy"
- "3. ISA225      Inv to Furnish Nucleotide and/or Amino Acid Seq Listing Complying with Standard"
- "4. RO101      PCT/RO/101 Form Record Copy"
- "5. RO101S      PCT/RO/101 FORM SEARCH COPY"
- "6. RO102N      Notification concerning Payment of Prescribed Fees-No Reply"
- "7. RO105      Notification of The International Application # and of the Intl. Filing Date"
- "8. RO106      Invitation To Correct Defects in The International Application (Incl. Annex ABC)"